Full wwPDB EM Validation Report (i)

Aug 4, 2026 – 06:30 PM EDT

PDB ID	:	8VAM / pdb_00008vam
EMDB ID	:	EMD-43095
Title	:	Structure of the E. coli clamp loader bound to the beta clamp in a Semi-Open conformation
Authors	:	Landeck, J.T.; Kelch, B.A.
Deposited on	:	2023-12-11
Resolution	:	3.90 Å(reported)
Based on initial models	:	3GLF, 2POL

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 (i) 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 (i)) were used in the production of this report:

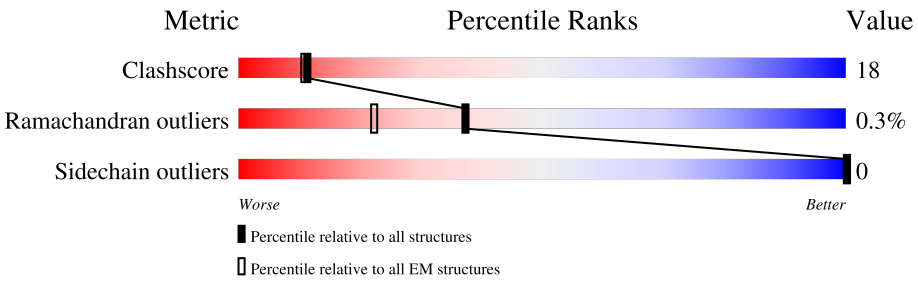
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data 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)	:	2.50

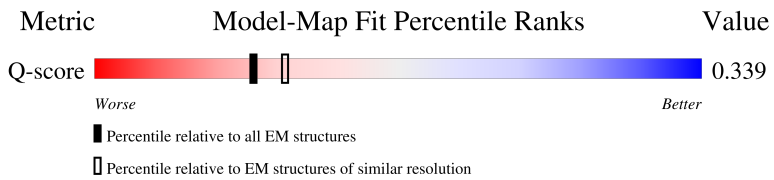
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.90 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	8855 (3.40 - 4.40)

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

Mol	Chain	Length	Quality of chain
1	A	333	50% 60% 39%
2	B	376	45% 62% 36% •
2	C	376	8% 54% 43% • •
2	D	376	• 69% 27% •

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Mol	Chain	Length	Quality of chain
3	E	337	5% 70% 30%
4	F	369	37% 57% 42%
4	G	369	41% 26% 33%

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
7	BEF	C	402	-	-	X	-

2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 18771 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 DNA polymerase III subunit delta.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	333	2651	1678	482	481	10	0	0

- Molecule 2 is a protein called DNA polymerase III subunit tau.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	371	2885	1814	521	533	17	0	0
2	C	370	2878	1809	520	532	17	0	0
2	D	363	2821	1772	510	523	16	0	0

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-2	GLY	-	expression tag	UNP P06710
B	-1	PRO	-	expression tag	UNP P06710
B	0	HIS	-	expression tag	UNP P06710
C	-2	GLY	-	expression tag	UNP P06710
C	-1	PRO	-	expression tag	UNP P06710
C	0	HIS	-	expression tag	UNP P06710
D	-2	GLY	-	expression tag	UNP P06710
D	-1	PRO	-	expression tag	UNP P06710
D	0	HIS	-	expression tag	UNP P06710

- Molecule 3 is a protein called DNA polymerase III subunit delta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	E	337	2623	1668	473	469	13	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	-2	GLY	-	expression tag	UNP P28631
E	-1	PRO	-	expression tag	UNP P28631
E	0	HIS	-	expression tag	UNP P28631

- Molecule 4 is a protein called Beta sliding clamp.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	F	369	2865	1799	503	544	19	0	0
			Total	C	N	O	S		
4	G	248	1948	1220	339	375	14	0	0

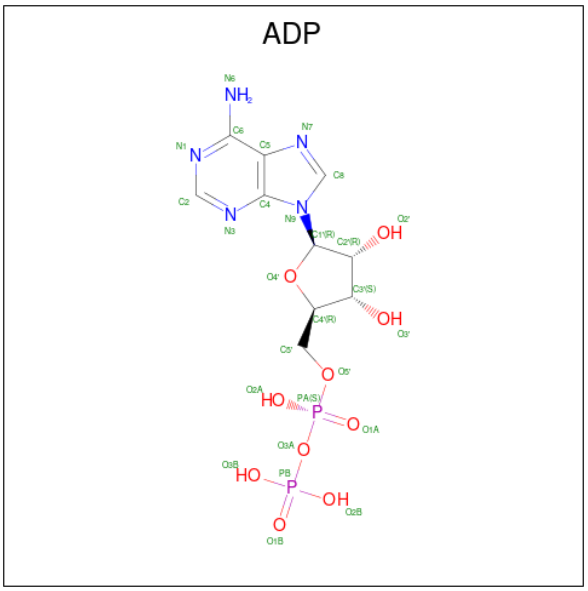
There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	-2	GLY	-	expression tag	UNP P0A988
F	-1	PRO	-	expression tag	UNP P0A988
F	0	HIS	-	expression tag	UNP P0A988
G	-2	GLY	-	expression tag	UNP P0A988
G	-1	PRO	-	expression tag	UNP P0A988
G	0	HIS	-	expression tag	UNP P0A988

- Molecule 5 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

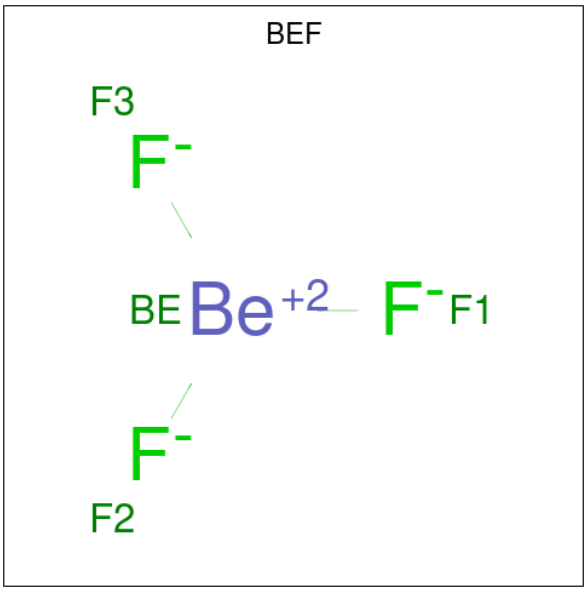
Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
5	B	1	1	1	0
			Total	Zn	
5	C	1	1	1	0
			Total	Zn	
5	D	1	1	1	0
			Total	Zn	
5	E	1	1	1	0

- Molecule 6 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
6	B	1	27	10	5	10	2	0
			Total	C	N	O	P	
6	C	1	27	10	5	10	2	0
			Total	C	N	O	P	
6	D	1	27	10	5	10	2	0

- Molecule 7 is BERYLLIUM TRIFLUORIDE ION (CCD ID: BEF) (formula: BeF_3) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
			Total	Be	F	
7	B	1	4	1	3	0
7	C	1	4	1	3	0
7	D	1	4	1	3	0

- Molecule 8 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

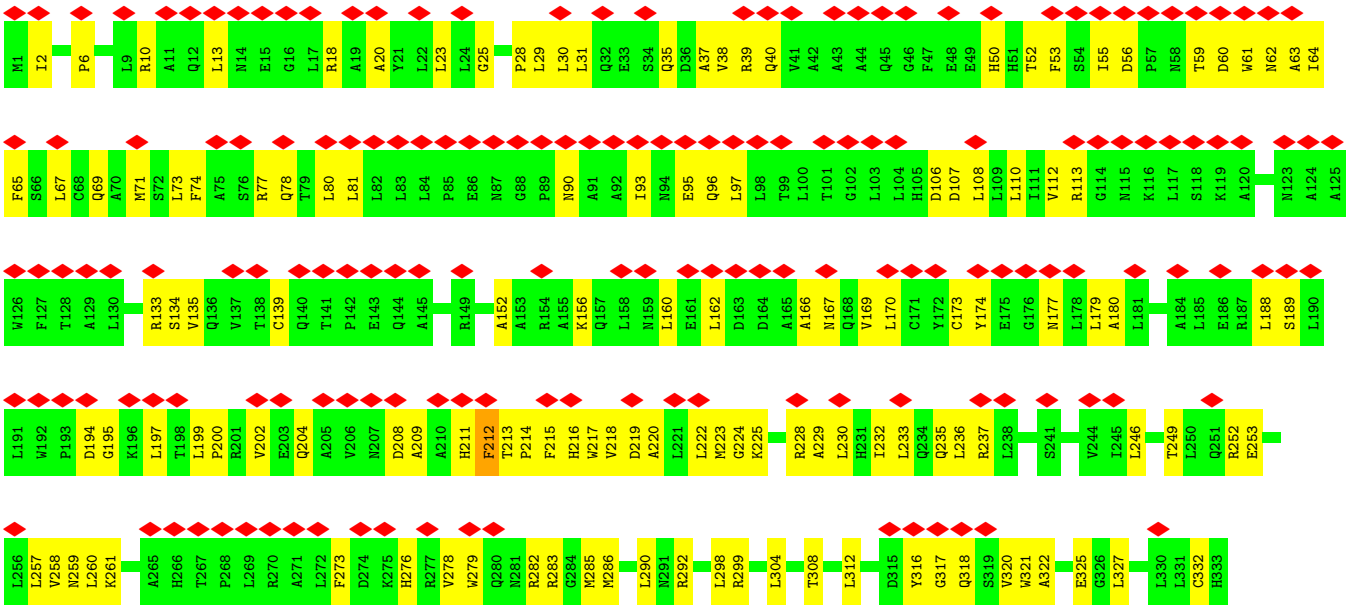
Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
8	B	1	1	1	0
8	C	1	1	1	0
8	D	1	1	1	0

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.

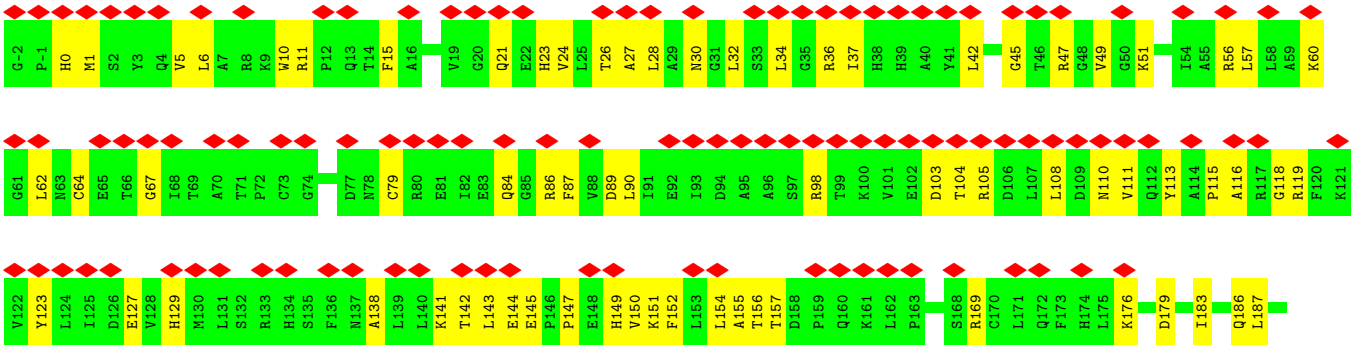
- Molecule 1: DNA polymerase III subunit delta

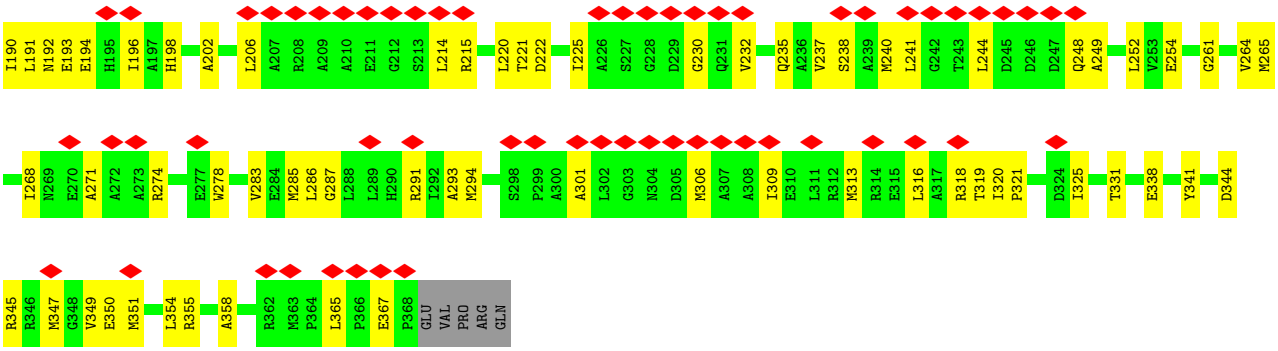
Chain A:



- Molecule 2: DNA polymerase III subunit tau

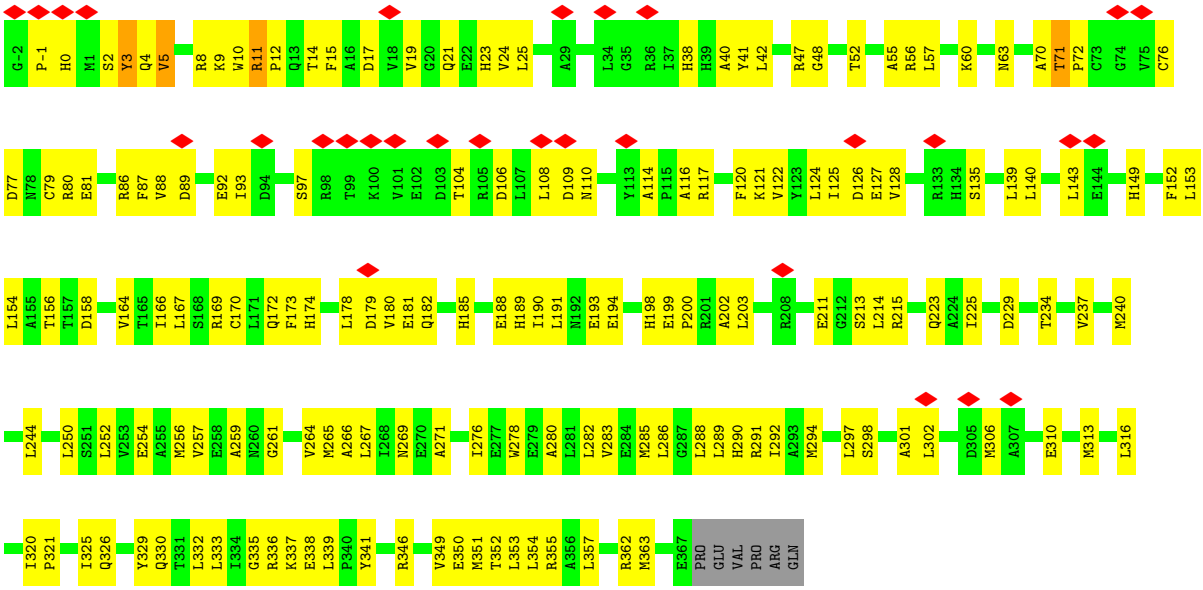
Chain B:





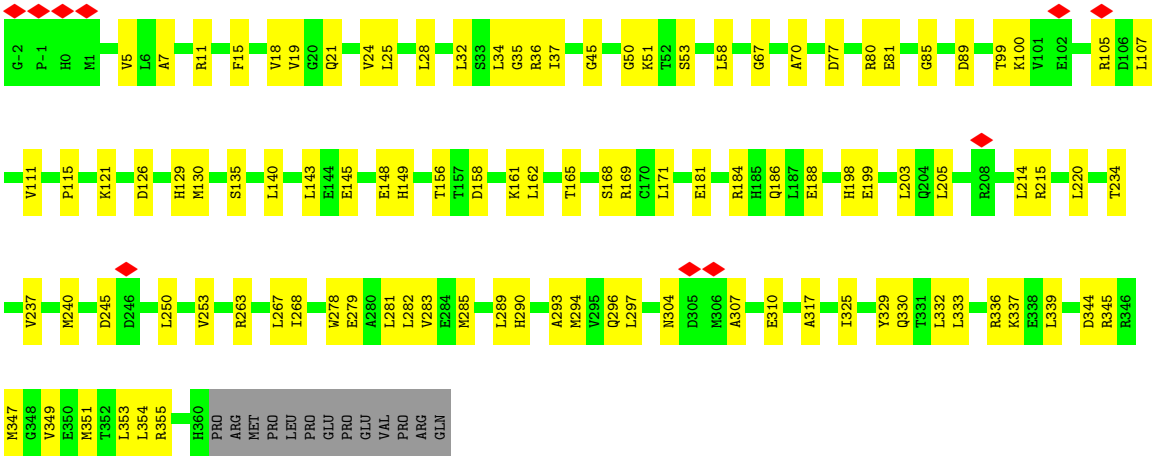
• Molecule 2: DNA polymerase III subunit tau

Chain C:



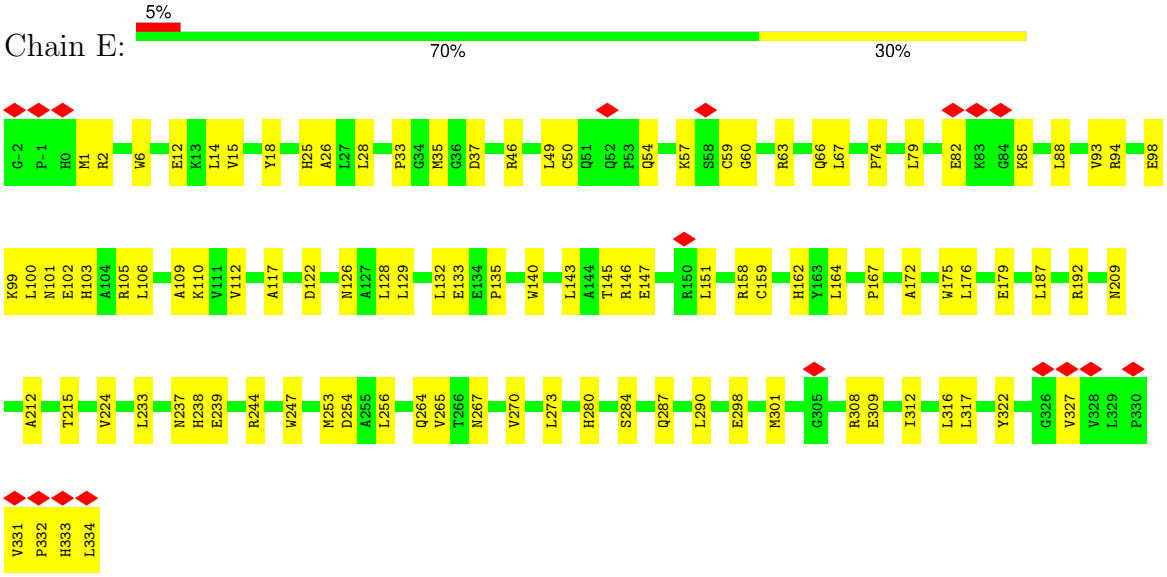
• Molecule 2: DNA polymerase III subunit tau

Chain D:



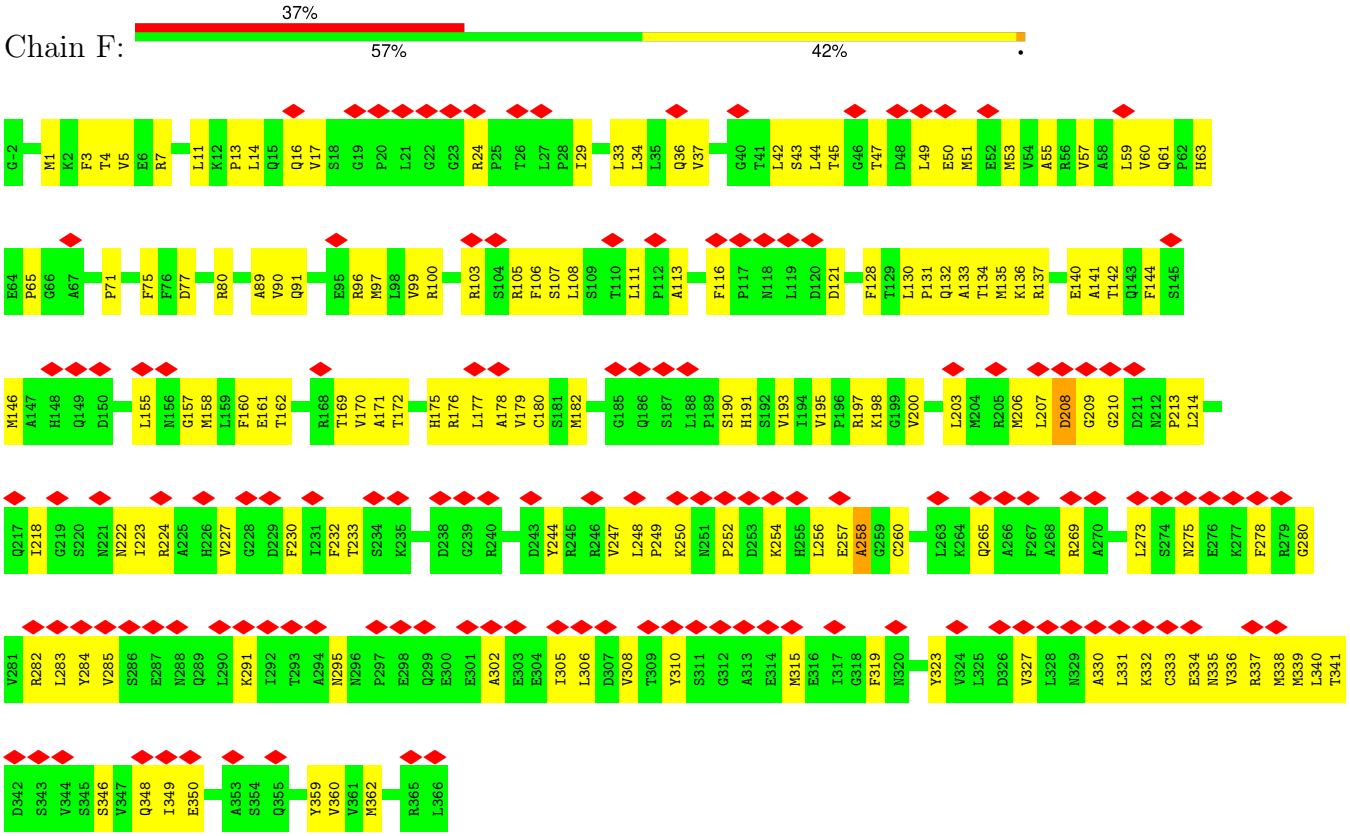
- Molecule 3: DNA polymerase III subunit delta'

Chain E:



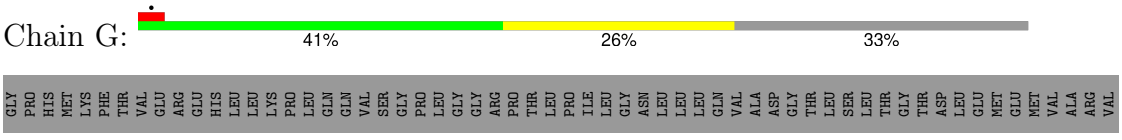
- Molecule 4: Beta sliding clamp

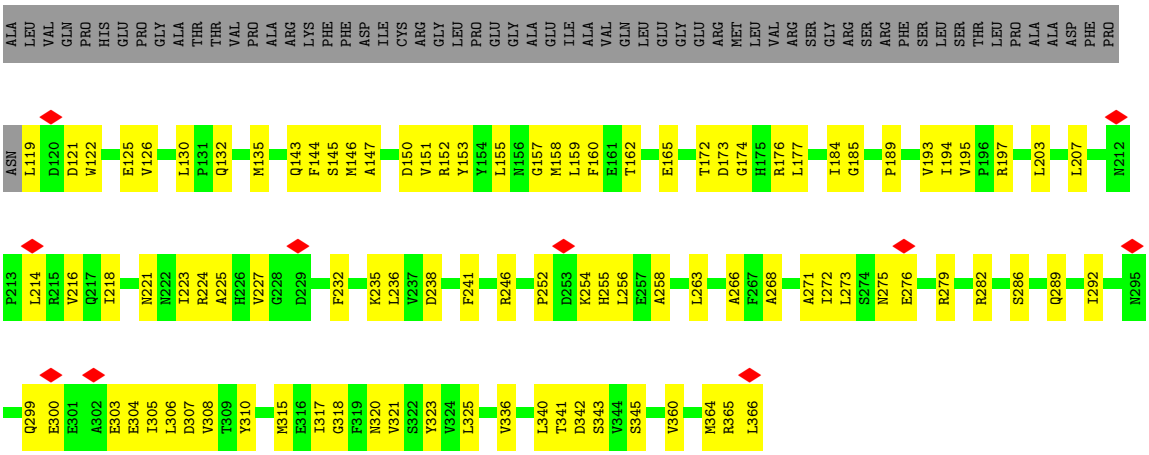
Chain F:



- Molecule 4: Beta sliding clamp

Chain G:




ALA LEU VAL GLN PRO HIS GLU PRO GLY ALA THR THR VAL PRO ALA ARG LYS PHE PHE ASP ILE CYS ARG GLY LEU PRO GLU GLY ALA GLU ILE ALA VAL GLN LEU GLU GLY GLU ARG MET LEU VAL ARG SER GLY ARG SER ARG PHE SER LEU SER THR LEU PRO ALA ALA ASP PHE PRO
ASN L119 D120 D121 W122 E125 V126 L130 P131 Q132 M135 Q143 F144 S145 M146 A147 D150 V151 R152 Y153 Y154 L155 N156 G157 M158 L159 F160 E161 T162 E165 T172 D173 G174 H175 R176 L177 I184 G185 P189 V193 I194 V195 P196 R197 L203 L207 N212
P213 L214 R215 V216 Q217 I218 N221 N222 I223 R224 A225 H226 V227 G228 D229 F232 K235 L236 V237 D238 F241 R246 P252 D253 K254 H255 L256 E257 A258 L263 A266 F267 A268 A271 I272 L273 S274 N275 E276 R279 R282 S286 Q289 I292 N295
Q299 E300 E301 A302 E303 E304 I305 L306 D307 V308 T309 Y310 M315 E316 I317 G318 F319 N320 V321 S322 Y323 V324 L325 V336 L340 T341 D342 S343 V344 S345 V360 M364 R365 L366

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	37816	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	49.86	Depositor
Minimum defocus (nm)	1100	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.620	Depositor
Minimum map value	-0.357	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.015	Depositor
Recommended contour level	0.09	Depositor
Map size (Å)	292.16, 292.16, 292.16	wwPDB
Map dimensions	352, 352, 352	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83, 0.83, 0.83	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: ADP, BEF, ZN, 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	0.13	0/2698	0.34	0/3664
2	B	0.13	0/2935	0.30	0/3980
2	C	0.21	0/2927	0.43	1/3968 (0.0%)
2	D	0.22	0/2867	0.34	0/3885
3	E	0.21	0/2690	0.35	0/3671
4	F	0.14	0/2916	0.35	0/3947
4	G	0.19	0/1980	0.35	0/2677
All	All	0.18	0/19013	0.35	1/25792 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	11	ARG	CB-CG-CD	5.81	124.67	111.30

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	2651	0	2703	104	0
2	B	2885	0	2929	108	0
2	C	2878	0	2923	150	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	2821	0	2863	93	0
3	E	2623	0	2620	85	0
4	F	2865	0	2878	129	0
4	G	1948	0	1934	78	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
5	E	1	0	0	0	0
6	B	27	0	12	3	0
6	C	27	0	12	3	0
6	D	27	0	12	6	0
7	B	4	0	0	0	0
7	C	4	0	0	3	0
7	D	4	0	0	0	0
8	B	1	0	0	0	0
8	C	1	0	0	0	0
8	D	1	0	0	0	0
All	All	18771	0	18886	679	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 18.

All (679) 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)
2:C:215:ARG:HH21	2:D:168:SER:HB2	1.39	0.86
4:F:146:MET:HG3	4:F:158:MET:HE1	1.57	0.86
2:B:108:LEU:HD11	2:B:138:ALA:HB1	1.59	0.84
4:F:157:GLY:HA3	4:F:195:VAL:O	1.78	0.83
2:C:11:ARG:HG2	6:C:401:ADP:O3'	1.80	0.81
2:C:223:GLN:HB2	2:D:171:LEU:HD11	1.61	0.81
3:E:25:HIS:NE2	3:E:132:LEU:O	2.14	0.81
2:C:215:ARG:NH2	2:D:165:THR:O	2.15	0.80
2:B:45:GLY:HA3	2:B:49:VAL:HG11	1.64	0.79
2:D:214:LEU:HD22	6:D:401:ADP:H1'	1.64	0.79
4:G:126:VAL:HB	4:G:218:ILE:HB	1.66	0.78
2:B:358:ALA:HA	2:B:365:LEU:HB2	1.65	0.77
2:B:293:ALA:HB2	2:B:325:ILE:HG21	1.67	0.77
1:A:64:ILE:HG13	1:A:67:LEU:HD12	1.67	0.76
4:F:157:GLY:CA	4:F:195:VAL:O	2.34	0.76
4:F:144:PHE:HB3	4:F:176:ARG:HH11	1.51	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:186:GLN:HG2	2:D:214:LEU:HD11	1.69	0.75
2:B:309:ILE:HG22	2:B:313:MET:HB2	1.68	0.75
1:A:230:LEU:HD21	2:B:301:ALA:HA	1.69	0.75
2:B:108:LEU:O	2:B:111:VAL:HG12	1.85	0.75
2:B:186:GLN:HG2	2:B:214:LEU:HD21	1.68	0.74
3:E:100:LEU:O	3:E:110:LYS:NZ	2.21	0.74
1:A:162:LEU:HD13	1:A:167:ASN:HB2	1.69	0.74
2:B:144:GLU:HG3	2:B:145:GLU:HG3	1.68	0.74
1:A:223:MET:HG3	1:A:225:LYS:HG3	1.67	0.73
1:A:173:CYS:HB3	1:A:209:ALA:HB2	1.69	0.73
3:E:128:LEU:HG	3:E:132:LEU:HD23	1.71	0.73
2:D:215:ARG:NH2	3:E:133:GLU:OE2	2.21	0.73
4:G:146:MET:HE3	4:G:197:ARG:HD2	1.69	0.73
2:C:261:GLY:HA3	2:D:297:LEU:HD11	1.70	0.72
2:D:18:VAL:HB	2:D:25:LEU:HD21	1.70	0.72
2:B:10:TRP:HZ2	2:B:194:GLU:HG2	1.54	0.71
2:C:106:ASP:O	2:C:110:ASN:ND2	2.24	0.71
2:C:215:ARG:CZ	7:C:402:BEF:F2	2.29	0.71
4:F:162:THR:O	4:F:190:SER:HA	1.91	0.71
4:F:51:MET:HE1	4:F:198:LYS:HB2	1.73	0.70
4:G:289:GLN:HG3	4:G:305:ILE:HG23	1.73	0.70
2:C:47:ARG:HB2	7:C:402:BEF:F3	1.81	0.70
2:B:110:ASN:HD22	2:B:113:TYR:HE2	1.39	0.69
2:D:156:THR:HG21	2:D:162:LEU:HD21	1.74	0.69
2:D:278:TRP:HB3	2:D:349:VAL:HG21	1.74	0.69
4:F:131:PRO:HA	4:F:213:PRO:HA	1.73	0.69
4:F:141:ALA:HA	4:F:330:ALA:HB1	1.73	0.69
4:F:169:THR:O	4:F:179:VAL:HA	1.92	0.69
4:G:150:ASP:OD2	4:G:152:ARG:NH2	2.26	0.68
2:D:11:ARG:NH1	2:D:53:SER:OG	2.26	0.68
2:B:60:LYS:NZ	2:B:79:CYS:O	2.22	0.68
3:E:237:ASN:ND2	3:E:309:GLU:OE2	2.26	0.68
4:G:246:ARG:O	4:G:246:ARG:NH1	2.26	0.68
2:C:350:GLU:HB3	2:D:290:HIS:HE1	1.57	0.68
2:C:302:LEU:HD21	2:C:313:MET:HG3	1.74	0.68
1:A:312:LEU:HD13	1:A:317:GLY:HA2	1.77	0.67
4:F:158:MET:HG2	4:F:200:VAL:HG21	1.76	0.67
1:A:312:LEU:HD11	1:A:320:VAL:HB	1.77	0.67
4:F:132:GLN:OE1	4:F:207:LEU:HG	1.94	0.67
2:C:285:MET:HE1	2:C:353:LEU:HD21	1.76	0.66
2:C:215:ARG:CZ	2:D:169:ARG:HB3	2.25	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:194:GLU:OE1	2:D:36:ARG:NH2	2.28	0.66
4:F:133:ALA:HA	4:F:136:LYS:HD3	1.77	0.66
1:A:304:LEU:HD11	1:A:327:LEU:HD13	1.78	0.66
1:A:223:MET:SD	1:A:225:LYS:NZ	2.68	0.66
1:A:258:VAL:HG22	1:A:298:LEU:HD13	1.78	0.66
2:C:271:ALA:HB1	2:C:276:ILE:HD11	1.76	0.65
1:A:25:GLY:HA3	1:A:139:CYS:HB3	1.79	0.65
4:F:33:LEU:HD21	4:F:44:LEU:HB3	1.77	0.65
2:B:56:ARG:O	2:B:60:LYS:HG2	1.96	0.65
2:C:181:GLU:OE2	2:C:185:HIS:NE2	2.28	0.65
4:F:128:PHE:CD1	4:F:130:LEU:HB2	2.32	0.64
1:A:2:ILE:HB	1:A:135:VAL:HG22	1.80	0.64
1:A:292:ARG:NH2	1:A:332:CYS:O	2.30	0.64
4:F:193:VAL:HG11	4:F:218:ILE:HG21	1.80	0.64
1:A:29:LEU:HB2	1:A:179:LEU:HD22	1.78	0.64
2:D:290:HIS:O	2:D:294:MET:HG2	1.98	0.64
4:F:132:GLN:HG2	4:F:210:GLY:HA2	1.79	0.64
2:D:336:ARG:HA	2:D:339:LEU:HD23	1.80	0.64
2:D:250:LEU:HA	2:D:253:VAL:HG12	1.80	0.64
2:B:67:GLY:HA2	2:B:119:ARG:HH12	1.62	0.63
2:C:104:THR:HG21	2:C:135:SER:HB2	1.79	0.63
4:G:145:SER:HA	4:G:176:ARG:HE	1.63	0.63
2:C:215:ARG:HH12	2:D:169:ARG:CZ	2.12	0.63
2:D:354:LEU:HD11	3:E:256:LEU:HB3	1.79	0.63
2:C:341:TYR:O	2:D:336:ARG:NE	2.32	0.63
4:F:175:HIS:ND1	4:F:362:MET:O	2.32	0.63
2:D:351:MET:HG3	3:E:253:MET:HE1	1.81	0.63
2:C:63:ASN:HD21	2:C:120:PHE:H	1.47	0.63
2:C:185:HIS:O	2:C:189:HIS:ND1	2.29	0.63
4:F:36:GLN:HG3	4:F:43:SER:HB3	1.79	0.63
2:C:15:PHE:HB2	2:C:71:THR:HG21	1.79	0.63
4:G:143:GLN:HA	4:G:158:MET:HE1	1.80	0.63
2:B:87:PHE:HB3	2:B:90:LEU:HB3	1.81	0.63
2:B:338:GLU:OE2	2:C:330:GLN:NE2	2.26	0.63
2:D:18:VAL:HG11	2:D:25:LEU:HD11	1.81	0.62
2:B:249:ALA:HA	2:B:252:LEU:HB2	1.79	0.62
2:C:337:LYS:HZ2	3:E:334:LEU:HD22	1.64	0.62
3:E:103:HIS:ND1	4:G:221:ASN:OD1	2.31	0.62
2:C:97:SER:O	2:D:105:ARG:NH2	2.32	0.62
2:D:32:LEU:HA	2:D:37:ILE:HD11	1.81	0.62
2:B:15:PHE:HZ	2:B:28:LEU:HD22	1.65	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:354:LEU:HD21	3:E:256:LEU:HD13	1.82	0.62
2:B:89:ASP:OD2	2:B:118:GLY:N	2.26	0.62
2:B:192:ASN:OD1	2:B:198:HIS:NE2	2.29	0.62
2:C:77:ASP:O	2:C:80:ARG:HG2	2.00	0.62
4:F:97:MET:HB3	4:F:108:LEU:HB2	1.80	0.62
2:C:181:GLU:OE1	2:C:182:GLN:NE2	2.30	0.62
1:A:249:THR:HA	1:A:252:ARG:HE	1.63	0.61
2:C:215:ARG:NH1	2:D:169:ARG:HB3	2.15	0.61
4:F:13:PRO:HG2	4:F:57:VAL:HG22	1.81	0.61
4:G:172:THR:HG22	4:G:174:GLY:H	1.65	0.61
2:D:304:ASN:HA	2:D:307:ALA:HB2	1.81	0.61
3:E:192:ARG:NH1	3:E:265:VAL:O	2.33	0.61
2:B:191:LEU:HG	2:B:196:ILE:HD11	1.82	0.61
2:C:47:ARG:HH22	2:C:211:GLU:HB2	1.65	0.61
2:C:81:GLU:HB3	2:C:86:ARG:HB2	1.82	0.61
4:F:282:ARG:NH2	4:F:295:ASN:OD1	2.31	0.61
4:F:17:VAL:HG12	4:F:53:MET:HG3	1.82	0.61
2:C:125:ILE:HB	2:C:154:LEU:CD2	2.31	0.61
2:D:184:ARG:NH2	2:D:188:GLU:OE1	2.33	0.61
1:A:18:ARG:HA	1:A:133:ARG:HH21	1.66	0.60
2:D:51:LYS:N	6:D:401:ADP:O2B	2.34	0.60
1:A:215:PHE:O	1:A:219:ASP:HB2	2.01	0.60
2:D:32:LEU:HD13	2:D:70:ALA:HA	1.83	0.60
1:A:80:LEU:HB2	1:A:108:LEU:HD11	1.81	0.60
2:B:271:ALA:HA	2:B:274:ARG:HH21	1.66	0.60
4:F:155:LEU:HD22	4:F:172:THR:HB	1.83	0.60
2:C:128:VAL:HG12	2:C:156:THR:HB	1.82	0.60
2:D:296:GLN:NE2	2:D:317:ALA:O	2.35	0.60
1:A:6:PRO:HG2	1:A:30:LEU:HD13	1.84	0.60
2:D:198:HIS:CE1	2:D:203:LEU:HD11	2.37	0.60
1:A:217:TRP:CE2	1:A:233:LEU:HD21	2.36	0.60
2:C:76:CYS:HB3	2:C:79:CYS:SG	2.42	0.59
1:A:52:THR:O	2:B:141:LYS:NZ	2.36	0.59
1:A:174:TYR:HD2	1:A:180:ALA:HB1	1.66	0.59
3:E:105:ARG:HD3	4:G:235:LYS:HD2	1.84	0.59
4:G:121:ASP:OD2	4:G:224:ARG:NH2	2.36	0.59
2:B:341:TYR:O	2:C:336:ARG:NH1	2.36	0.59
1:A:273:PHE:HB3	1:A:283:ARG:HD3	1.83	0.59
4:F:348:GLN:NE2	4:F:350:GLU:OE2	2.35	0.59
2:D:215:ARG:NH2	6:D:401:ADP:O2A	2.35	0.59
3:E:101:ASN:HD22	4:G:153:TYR:HB2	1.68	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:5:VAL:HG12	2:D:7:ALA:H	1.67	0.59
3:E:59:CYS:SG	3:E:60:GLY:N	2.76	0.59
4:G:165:GLU:O	4:G:184:ILE:N	2.32	0.59
3:E:46:ARG:NH1	3:E:46:ARG:HB2	2.18	0.58
1:A:55:ILE:HG21	1:A:93:ILE:HD12	1.85	0.58
1:A:299:ARG:HG3	3:E:317:LEU:HB3	1.85	0.58
4:F:244:TYR:HA	4:F:247:VAL:HG22	1.85	0.58
2:B:64:CYS:O	2:B:119:ARG:NH2	2.36	0.58
2:C:56:ARG:NH2	2:D:145:GLU:OE2	2.36	0.58
3:E:67:LEU:HD23	3:E:74:PRO:HD3	1.85	0.58
4:F:203:LEU:HA	4:F:206:MET:HE2	1.86	0.58
4:F:132:GLN:CG	4:F:210:GLY:HA2	2.34	0.58
2:B:34:LEU:HD22	2:B:36:ARG:HG2	1.84	0.58
2:C:48:GLY:N	6:C:401:ADP:O3B	2.34	0.58
1:A:73:LEU:O	4:F:175:HIS:NE2	2.37	0.58
4:F:34:LEU:HB2	4:F:45:THR:HB	1.86	0.58
2:B:113:TYR:O	2:B:149:HIS:NE2	2.36	0.58
2:C:89:ASP:HB3	2:C:121:LYS:HA	1.86	0.58
2:B:350:GLU:OE1	2:C:290:HIS:NE2	2.31	0.58
4:F:260:CYS:HB2	4:F:336:VAL:HG13	1.86	0.58
4:G:315:MET:HE1	4:G:340:LEU:HD13	1.85	0.57
2:C:341:TYR:HB3	2:D:336:ARG:HE	1.68	0.57
3:E:253:MET:HE2	3:E:290:LEU:HD11	1.85	0.57
2:C:23:HIS:CD2	2:C:24:VAL:HG13	2.40	0.57
4:F:121:ASP:O	4:F:222:ASN:ND2	2.36	0.57
2:B:214:LEU:HD23	6:B:402:ADP:C4	2.40	0.57
2:C:338:GLU:HB2	2:D:333:LEU:HD21	1.86	0.57
3:E:33:PRO:HD3	3:E:146:ARG:HG3	1.86	0.57
2:B:1:MET:HG2	2:B:5:VAL:HA	1.85	0.57
3:E:133:GLU:HB2	3:E:158:ARG:NE	2.20	0.57
1:A:211:HIS:CE1	1:A:235:GLN:HB3	2.40	0.56
2:B:306:MET:HB3	2:B:309:ILE:HB	1.86	0.56
4:G:315:MET:HE3	4:G:317:ILE:HB	1.87	0.56
1:A:152:ALA:HA	1:A:162:LEU:HD21	1.87	0.56
4:F:131:PRO:O	4:F:134:THR:OG1	2.22	0.56
1:A:325:GLU:OE2	2:B:291:ARG:NH1	2.39	0.56
2:B:354:LEU:HD11	2:C:297:LEU:HD23	1.87	0.56
4:G:194:ILE:HD11	4:G:241:PHE:HB2	1.88	0.56
4:F:161:GLU:HA	4:F:191:HIS:O	2.05	0.56
4:F:273:LEU:HD12	4:F:302:ALA:HB2	1.85	0.56
2:B:6:LEU:HG	2:B:222:ASP:OD1	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:84:GLN:HB3	2:B:86:ARG:HH21	1.71	0.56
2:C:188:GLU:HG3	2:C:198:HIS:CE1	2.41	0.56
2:D:81:GLU:O	2:D:85:GLY:N	2.38	0.56
3:E:128:LEU:HG	3:E:132:LEU:CD2	2.36	0.56
4:G:144:PHE:O	4:G:176:ARG:NH2	2.38	0.56
2:B:225:ILE:HG23	2:B:230:GLY:HA2	1.88	0.56
2:C:5:VAL:O	2:C:8:ARG:N	2.39	0.56
2:C:122:VAL:HG23	2:C:153:LEU:HD13	1.88	0.56
2:B:220:LEU:HD12	2:B:240:MET:HE1	1.87	0.56
2:C:38:HIS:HB2	2:C:41:TYR:HE1	1.71	0.56
2:C:354:LEU:HD22	2:D:293:ALA:HB1	1.88	0.56
2:C:215:ARG:NH2	2:D:168:SER:HB2	2.17	0.55
3:E:6:TRP:HH2	3:E:35:MET:HG3	1.70	0.55
2:B:244:LEU:HB2	2:C:167:LEU:HD13	1.88	0.55
3:E:79:LEU:HB3	3:E:88:LEU:HD11	1.87	0.55
4:F:180:CYS:HB3	4:F:182:MET:HE3	1.88	0.55
4:G:130:LEU:HD23	4:G:135:MET:HB2	1.88	0.55
2:D:89:ASP:HB3	2:D:121:LYS:HA	1.87	0.55
3:E:254:ASP:OD2	3:E:267:ASN:ND2	2.39	0.55
2:D:50:GLY:HA2	6:D:401:ADP:O1A	2.07	0.55
4:F:214:LEU:HD22	4:F:227:VAL:HA	1.88	0.55
2:B:331:THR:HG23	2:B:355:ARG:HD2	1.89	0.55
1:A:199:LEU:HA	1:A:202:VAL:HG22	1.89	0.55
4:F:16:GLN:HG2	4:F:53:MET:HE2	1.88	0.55
4:F:175:HIS:HB2	4:F:323:TYR:CE2	2.42	0.55
4:F:208:ASP:OD1	4:F:209:GLY:N	2.40	0.55
2:C:254:GLU:HG2	2:C:316:LEU:HD21	1.89	0.54
2:B:1:MET:HG3	2:B:222:ASP:OD1	2.06	0.54
4:F:3:PHE:HB2	4:F:90:VAL:HB	1.90	0.54
4:G:275:ASN:OD1	4:G:276:GLU:N	2.40	0.54
1:A:220:ALA:O	1:A:224:GLY:N	2.41	0.54
2:D:21:GLN:OE1	6:D:401:ADP:N6	2.40	0.54
4:F:128:PHE:HD1	4:F:130:LEU:HB2	1.68	0.54
4:G:145:SER:HA	4:G:176:ARG:NE	2.21	0.54
4:G:318:GLY:O	4:G:364:MET:N	2.35	0.54
2:B:26:THR:O	2:B:30:ASN:ND2	2.41	0.54
2:C:93:ILE:HB	2:C:125:ILE:HD13	1.88	0.54
4:G:193:VAL:HG23	4:G:236:LEU:HD13	1.89	0.54
2:C:15:PHE:CZ	2:C:25:LEU:HB2	2.43	0.54
3:E:212:ALA:HB1	3:E:244:ARG:HH12	1.72	0.54
3:E:94:ARG:O	3:E:98:GLU:HG2	2.07	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:160:LEU:HD11	1:A:189:SER:HB2	1.90	0.53
2:B:15:PHE:CZ	2:B:28:LEU:HD22	2.42	0.53
1:A:261:LYS:NZ	1:A:290:LEU:O	2.30	0.53
2:C:87:PHE:O	2:C:117:ARG:NH2	2.42	0.53
1:A:18:ARG:HG3	1:A:135:VAL:HG23	1.91	0.53
4:F:142:THR:HG21	4:F:169:THR:HG22	1.90	0.53
2:B:127:GLU:N	2:B:155:ALA:O	2.42	0.53
4:F:77:ASP:OD1	4:F:80:ARG:NH2	2.42	0.53
4:F:214:LEU:HD13	4:F:227:VAL:HG22	1.91	0.53
4:F:177:LEU:HD23	4:F:360:VAL:HB	1.91	0.53
4:G:225:ALA:H	4:G:232:PHE:HB3	1.74	0.53
3:E:238:HIS:ND1	3:E:238:HIS:O	2.41	0.53
4:F:71:PRO:HG2	4:F:108:LEU:HD12	1.91	0.53
4:F:252:PRO:HB3	4:F:339:MET:HB3	1.91	0.53
3:E:100:LEU:HD11	3:E:112:VAL:HG21	1.90	0.52
2:C:252:LEU:HA	2:C:267:LEU:HD13	1.92	0.52
3:E:46:ARG:HB2	3:E:46:ARG:HH11	1.75	0.52
3:E:82:GLU:HB2	3:E:85:LYS:HE2	1.90	0.52
4:F:100:ARG:HG2	4:F:105:ARG:HG2	1.92	0.52
2:B:344:ASP:HB3	2:B:347:MET:HG2	1.90	0.52
4:G:214:LEU:HD23	4:G:227:VAL:HG22	1.92	0.52
2:C:252:LEU:HD11	2:C:264:VAL:HG13	1.92	0.52
4:F:257:GLU:HG3	4:F:337:ARG:HG2	1.91	0.52
2:B:198:HIS:HA	2:B:232:VAL:HB	1.91	0.52
2:C:92:GLU:OE1	2:C:92:GLU:N	2.42	0.52
2:B:215:ARG:HB2	6:B:402:ADP:H5'1	1.92	0.52
4:G:193:VAL:HG21	4:G:218:ILE:HD12	1.91	0.52
1:A:260:LEU:HB3	1:A:290:LEU:HD11	1.91	0.51
2:B:367:GLU:HG3	2:C:321:PRO:HB3	1.92	0.51
2:C:15:PHE:HD1	2:C:57:LEU:HD21	1.75	0.51
2:C:108:LEU:HD21	2:C:139:LEU:HA	1.91	0.51
3:E:126:ASN:HA	3:E:129:LEU:HG	1.92	0.51
3:E:284:SER:O	3:E:287:GLN:HG3	2.11	0.51
3:E:298:GLU:HA	3:E:301:MET:HE3	1.91	0.51
1:A:219:ASP:HA	1:A:222:LEU:HD12	1.92	0.51
1:A:220:ALA:HB1	1:A:225:LYS:HB2	1.93	0.51
2:D:21:GLN:HB3	2:D:24:VAL:HG12	1.91	0.51
1:A:53:PHE:CZ	1:A:63:ALA:HB1	2.45	0.51
1:A:278:VAL:O	1:A:283:ARG:NE	2.40	0.51
2:C:0:HIS:CG	2:D:35:GLY:HA2	2.46	0.51
4:F:99:VAL:HG23	4:F:106:PHE:HB2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:64:ILE:HD13	1:A:96:GLN:HB3	1.92	0.51
1:A:217:TRP:CH2	1:A:246:LEU:HB3	2.45	0.51
2:C:282:LEU:HD12	2:C:339:LEU:HD22	1.93	0.51
2:C:338:GLU:CB	2:D:333:LEU:HD21	2.41	0.51
1:A:55:ILE:HG12	1:A:59:THR:HG21	1.93	0.51
4:F:130:LEU:HD23	4:F:135:MET:HB3	1.93	0.51
2:C:164:VAL:HA	2:C:167:LEU:HD12	1.92	0.51
4:F:252:PRO:HA	4:F:341:THR:HG22	1.92	0.51
4:G:342:ASP:OD1	4:G:343:SER:N	2.42	0.51
2:D:115:PRO:HG3	2:D:149:HIS:ND1	2.26	0.51
4:F:179:VAL:HG11	4:F:248:LEU:HD12	1.92	0.51
4:F:254:LYS:HB2	4:F:340:LEU:HB2	1.92	0.51
4:F:224:ARG:HG2	4:F:233:THR:HG23	1.93	0.50
4:F:283:LEU:HB2	4:F:319:PHE:HE1	1.76	0.50
1:A:194:ASP:OD1	1:A:195:GLY:N	2.44	0.50
2:B:206:LEU:HG	2:B:221:THR:HG22	1.92	0.50
2:C:266:ALA:HA	2:C:269:ASN:HD21	1.76	0.50
2:C:294:MET:O	2:C:297:LEU:HG	2.10	0.50
2:D:181:GLU:HA	2:D:184:ARG:HG2	1.93	0.50
4:F:96:ARG:NH2	4:G:299:GLN:O	2.45	0.50
2:B:183:ILE:HG23	2:B:214:LEU:HD13	1.92	0.50
1:A:188:LEU:HD21	1:A:202:VAL:HG12	1.93	0.50
4:G:282:ARG:HH21	4:G:366:LEU:HD22	1.76	0.50
4:F:90:VAL:HG22	4:F:99:VAL:HG12	1.91	0.50
4:G:177:LEU:HB3	4:G:360:VAL:HB	1.92	0.50
1:A:52:THR:OG1	2:B:141:LYS:NZ	2.42	0.50
2:C:70:ALA:C	2:C:72:PRO:HD2	2.36	0.50
3:E:224:VAL:O	3:E:280:HIS:ND1	2.45	0.50
4:F:206:MET:HE1	4:F:232:PHE:HB3	1.94	0.50
4:G:132:GLN:HE22	4:G:207:LEU:HB2	1.76	0.50
1:A:212:PHE:O	1:A:236:LEU:HD21	2.12	0.50
1:A:217:TRP:HD1	1:A:229:ALA:HB1	1.77	0.50
2:C:0:HIS:HE2	2:C:3:TYR:HE1	1.59	0.50
2:C:55:ALA:HB1	2:C:124:LEU:HD21	1.94	0.50
4:F:132:GLN:HG3	4:F:136:LYS:HD2	1.94	0.50
2:B:98:ARG:HH22	4:F:24:ARG:HH22	1.59	0.49
2:B:143:LEU:HB3	2:B:169:ARG:HG2	1.94	0.49
3:E:122:ASP:O	3:E:126:ASN:ND2	2.45	0.49
4:G:203:LEU:HB2	4:G:232:PHE:CE1	2.47	0.49
2:C:250:LEU:HD13	2:C:313:MET:HE1	1.93	0.49
1:A:174:TYR:CD2	1:A:180:ALA:HB1	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:291:ARG:HH11	2:C:301:ALA:HB1	1.77	0.49
2:D:148:GLU:HG3	4:G:365:ARG:HH12	1.77	0.49
3:E:117:ALA:HB3	3:E:145:THR:HG22	1.94	0.49
4:F:108:LEU:HD13	4:G:300:GLU:OE2	2.13	0.49
4:F:248:LEU:HB3	4:F:249:PRO:HD3	1.94	0.49
1:A:56:ASP:H	1:A:59:THR:HB	1.78	0.49
2:C:3:TYR:HB3	2:D:36:ARG:HA	1.95	0.49
2:C:257:VAL:HG13	2:C:320:ILE:HD11	1.93	0.49
2:C:355:ARG:NH2	2:D:330:GLN:OE1	2.45	0.49
3:E:331:VAL:O	3:E:333:HIS:ND1	2.35	0.49
2:B:23:HIS:CD2	2:B:24:VAL:HG23	2.47	0.49
2:B:129:HIS:ND1	2:B:156:THR:OG1	2.44	0.49
2:B:338:GLU:OE1	2:B:355:ARG:NH2	2.45	0.49
2:D:337:LYS:NZ	3:E:334:LEU:OXT	2.40	0.49
2:B:51:LYS:HB3	2:B:155:ALA:HB1	1.94	0.49
2:C:215:ARG:HH21	2:D:168:SER:CB	2.20	0.49
3:E:322:TYR:HA	3:E:327:VAL:HG11	1.94	0.49
4:F:47:THR:HG22	4:F:49:LEU:H	1.76	0.49
4:F:284:TYR:HB3	4:F:291:LYS:HB3	1.95	0.49
1:A:37:ALA:O	1:A:40:GLN:HG3	2.13	0.49
1:A:53:PHE:HZ	1:A:63:ALA:HB1	1.78	0.49
2:D:289:LEU:HD22	2:D:325:ILE:HG23	1.95	0.49
4:F:53:MET:HE1	4:F:230:PHE:HB3	1.94	0.49
4:G:292:ILE:HD11	4:G:304:GLU:OE2	2.13	0.49
2:C:116:ALA:O	2:C:117:ARG:HG2	2.13	0.48
3:E:18:TYR:HE2	3:E:140:TRP:CD1	2.30	0.48
4:F:36:GLN:O	4:F:42:LEU:HD12	2.13	0.48
4:F:130:LEU:HG	4:F:134:THR:OG1	2.12	0.48
4:F:137:ARG:HA	4:F:140:GLU:HG3	1.95	0.48
1:A:216:HIS:CD2	1:A:228:ARG:HH21	2.30	0.48
1:A:273:PHE:HE1	1:A:286:MET:HB2	1.78	0.48
2:D:355:ARG:CZ	3:E:332:PRO:HG2	2.43	0.48
2:C:63:ASN:HD21	2:C:120:PHE:N	2.11	0.48
2:C:158:ASP:OD1	2:C:158:ASP:N	2.44	0.48
4:F:254:LYS:HB3	4:F:310:TYR:HE1	1.78	0.48
2:C:265:MET:O	2:C:269:ASN:ND2	2.47	0.48
4:G:252:PRO:HA	4:G:341:THR:HG22	1.96	0.48
2:C:47:ARG:NH2	2:C:211:GLU:HB2	2.27	0.48
1:A:282:ARG:O	1:A:286:MET:HG2	2.13	0.48
2:B:32:LEU:HD12	2:B:37:ILE:HD11	1.95	0.48
3:E:79:LEU:HD13	3:E:93:VAL:HG12	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:50:GLU:HG2	4:F:51:MET:HG3	1.95	0.48
2:B:264:VAL:HG13	2:B:265:MET:HE2	1.95	0.48
2:D:129:HIS:HB2	2:D:161:LYS:HB2	1.95	0.48
4:G:271:ALA:HB2	4:G:321:VAL:HG21	1.95	0.48
2:C:48:GLY:HA3	2:C:213:SER:HB2	1.94	0.48
2:D:28:LEU:HD11	2:D:58:LEU:HD22	1.96	0.48
2:D:281:LEU:O	2:D:285:MET:HG3	2.14	0.48
3:E:14:LEU:HD11	3:E:162:HIS:CD2	2.48	0.48
4:F:60:VAL:HG23	4:F:61:GLN:HG3	1.96	0.48
2:C:191:LEU:HD11	2:C:225:ILE:HD11	1.96	0.48
2:C:244:LEU:HD23	2:C:244:LEU:H	1.79	0.48
2:C:362:ARG:O	2:C:363:MET:HE2	2.14	0.48
3:E:175:TRP:HE3	3:E:176:LEU:HD22	1.77	0.48
4:F:36:GLN:HE21	4:F:43:SER:HB3	1.79	0.48
4:F:334:GLU:OE1	4:F:335:ASN:ND2	2.46	0.48
2:B:10:TRP:CE2	2:B:190:ILE:HG23	2.48	0.48
2:C:14:THR:HG22	2:C:14:THR:O	2.14	0.48
4:F:3:PHE:HB3	4:F:5:VAL:HG23	1.96	0.48
1:A:13:LEU:HD21	1:A:38:VAL:HG22	1.95	0.47
2:B:261:GLY:O	2:B:265:MET:HG2	2.14	0.47
2:B:111:VAL:HA	2:B:123:TYR:HE2	1.79	0.47
2:C:128:VAL:HG21	2:C:154:LEU:HD13	1.96	0.47
2:D:310:GLU:OE1	2:D:310:GLU:N	2.45	0.47
4:F:135:MET:HG2	4:F:207:LEU:HD21	1.96	0.47
4:G:258:ALA:HB2	4:G:308:VAL:HG12	1.95	0.47
4:G:282:ARG:NH2	4:G:366:LEU:HD22	2.29	0.47
1:A:61:TRP:NE1	1:A:95:GLU:OE1	2.48	0.47
1:A:77:ARG:HG2	1:A:107:ASP:HA	1.95	0.47
2:B:15:PHE:HE1	2:B:57:LEU:HB3	1.80	0.47
2:B:318:ARG:HH11	2:B:319:THR:HG22	1.79	0.47
2:C:57:LEU:HD12	2:C:60:LYS:NZ	2.30	0.47
2:D:19:VAL:HG21	2:D:186:GLN:HB2	1.96	0.47
1:A:73:LEU:HB3	4:F:362:MET:HE2	1.95	0.47
1:A:162:LEU:HB3	1:A:197:LEU:HD12	1.96	0.47
2:C:189:HIS:O	2:C:193:GLU:HG2	2.14	0.47
2:D:99:THR:O	2:D:135:SER:OG	2.31	0.47
4:F:106:PHE:HD2	4:G:273:LEU:HD12	1.79	0.47
1:A:308:THR:O	1:A:312:LEU:HD23	2.14	0.47
2:C:351:MET:HG2	2:D:329:TYR:CE2	2.49	0.47
1:A:219:ASP:O	1:A:223:MET:HG2	2.15	0.47
2:B:67:GLY:HA2	2:B:119:ARG:NH1	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:45:GLY:N	2:D:51:LYS:HD3	2.29	0.47
3:E:28:LEU:HD11	3:E:151:LEU:HD22	1.96	0.47
3:E:237:ASN:CG	3:E:308:ARG:HE	2.20	0.47
1:A:325:GLU:CD	2:B:291:ARG:NH1	2.73	0.47
2:C:41:TYR:HB2	2:C:153:LEU:HG	1.97	0.47
2:C:199:GLU:OE1	2:C:234:THR:N	2.45	0.47
2:D:158:ASP:OD1	2:D:158:ASP:N	2.47	0.47
3:E:122:ASP:N	3:E:122:ASP:OD1	2.46	0.47
3:E:270:VAL:HB	3:E:273:LEU:HB2	1.96	0.47
4:G:132:GLN:HA	4:G:214:LEU:HD11	1.97	0.47
2:C:302:LEU:HD13	2:C:310:GLU:HG3	1.96	0.47
2:C:215:ARG:HH12	2:D:169:ARG:NE	2.13	0.47
1:A:52:THR:HG22	1:A:81:LEU:HB3	1.97	0.46
4:G:160:PHE:HE2	4:G:195:VAL:HB	1.80	0.46
1:A:212:PHE:HZ	1:A:216:HIS:HB2	1.79	0.46
1:A:218:VAL:O	1:A:222:LEU:HG	2.16	0.46
1:A:177:ASN:HD21	1:A:179:LEU:HD23	1.81	0.46
1:A:208:ASP:OD1	1:A:208:ASP:N	2.49	0.46
2:C:-1:PRO:HG3	2:D:67:GLY:HA3	1.98	0.46
2:D:107:LEU:O	2:D:111:VAL:HG13	2.16	0.46
3:E:12:GLU:O	3:E:15:VAL:HG12	2.16	0.46
4:F:256:LEU:HD21	4:F:285:VAL:HG13	1.96	0.46
1:A:69:GLN:HE22	1:A:74:PHE:HZ	1.64	0.46
4:F:13:PRO:HB3	4:F:55:ALA:HB1	1.96	0.46
4:F:113:ALA:HA	4:F:116:PHE:CE1	2.50	0.46
3:E:172:ALA:O	3:E:176:LEU:HD23	2.15	0.46
4:F:218:ILE:HG12	4:F:223:ILE:HG13	1.97	0.46
4:F:331:LEU:HB3	4:F:333:CYS:SG	2.55	0.46
2:B:202:ALA:HB1	2:B:237:VAL:HG21	1.97	0.46
2:C:24:VAL:HG12	2:C:173:PHE:HB3	1.98	0.46
2:B:51:LYS:HD2	2:B:155:ALA:HB1	1.98	0.46
2:C:52:THR:O	2:C:56:ARG:HG2	2.16	0.46
2:C:178:LEU:HD22	2:C:214:LEU:HG	1.97	0.46
1:A:259:ASN:HB3	1:A:276:HIS:NE2	2.30	0.46
2:B:285:MET:HE3	2:B:285:MET:HB3	1.74	0.46
4:G:173:ASP:OD2	4:G:176:ARG:NH1	2.47	0.46
3:E:46:ARG:O	3:E:50:CYS:HB2	2.15	0.46
2:C:104:THR:O	2:C:108:LEU:HG	2.16	0.46
1:A:218:VAL:HG11	1:A:253:GLU:CD	2.40	0.45
4:F:130:LEU:HD23	4:F:135:MET:HE3	1.98	0.45
4:G:320:ASN:HB3	4:G:323:TYR:CD2	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:60:ASP:H	1:A:63:ALA:HB3	1.81	0.45
2:C:240:MET:HE3	2:C:240:MET:HB3	1.87	0.45
2:D:15:PHE:HZ	2:D:28:LEU:HD23	1.81	0.45
4:G:165:GLU:N	4:G:165:GLU:OE1	2.49	0.45
1:A:28:PRO:HA	1:A:31:LEU:HD12	1.98	0.45
2:B:87:PHE:HE2	2:B:89:ASP:HB2	1.80	0.45
2:B:115:PRO:HD3	2:B:149:HIS:CD2	2.52	0.45
2:B:294:MET:HE3	2:B:294:MET:HB2	1.78	0.45
2:C:42:LEU:HA	2:C:154:LEU:O	2.16	0.45
2:C:125:ILE:HB	2:C:154:LEU:HD22	1.97	0.45
2:C:215:ARG:HH12	2:D:169:ARG:NH2	2.14	0.45
1:A:62:ASN:HA	1:A:65:PHE:CD1	2.52	0.45
1:A:166:ALA:O	1:A:170:LEU:HD23	2.16	0.45
2:C:12:PRO:HA	2:C:17:ASP:HB3	1.97	0.45
2:C:140:LEU:HA	2:C:143:LEU:HB2	1.99	0.45
2:D:199:GLU:OE2	2:D:234:THR:OG1	2.19	0.45
3:E:103:HIS:CE1	4:G:238:ASP:OD1	2.70	0.45
1:A:220:ALA:HB3	1:A:229:ALA:HB2	1.98	0.45
2:D:130:MET:HB3	2:D:130:MET:HE2	1.74	0.45
4:G:155:LEU:O	4:G:157:GLY:N	2.47	0.45
1:A:257:LEU:HD22	1:A:298:LEU:HD21	1.98	0.45
2:B:338:GLU:HB3	2:C:333:LEU:HD21	1.98	0.45
3:E:298:GLU:HA	3:E:301:MET:HG2	1.97	0.45
2:B:351:MET:SD	2:C:326:GLN:NE2	2.71	0.45
4:F:280:GLY:HA2	4:F:319:PHE:O	2.16	0.45
4:F:283:LEU:HB2	4:F:319:PHE:CE1	2.52	0.45
2:C:292:ILE:HG23	2:C:325:ILE:HD13	1.99	0.45
2:D:100:LYS:NZ	3:E:94:ARG:HH22	2.14	0.45
1:A:31:LEU:HG	1:A:139:CYS:SG	2.57	0.45
2:B:344:ASP:OD1	2:B:345:ARG:N	2.50	0.45
2:C:11:ARG:CG	6:C:401:ADP:O3'	2.58	0.45
2:C:215:ARG:NH1	7:C:402:BEF:F2	2.39	0.45
2:C:350:GLU:HB3	2:D:290:HIS:CE1	2.44	0.45
2:D:279:GLU:O	2:D:283:VAL:HG13	2.16	0.44
4:F:305:ILE:C	4:F:306:LEU:HD12	2.42	0.44
4:G:263:LEU:HD12	4:G:336:VAL:HG11	2.00	0.44
1:A:35:GLN:NE2	1:A:81:LEU:HD22	2.32	0.44
1:A:93:ILE:HG12	1:A:97:LEU:HG	1.99	0.44
2:C:114:ALA:HB2	2:C:149:HIS:ND1	2.31	0.44
3:E:239:GLU:CD	3:E:308:ARG:HH12	2.25	0.44
4:F:280:GLY:CA	4:F:319:PHE:O	2.66	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:122:TRP:HZ2	4:G:224:ARG:HG3	1.81	0.44
4:G:258:ALA:O	4:G:336:VAL:HG12	2.17	0.44
4:F:203:LEU:HG	4:F:206:MET:HE2	1.98	0.44
2:B:179:ASP:O	2:B:183:ILE:HG13	2.18	0.44
2:C:106:ASP:HA	2:C:109:ASP:OD2	2.18	0.44
3:E:88:LEU:HD21	3:E:93:VAL:HG13	2.00	0.44
4:G:341:THR:HG1	4:G:345:SER:HG	1.53	0.44
1:A:228:ARG:NH1	1:A:232:ILE:HD11	2.32	0.44
2:C:10:TRP:CG	2:C:190:ILE:HD12	2.53	0.44
2:D:126:ASP:OD1	2:D:126:ASP:N	2.49	0.44
4:F:171:ALA:O	4:F:177:LEU:HD12	2.18	0.44
4:G:159:LEU:HD22	4:G:241:PHE:HB3	2.00	0.44
1:A:156:LYS:HD3	1:A:156:LYS:HA	1.84	0.44
2:C:259:ALA:HA	2:C:357:LEU:CD1	2.48	0.44
2:D:347:MET:HG2	2:D:351:MET:HE2	2.00	0.44
4:G:286:SER:C	4:G:310:TYR:HD2	2.26	0.44
4:G:289:GLN:HE21	4:G:305:ILE:HD12	1.82	0.44
2:B:176:LYS:HD2	2:B:176:LYS:HA	1.70	0.44
2:B:235:GLN:O	2:B:238:SER:OG	2.36	0.44
3:E:63:ARG:HA	3:E:66:GLN:HB3	1.99	0.44
4:G:255:HIS:C	4:G:256:LEU:HD12	2.43	0.44
2:B:87:PHE:CE2	2:B:89:ASP:HB2	2.53	0.44
2:B:351:MET:HG2	2:C:329:TYR:CE1	2.53	0.44
2:C:229:ASP:HA	2:D:34:LEU:HD11	1.99	0.44
3:E:176:LEU:HB3	3:E:187:LEU:HD12	1.99	0.44
4:F:331:LEU:O	4:F:332:LYS:HG3	2.17	0.44
4:G:275:ASN:O	4:G:279:ARG:HG2	2.18	0.44
2:B:98:ARG:NH1	2:B:103:ASP:OD2	2.51	0.44
2:B:187:LEU:HD11	2:B:221:THR:HG21	1.99	0.44
2:B:254:GLU:HG3	2:B:316:LEU:HD21	1.99	0.44
2:C:143:LEU:HD23	2:C:152:PHE:HD2	1.83	0.44
3:E:2:ARG:HH22	3:E:179:GLU:CD	2.25	0.44
4:F:37:VAL:HB	4:F:65:PRO:HA	2.00	0.44
4:F:285:VAL:HB	4:F:315:MET:HB3	2.00	0.44
1:A:162:LEU:HA	1:A:197:LEU:HB2	2.00	0.43
2:C:291:ARG:NH1	2:C:301:ALA:O	2.51	0.43
3:E:117:ALA:HB2	3:E:143:LEU:HD23	2.00	0.43
4:G:254:LYS:HE3	4:G:315:MET:SD	2.58	0.43
2:B:27:ALA:HA	2:B:30:ASN:HD21	1.84	0.43
3:E:101:ASN:ND2	4:G:153:TYR:HB2	2.31	0.43
3:E:192:ARG:NH1	3:E:264:GLN:OE1	2.45	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:14:LEU:HD21	4:F:75:PHE:HD2	1.81	0.43
4:F:29:ILE:HG22	4:F:111:LEU:HD13	1.99	0.43
4:F:254:LYS:O	4:F:339:MET:HA	2.18	0.43
4:F:338:MET:HG3	4:F:349:ILE:HG12	2.01	0.43
2:B:11:ARG:HA	6:B:402:ADP:O3'	2.17	0.43
2:B:248:GLN:HG3	2:B:274:ARG:HH22	1.82	0.43
2:C:289:LEU:O	2:C:292:ILE:HG22	2.18	0.43
2:D:143:LEU:HD23	2:D:143:LEU:HA	1.80	0.43
3:E:25:HIS:CD2	3:E:135:PRO:HG3	2.54	0.43
4:F:144:PHE:CZ	4:F:327:VAL:HA	2.52	0.43
4:F:258:ALA:HB3	4:F:308:VAL:HG22	2.00	0.43
2:B:0:HIS:O	2:B:1:MET:HB3	2.18	0.43
2:C:278:TRP:CE2	2:C:346:ARG:HB2	2.53	0.43
2:C:282:LEU:HD23	2:C:282:LEU:HA	1.82	0.43
4:G:266:ALA:HB1	4:G:306:LEU:HD11	1.99	0.43
3:E:167:PRO:HG2	3:E:172:ALA:HB2	2.00	0.43
4:F:4:THR:O	4:F:61:GLN:NE2	2.51	0.43
2:C:126:ASP:O	2:C:127:GLU:HG3	2.18	0.43
3:E:54:GLN:HB3	3:E:57:LYS:HB2	2.00	0.43
2:C:23:HIS:NE2	2:C:174:HIS:O	2.49	0.43
3:E:209:ASN:HB3	3:E:247:TRP:HH2	1.83	0.43
2:B:21:GLN:HA	2:B:23:HIS:CE1	2.53	0.43
2:C:202:ALA:HB1	2:C:237:VAL:HG21	2.01	0.43
2:C:289:LEU:HD23	2:C:289:LEU:HA	1.83	0.43
2:D:77:ASP:O	2:D:80:ARG:N	2.52	0.43
2:D:344:ASP:OD1	2:D:345:ARG:N	2.51	0.43
3:E:26:ALA:HB1	3:E:159:CYS:SG	2.59	0.43
3:E:164:LEU:HD23	3:E:164:LEU:HA	1.84	0.43
4:G:130:LEU:O	4:G:214:LEU:HB2	2.19	0.43
1:A:39:ARG:CZ	1:A:50:HIS:HB3	2.49	0.43
2:B:147:PRO:HD2	2:B:150:VAL:HG21	2.00	0.43
2:C:200:PRO:HA	2:C:203:LEU:HD12	2.00	0.43
3:E:128:LEU:O	3:E:132:LEU:HD23	2.19	0.43
3:E:239:GLU:HA	3:E:308:ARG:NH1	2.33	0.43
4:F:141:ALA:HB1	4:F:359:TYR:OH	2.18	0.43
4:F:170:VAL:HA	4:F:178:ALA:O	2.18	0.43
1:A:18:ARG:HB3	1:A:133:ARG:O	2.19	0.43
4:F:160:PHE:HB2	4:F:193:VAL:HG12	2.01	0.43
4:F:206:MET:HE3	4:F:227:VAL:HG21	2.01	0.43
1:A:62:ASN:HA	1:A:65:PHE:HD1	1.84	0.42
2:B:241:LEU:O	2:B:244:LEU:HG	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:4:GLN:CG	2:C:9:LYS:HB2	2.48	0.42
3:E:63:ARG:HG2	4:G:119:LEU:HD13	2.00	0.42
4:F:170:VAL:HG22	4:F:179:VAL:HG23	2.00	0.42
2:B:306:MET:HG2	2:B:309:ILE:HD12	2.01	0.42
2:C:2:SER:O	2:C:3:TYR:CD1	2.73	0.42
2:C:297:LEU:HD12	2:C:298:SER:HB3	2.02	0.42
2:C:302:LEU:HB3	2:C:306:MET:HB2	2.01	0.42
2:D:205:LEU:HD22	2:D:237:VAL:HG13	2.01	0.42
4:F:275:ASN:HB3	4:F:278:PHE:O	2.19	0.42
4:F:339:MET:HE2	4:F:348:GLN:HB3	2.01	0.42
4:G:165:GLU:HB2	4:G:185:GLY:H	1.83	0.42
4:G:207:LEU:HD12	4:G:207:LEU:O	2.18	0.42
1:A:30:LEU:HB2	1:A:139:CYS:SG	2.58	0.42
1:A:200:PRO:O	1:A:204:GLN:NE2	2.52	0.42
1:A:237:ARG:HG3	1:A:321:TRP:CD1	2.55	0.42
2:B:127:GLU:HB3	2:B:129:HIS:HE1	1.85	0.42
2:C:57:LEU:HA	2:C:60:LYS:HZ3	1.83	0.42
3:E:1:MET:SD	3:E:1:MET:N	2.92	0.42
4:F:144:PHE:HZ	4:F:327:VAL:HA	1.84	0.42
2:B:278:TRP:CE3	2:B:349:VAL:HG21	2.54	0.42
4:G:272:ILE:HG22	4:G:273:LEU:HG	2.01	0.42
1:A:249:THR:HA	1:A:252:ARG:NE	2.33	0.42
1:A:316:TYR:HB3	1:A:318:GLN:HG2	2.01	0.42
2:B:36:ARG:HD2	2:B:36:ARG:HA	1.78	0.42
2:B:89:ASP:OD1	2:B:116:ALA:N	2.44	0.42
2:D:15:PHE:CZ	2:D:28:LEU:HD23	2.54	0.42
3:E:25:HIS:HA	3:E:140:TRP:CD1	2.55	0.42
4:F:59:LEU:HB3	4:F:63:HIS:ND1	2.34	0.42
1:A:23:LEU:N	1:A:112:VAL:O	2.49	0.42
2:B:142:THR:HG23	2:B:152:PHE:HE2	1.85	0.42
2:C:47:ARG:NH1	2:C:213:SER:OG	2.53	0.42
2:C:335:GLY:HA2	2:C:338:GLU:OE2	2.20	0.42
3:E:147:GLU:N	3:E:147:GLU:OE1	2.52	0.42
4:F:16:GLN:NE2	4:F:206:MET:HB2	2.35	0.42
4:F:175:HIS:HB2	4:F:323:TYR:CD2	2.55	0.42
4:F:346:SER:HB3	4:F:360:VAL:HG13	2.00	0.42
4:G:268:ALA:HA	4:G:325:LEU:HD11	2.00	0.42
1:A:169:VAL:HG13	1:A:170:LEU:HD22	2.02	0.42
2:B:351:MET:HE3	2:C:329:TYR:CD2	2.55	0.42
2:C:288:LEU:HD12	2:C:288:LEU:HA	1.87	0.42
2:D:282:LEU:HD23	2:D:282:LEU:HA	1.75	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:37:ASP:OD1	3:E:37:ASP:N	2.53	0.42
1:A:20:ALA:HA	1:A:110:LEU:HB2	2.02	0.42
2:C:42:LEU:HD23	2:C:172:GLN:HG2	2.01	0.42
2:D:19:VAL:N	6:D:401:ADP:N1	2.52	0.42
3:E:212:ALA:O	3:E:215:THR:HB	2.20	0.42
4:F:3:PHE:HA	4:F:63:HIS:CD2	2.54	0.42
4:F:170:VAL:HG11	4:F:244:TYR:HB3	2.01	0.42
4:F:250:LYS:HD3	4:F:346:SER:HB2	2.02	0.42
4:G:130:LEU:HD11	4:G:184:ILE:HD12	2.01	0.42
3:E:99:LYS:O	3:E:102:GLU:HG2	2.19	0.41
4:F:265:GLN:HB3	4:F:269:ARG:NH1	2.35	0.41
1:A:322:ALA:O	1:A:325:GLU:HG3	2.20	0.41
2:B:287:GLY:O	2:B:291:ARG:HG2	2.21	0.41
2:D:220:LEU:HD22	2:D:240:MET:HE1	2.02	0.41
2:D:263:ARG:O	2:D:267:LEU:HG	2.20	0.41
3:E:67:LEU:HD12	3:E:67:LEU:HA	1.83	0.41
4:F:96:ARG:HD3	4:F:107:SER:OG	2.21	0.41
4:F:128:PHE:CE1	4:F:130:LEU:HB2	2.55	0.41
4:G:218:ILE:HD11	4:G:223:ILE:HD12	2.00	0.41
2:B:62:LEU:HD21	2:B:151:LYS:HG3	2.02	0.41
2:C:179:ASP:OD1	2:C:180:VAL:N	2.54	0.41
2:C:289:LEU:HA	2:C:292:ILE:HG22	2.02	0.41
4:F:1:MET:O	4:F:91:GLN:HA	2.19	0.41
4:G:254:LYS:NZ	4:G:341:THR:O	2.53	0.41
4:G:263:LEU:HD23	4:G:306:LEU:HD22	2.01	0.41
1:A:71:MET:HG2	1:A:71:MET:O	2.20	0.41
3:E:209:ASN:HB3	3:E:247:TRP:CH2	2.56	0.41
4:F:257:GLU:O	4:F:308:VAL:HG13	2.20	0.41
4:G:150:ASP:OD1	4:G:151:VAL:N	2.53	0.41
1:A:23:LEU:HB2	1:A:113:ARG:HA	2.02	0.41
3:E:49:LEU:HD23	3:E:109:ALA:HB3	2.02	0.41
3:E:133:GLU:HB2	3:E:158:ARG:HE	1.83	0.41
2:B:47:ARG:H	2:B:157:THR:HG23	1.85	0.41
2:C:71:THR:N	2:C:72:PRO:HD2	2.35	0.41
2:D:140:LEU:HD22	2:D:169:ARG:CZ	2.50	0.41
4:F:7:ARG:CZ	4:F:11:LEU:HD11	2.51	0.41
4:G:214:LEU:O	4:G:216:VAL:HG23	2.21	0.41
1:A:106:ASP:OD1	1:A:106:ASP:N	2.53	0.41
2:C:280:ALA:HA	2:C:283:VAL:HG22	2.01	0.41
4:F:103:ARG:NH1	4:G:307:ASP:OD1	2.51	0.41
1:A:78:GLN:O	1:A:108:LEU:HA	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:90:ASN:H	1:A:93:ILE:HG22	1.85	0.41
2:B:42:LEU:HD13	2:B:154:LEU:HB3	2.02	0.41
2:B:320:ILE:HA	2:B:321:PRO:HD3	1.92	0.41
2:D:121:LYS:HE3	2:D:149:HIS:HE1	1.86	0.41
4:F:146:MET:HB2	4:F:197:ARG:HD3	2.03	0.41
4:F:175:HIS:HB2	4:F:323:TYR:HE2	1.86	0.41
4:G:153:TYR:HE2	4:G:238:ASP:O	2.03	0.41
1:A:20:ALA:HB3	1:A:134:SER:HB3	2.03	0.41
1:A:219:ASP:OD1	1:A:285:MET:HG3	2.21	0.41
1:A:299:ARG:HD3	3:E:317:LEU:O	2.20	0.41
2:B:10:TRP:CH2	2:B:193:GLU:HB3	2.55	0.41
2:C:5:VAL:HB	2:C:8:ARG:HB2	2.02	0.41
2:C:256:MET:HG3	2:C:357:LEU:HD22	2.03	0.41
2:C:332:LEU:HD23	2:C:352:THR:HG22	2.03	0.41
2:C:349:VAL:O	2:C:353:LEU:HD23	2.20	0.41
2:D:51:LYS:HE2	2:D:51:LYS:HB2	1.93	0.41
3:E:105:ARG:HG3	3:E:106:LEU:HD23	2.03	0.41
2:D:268:ILE:HD13	2:D:268:ILE:HA	1.85	0.41
4:F:323:TYR:O	4:F:327:VAL:HG23	2.21	0.41
4:G:125:GLU:HG2	4:G:126:VAL:HG23	2.02	0.41
2:C:19:VAL:HG23	2:C:178:LEU:HD21	2.03	0.40
3:E:308:ARG:O	3:E:312:ILE:HG13	2.21	0.40
4:F:3:PHE:O	4:F:89:ALA:HA	2.20	0.40
4:F:105:ARG:HH21	4:G:303:GLU:CD	2.28	0.40
4:F:161:GLU:CD	4:F:244:TYR:HE1	2.29	0.40
4:G:130:LEU:CD1	4:G:184:ILE:HD12	2.51	0.40
1:A:10:ARG:HH21	1:A:37:ALA:HB1	1.86	0.40
2:B:15:PHE:CD1	2:B:57:LEU:HD13	2.56	0.40
2:B:104:THR:O	2:B:108:LEU:HG	2.22	0.40
2:B:265:MET:O	2:B:268:ILE:HG22	2.21	0.40
2:C:3:TYR:HB3	2:D:35:GLY:O	2.21	0.40
2:C:166:ILE:HA	2:C:169:ARG:HG2	2.02	0.40
2:D:332:LEU:HD21	2:D:353:LEU:HD23	2.03	0.40
4:G:147:ALA:HB1	4:G:150:ASP:HB2	2.03	0.40
1:A:279:TRP:O	1:A:283:ARG:HG3	2.21	0.40
2:B:105:ARG:HA	2:B:108:LEU:HD12	2.03	0.40
2:C:21:GLN:HA	2:C:23:HIS:CE1	2.55	0.40
2:C:40:ALA:HB3	2:C:170:CYS:HB2	2.02	0.40
4:G:145:SER:HA	4:G:176:ARG:NH2	2.37	0.40
2:B:10:TRP:HH2	2:B:193:GLU:HB3	1.85	0.40
3:E:233:LEU:HG	3:E:316:LEU:HD12	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:283:VAL:O	2:B:286:LEU:HG	2.21	0.40
2:C:88:VAL:O	2:C:88:VAL:HG23	2.22	0.40
2:C:89:ASP:OD1	2:C:116:ALA:HB3	2.22	0.40
2:C:286:LEU:HA	2:C:286:LEU:HD23	1.78	0.40
2:D:245:ASP:OD1	2:D:245:ASP:N	2.53	0.40
4:F:260:CYS:N	4:F:334:GLU:O	2.31	0.40
4:G:162:THR:HG23	4:G:189:PRO:O	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	331/333 (99%)	303 (92%)	25 (8%)	3 (1%)	14	47
2	B	369/376 (98%)	356 (96%)	13 (4%)	0	100	100
2	C	368/376 (98%)	347 (94%)	18 (5%)	3 (1%)	16	50
2	D	361/376 (96%)	345 (96%)	16 (4%)	0	100	100
3	E	335/337 (99%)	318 (95%)	17 (5%)	0	100	100
4	F	367/369 (100%)	333 (91%)	32 (9%)	2 (0%)	24	59
4	G	246/369 (67%)	232 (94%)	14 (6%)	0	100	100
All	All	2377/2536 (94%)	2234 (94%)	135 (6%)	8 (0%)	37	69

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	71	THR
1	A	212	PHE
4	F	258	ALA
2	C	3	TYR

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Mol	Chain	Res	Type
2	C	5	VAL
1	A	213	THR
4	F	208	ASP
1	A	214	PRO

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	283/283 (100%)	283 (100%)	0	100	100
2	B	307/312 (98%)	307 (100%)	0	100	100
2	C	306/312 (98%)	306 (100%)	0	100	100
2	D	299/312 (96%)	299 (100%)	0	100	100
3	E	272/272 (100%)	272 (100%)	0	100	100
4	F	315/315 (100%)	315 (100%)	0	100	100
4	G	215/315 (68%)	215 (100%)	0	100	100
All	All	1997/2121 (94%)	1997 (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. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	140	GLN
1	A	216	HIS
2	B	0	HIS
2	B	23	HIS
2	B	137	ASN
2	B	182	GLN
2	B	195	HIS
2	B	223	GLN
2	B	248	GLN
2	B	296	GLN

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Mol	Chain	Res	Type
2	C	21	GLN
2	C	63	ASN
2	C	110	ASN
2	C	137	ASN
2	C	192	ASN
2	C	296	GLN
2	D	137	ASN
2	D	189	HIS
3	E	52	GLN
3	E	126	ASN
3	E	170	GLN
3	E	184	GLN
4	F	36	GLN
4	F	143	GLN
4	F	186	GLN
4	F	217	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 13 ligands modelled in this entry, 7 are monoatomic - leaving 6 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	BEF	B	403	6	0,3,3	-	-	-		
6	ADP	D	401	7,8	28,29,29	1.59	5 (17%)	43,45,45	1.70	12 (27%)
7	BEF	C	402	6	0,3,3	-	-	-		
7	BEF	D	402	6	0,3,3	-	-	-		
6	ADP	C	401	7,8	28,29,29	1.47	5 (17%)	43,45,45	1.88	10 (23%)
6	ADP	B	402	7,8	28,29,29	1.69	6 (21%)	43,45,45	1.75	13 (30%)

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	ADP	D	401	7,8	-	0/16/32/32	0/3/3/3
6	ADP	C	401	7,8	-	6/16/32/32	0/3/3/3
6	ADP	B	402	7,8	-	0/16/32/32	0/3/3/3

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	402	ADP	C5-C4	5.26	1.48	1.39
6	C	401	ADP	C5-C4	4.90	1.47	1.39
6	D	401	ADP	C5-C4	4.23	1.46	1.39
6	D	401	ADP	C5-N7	-3.41	1.32	1.39
6	B	402	ADP	PA-O3A	3.35	1.63	1.59
6	D	401	ADP	C4-N9	-3.27	1.30	1.37
6	B	402	ADP	C8-N7	2.45	1.36	1.31
6	B	402	ADP	C5-N7	-2.42	1.34	1.39
6	C	401	ADP	C8-N7	2.37	1.36	1.31
6	C	401	ADP	C5-C6	2.33	1.47	1.41
6	B	402	ADP	C5-C6	2.32	1.47	1.41
6	C	401	ADP	C4-N9	-2.08	1.33	1.37
6	B	402	ADP	C4-N9	-2.08	1.33	1.37
6	D	401	ADP	PA-O3A	2.05	1.61	1.59
6	D	401	ADP	C8-N9	-2.03	1.34	1.37
6	C	401	ADP	C5-N7	-2.00	1.35	1.39

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	C	401	ADP	C5-C4-N3	-5.13	119.65	126.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	B	402	ADP	C5-C4-N3	-4.64	120.33	126.72
6	C	401	ADP	N3-C4-N9	4.40	134.66	127.17
6	D	401	ADP	C5-C4-N3	-3.97	121.25	126.72
6	B	402	ADP	N3-C4-N9	3.75	133.54	127.17
6	D	401	ADP	N3-C4-N9	3.72	133.49	127.17
6	C	401	ADP	O2B-PB-O1B	3.53	124.58	110.83
6	C	401	ADP	C2-N3-C4	3.30	119.89	111.83
6	C	401	ADP	N3-C2-N1	-3.24	123.69	128.58
6	D	401	ADP	C4-N9-C8	3.21	109.11	105.74
6	B	402	ADP	C4-C5-N7	-2.83	107.35	110.58
6	D	401	ADP	O2B-PB-O1B	2.80	121.75	110.83
6	C	401	ADP	C4-N9-C8	2.79	108.67	105.74
6	C	401	ADP	C2'-C1'-N9	-2.69	106.63	113.30
6	D	401	ADP	N3-C2-N1	-2.66	124.55	128.58
6	B	402	ADP	O4'-C1'-N9	2.66	113.20	108.09
6	C	401	ADP	C2'-C3'-C4'	2.66	107.74	102.61
6	D	401	ADP	C2-N1-C6	2.60	123.00	118.73
6	D	401	ADP	O3'-C3'-C4'	-2.58	103.68	111.08
6	B	402	ADP	C2-N3-C4	2.56	118.08	111.83
6	C	401	ADP	C4-C5-N7	-2.55	107.66	110.58
6	D	401	ADP	N6-C6-N1	2.52	123.99	118.38
6	D	401	ADP	O3B-PB-O2B	-2.51	98.39	107.80
6	B	402	ADP	O2B-PB-O1B	2.44	120.35	110.83
6	C	401	ADP	C2-N1-C6	2.35	122.60	118.73
6	D	401	ADP	C2-N3-C4	2.28	117.39	111.83
6	B	402	ADP	C4-N9-C8	2.27	108.12	105.74
6	B	402	ADP	C2'-C1'-N9	-2.22	107.78	113.30
6	D	401	ADP	O2'-C2'-C1'	-2.22	102.45	110.10
6	B	402	ADP	O2'-C2'-C1'	-2.19	102.57	110.10
6	B	402	ADP	O3B-PB-O2B	-2.17	99.65	107.80
6	D	401	ADP	C4-C5-N7	-2.15	108.13	110.58
6	B	402	ADP	N3-C2-N1	-2.09	125.42	128.58
6	B	402	ADP	O5'-PA-O1A	-2.04	100.86	108.94
6	B	402	ADP	C5-N7-C8	2.02	106.62	103.45

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	C	401	ADP	PA-O3A-PB-O3B
6	C	401	ADP	C5'-O5'-PA-O1A
6	C	401	ADP	C5'-O5'-PA-O2A

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Mol	Chain	Res	Type	Atoms
6	C	401	ADP	C5'-O5'-PA-O3A
6	C	401	ADP	O4'-C4'-C5'-O5'
6	C	401	ADP	PA-O3A-PB-O2B

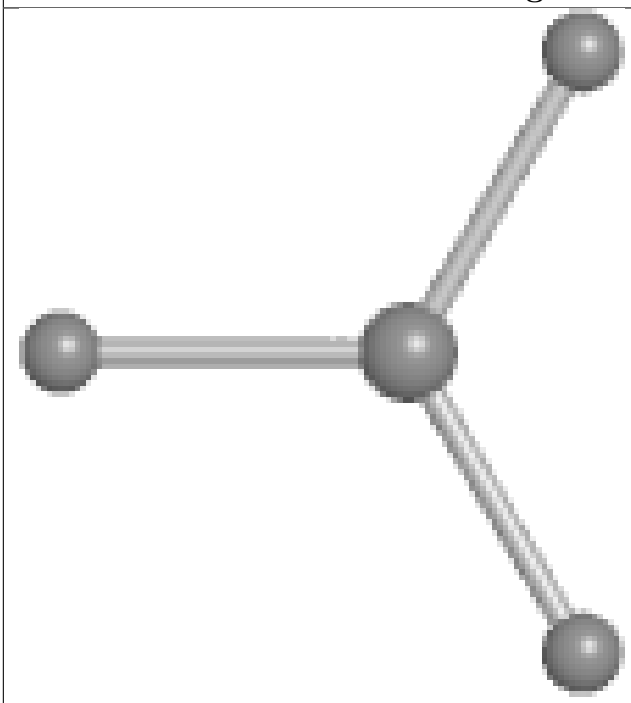
There are no ring outliers.

4 monomers are involved in 15 short contacts:

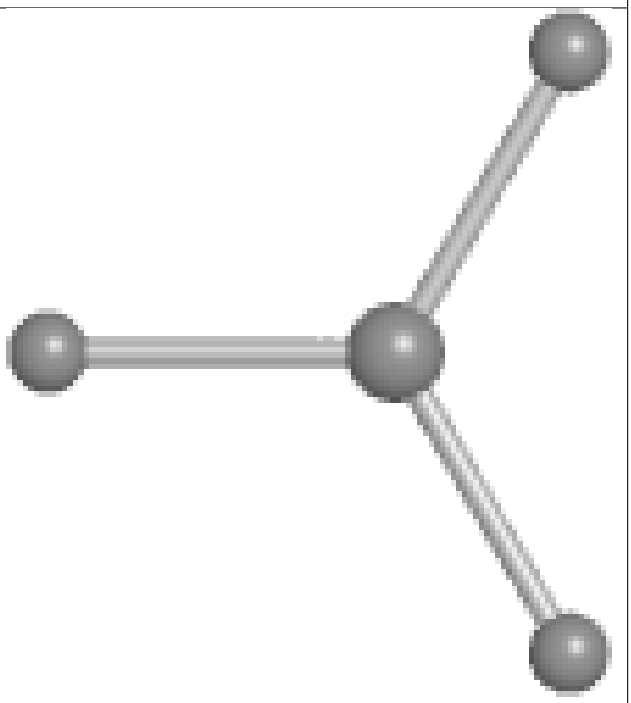
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	D	401	ADP	6	0
7	C	402	BEF	3	0
6	C	401	ADP	3	0
6	B	402	ADP	3	0

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

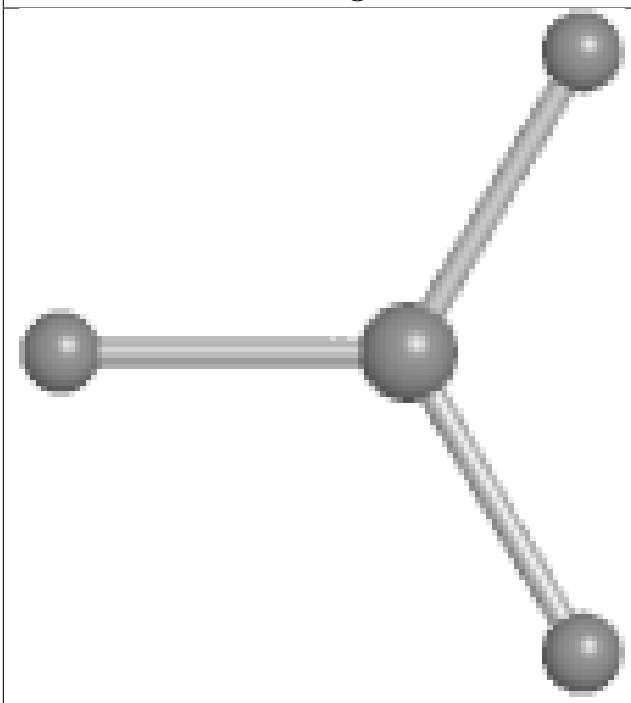
Ligand BEF B 403



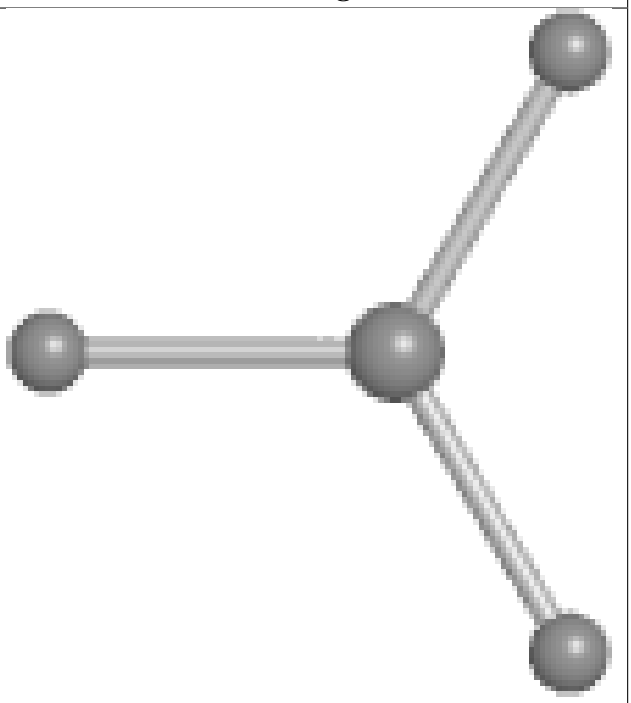
Bond lengths



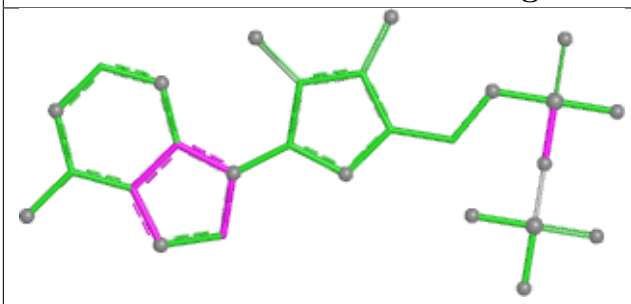
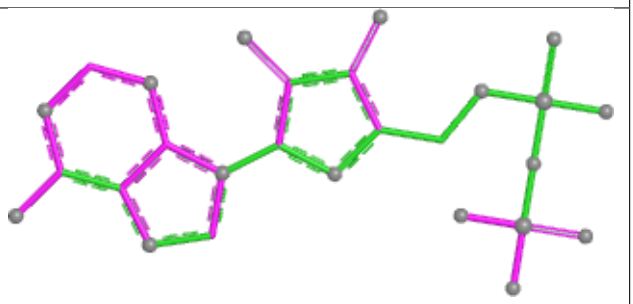
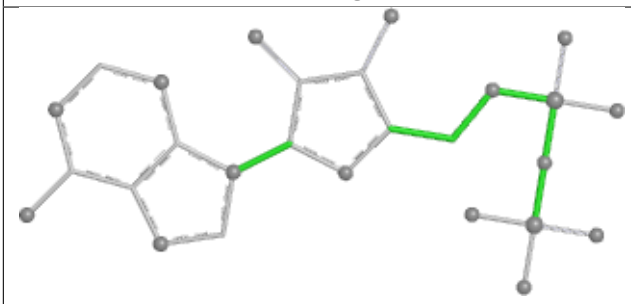
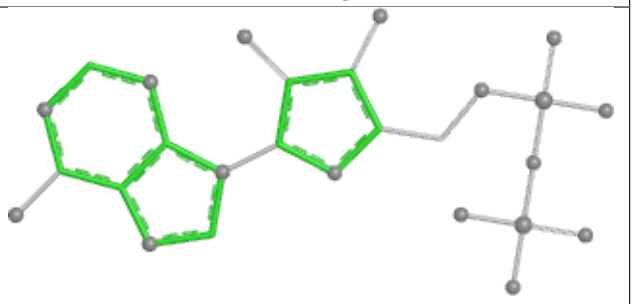
Bond angles

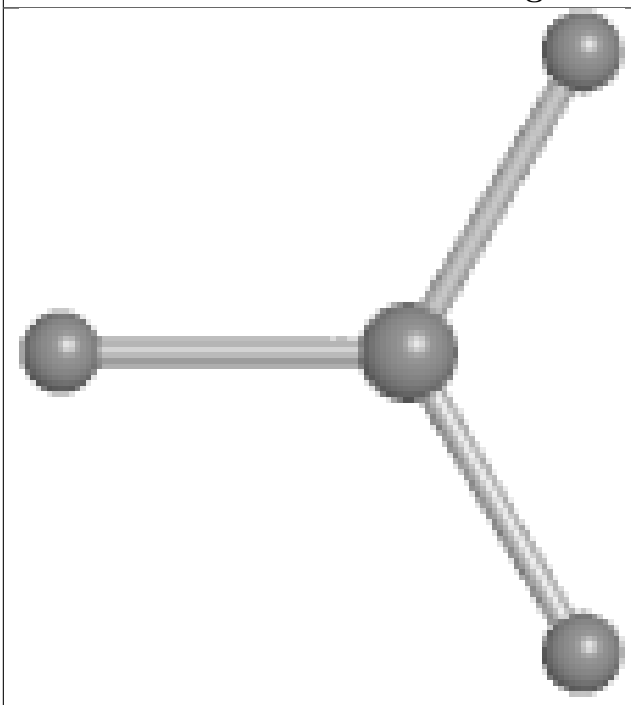
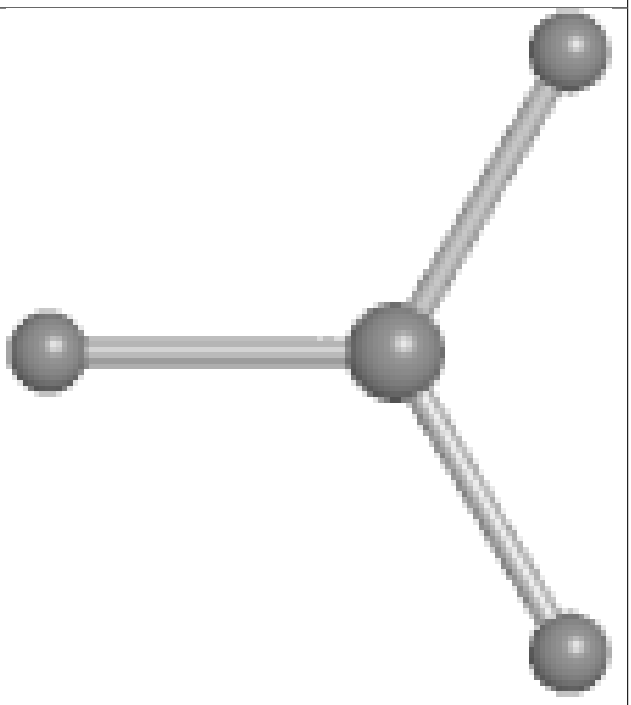
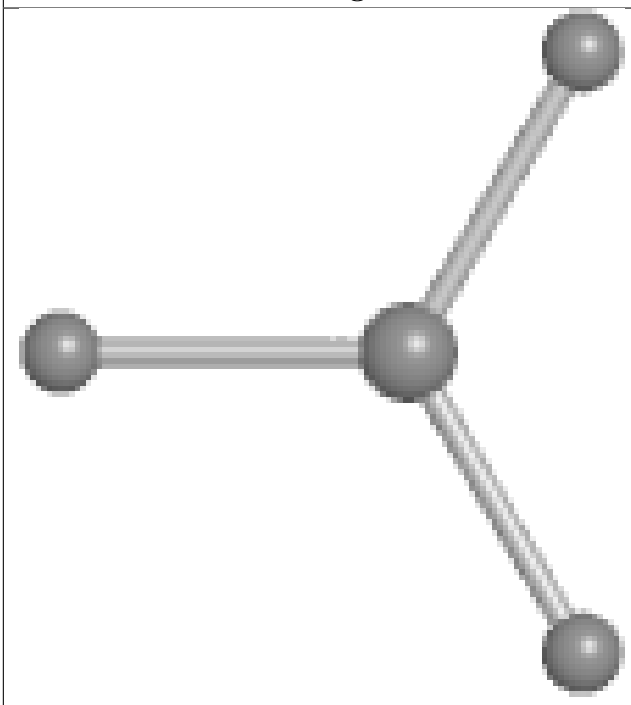
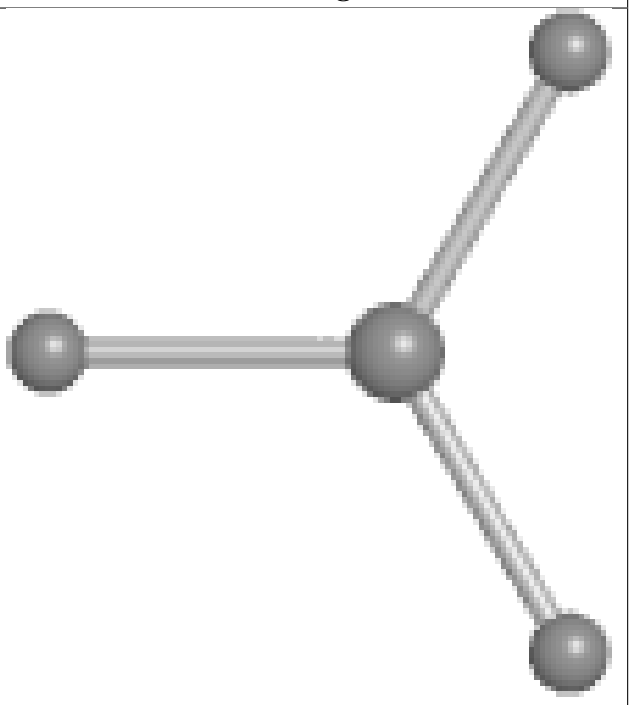


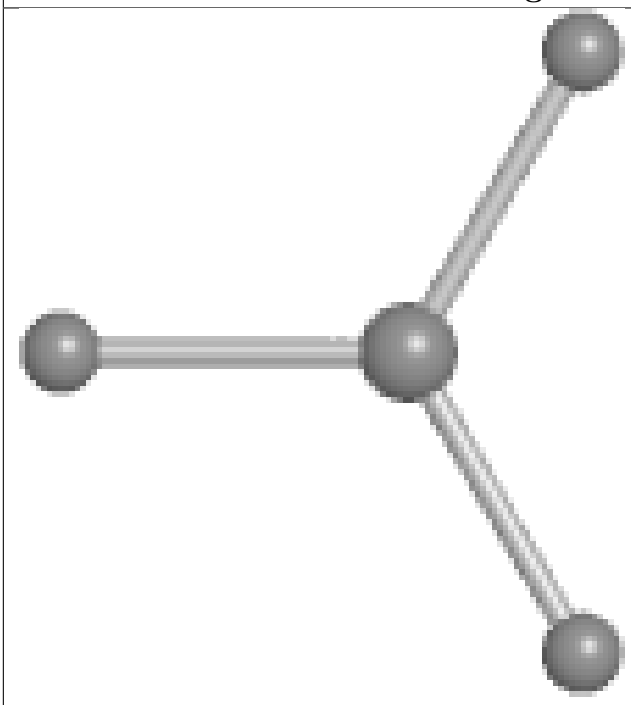
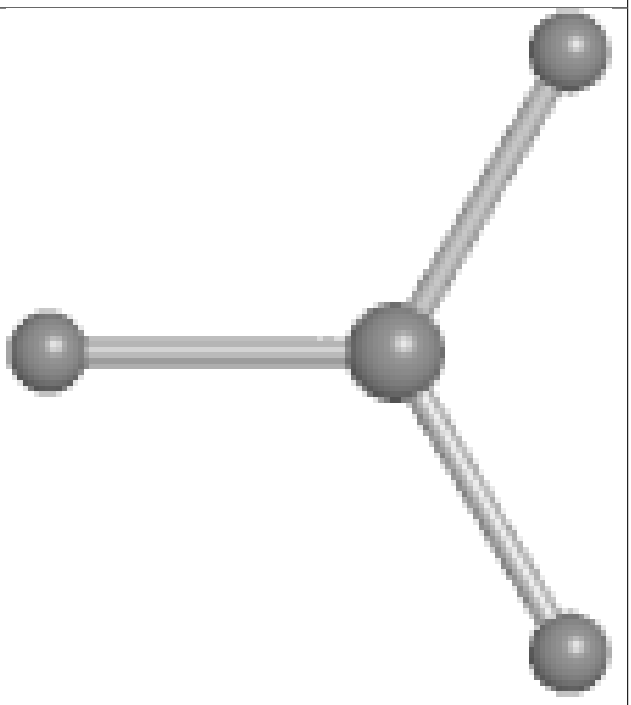
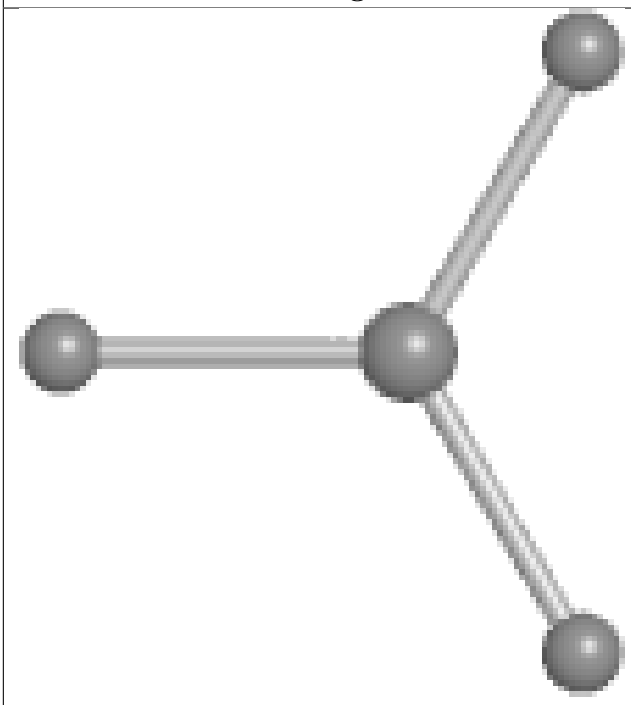
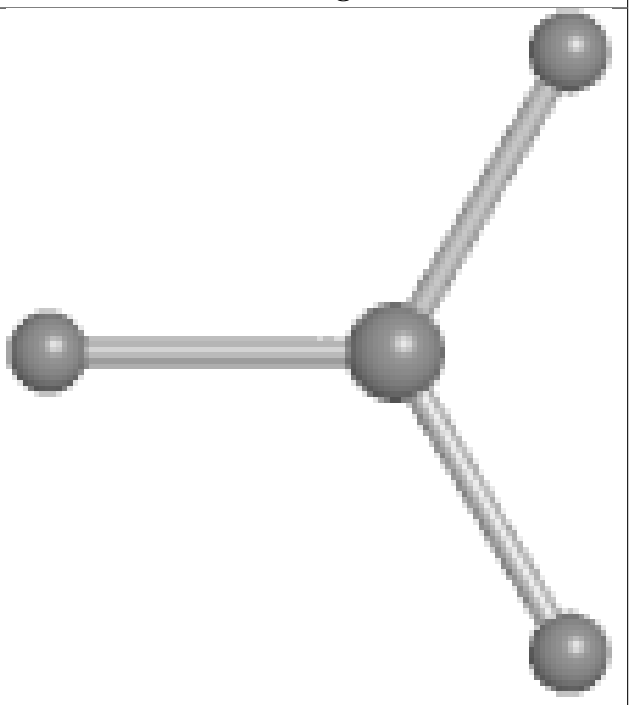
Torsions

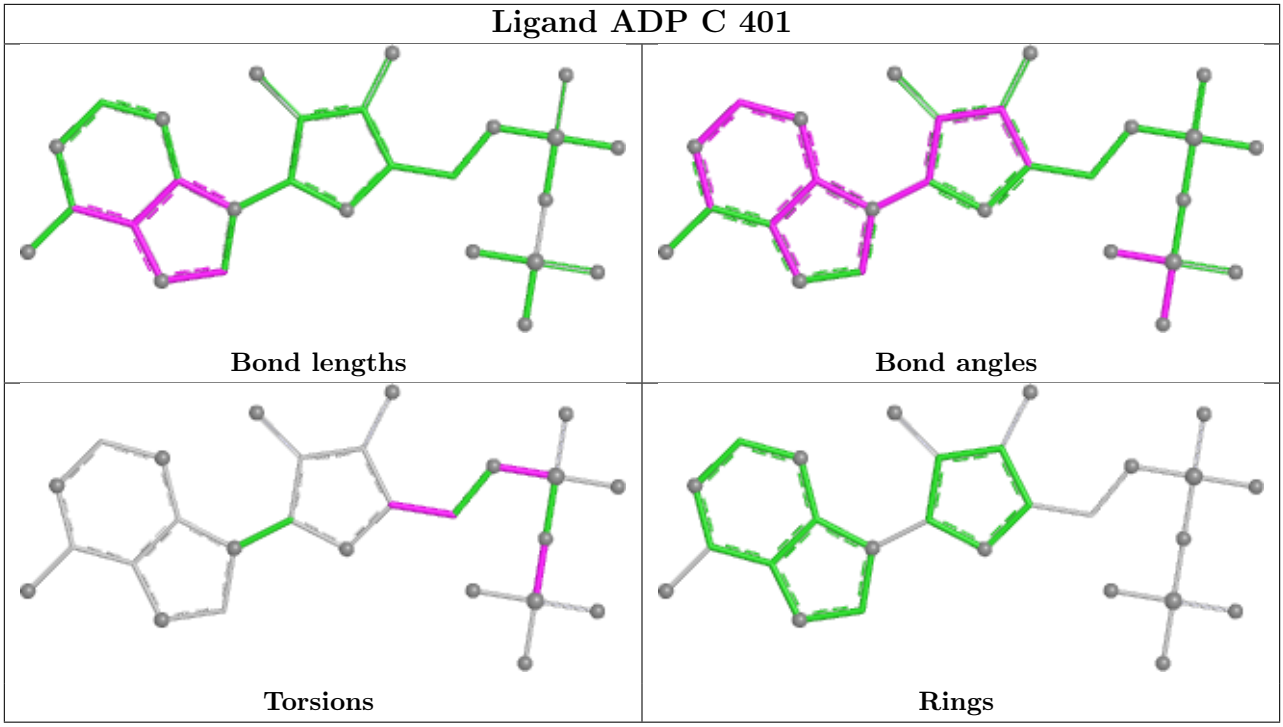


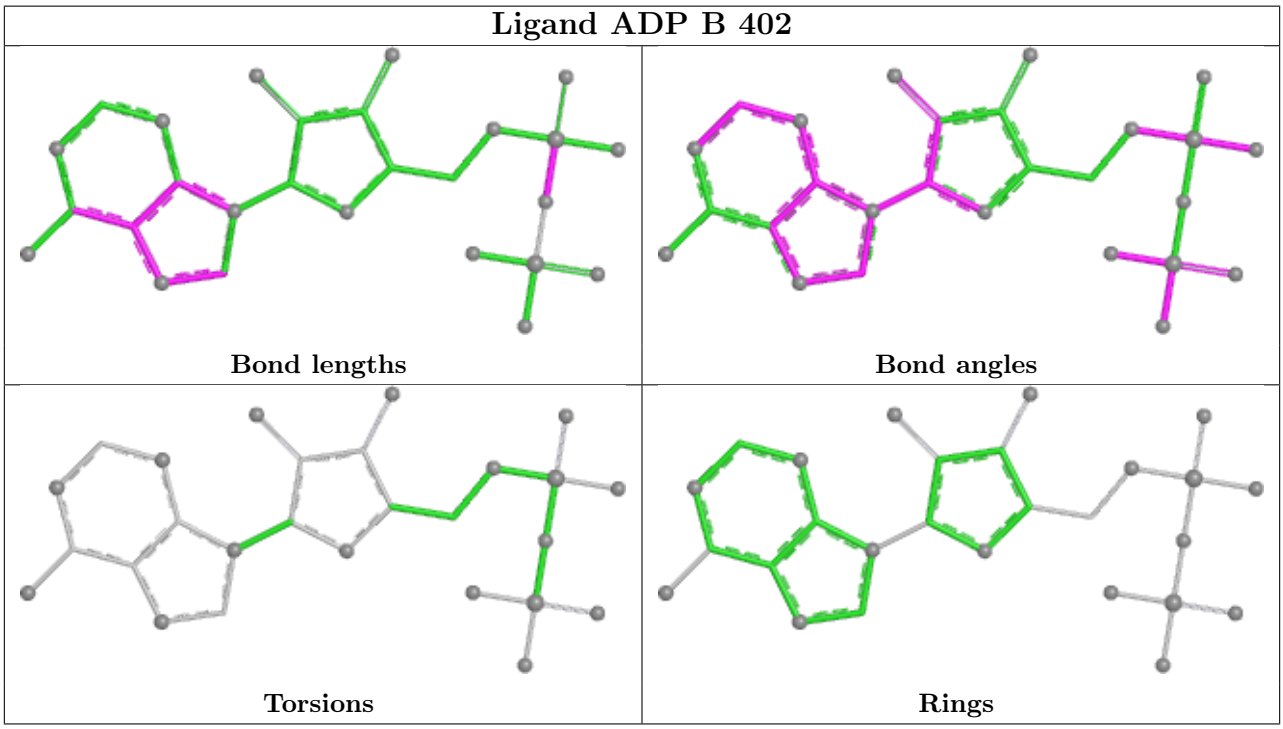
Rings

Ligand ADP D 401	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand BEF C 402	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand BEF D 402	
 Bond lengths	 Bond angles
 Torsions	 Rings





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.

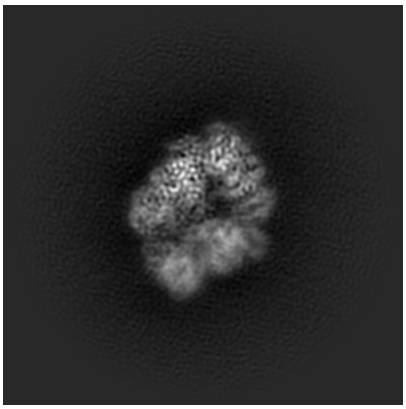
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-43095. These allow visual inspection of the internal detail of the map and identification of artifacts.

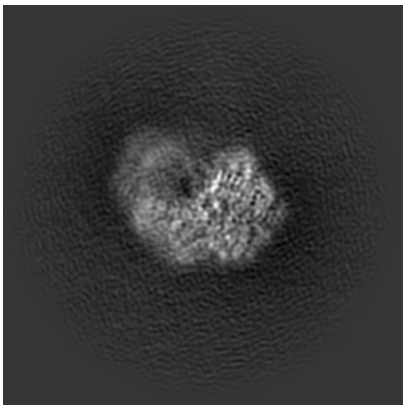
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

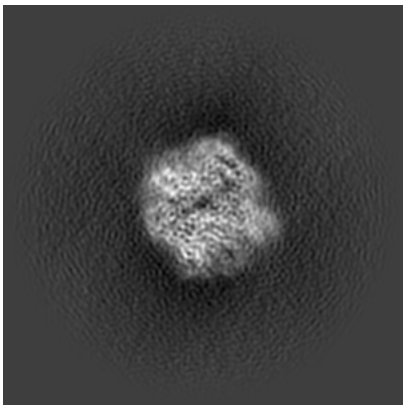
6.1.1 Primary map



X

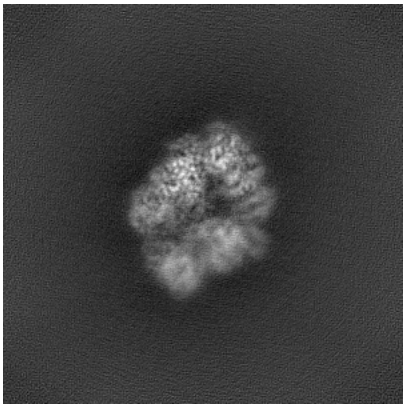


Y

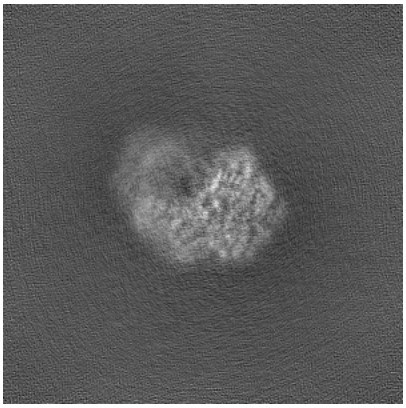


Z

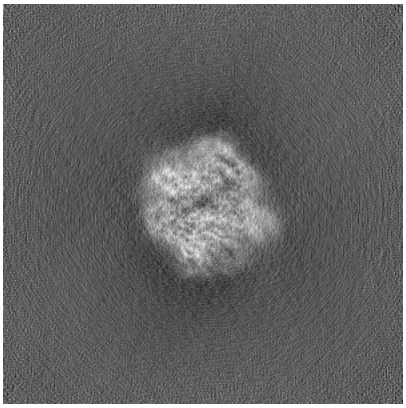
6.1.2 Raw map



X



Y

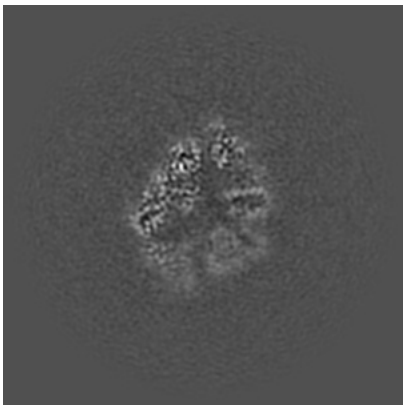


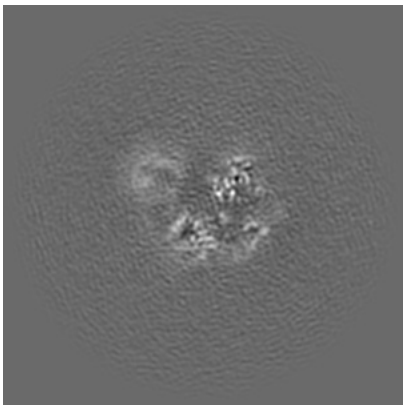
Z

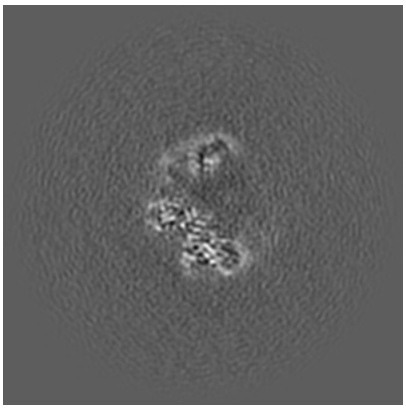
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

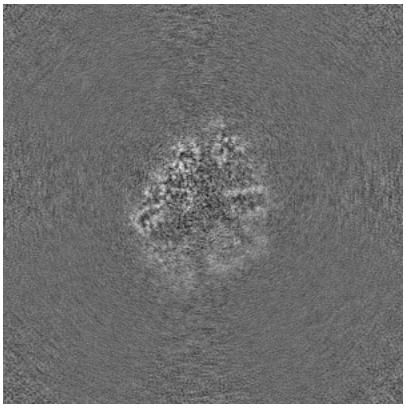
6.2.1 Primary map

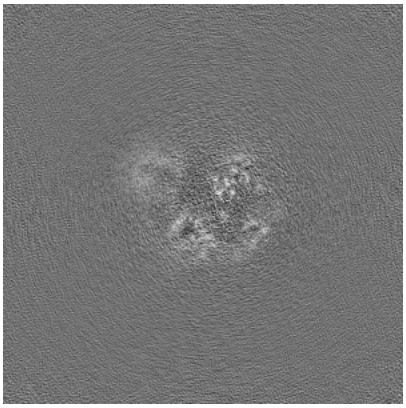

X Index: 176

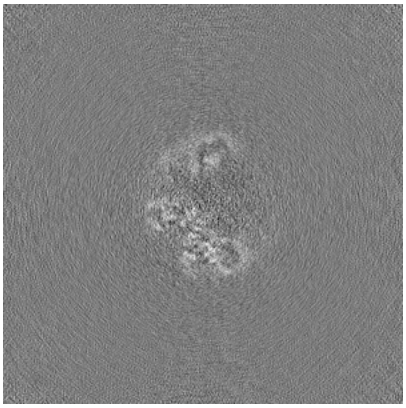

Y Index: 176


Z Index: 176

6.2.2 Raw map


X Index: 176

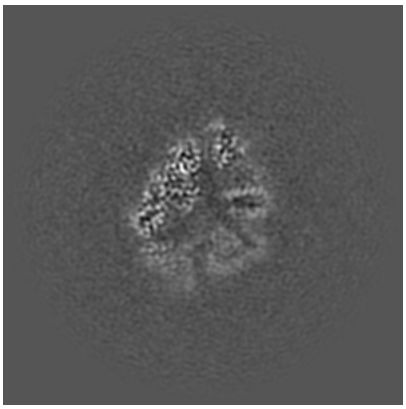

Y Index: 176

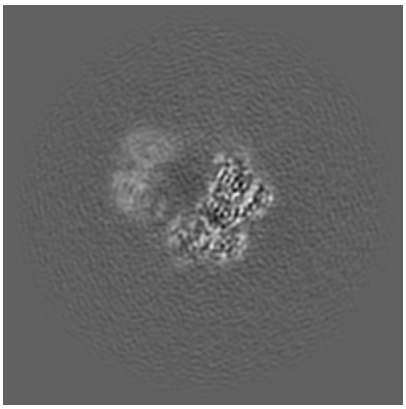

Z Index: 176

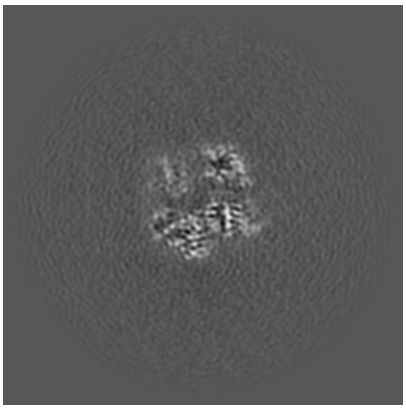
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

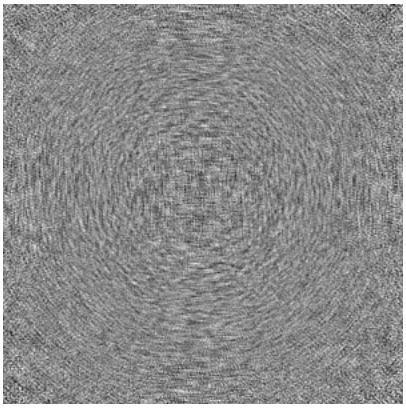
6.3.1 Primary map

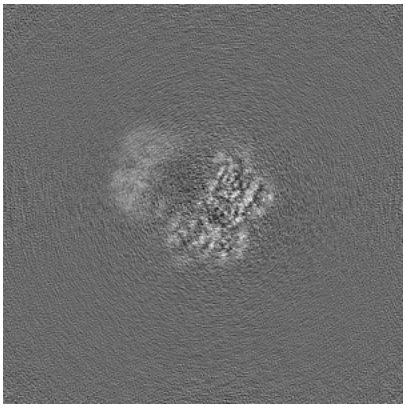

X Index: 175

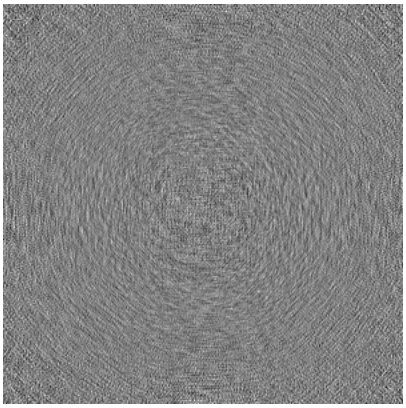

Y Index: 163


Z Index: 201

6.3.2 Raw map


X Index: 0

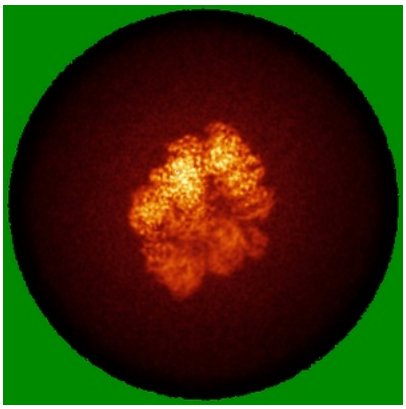

Y Index: 163

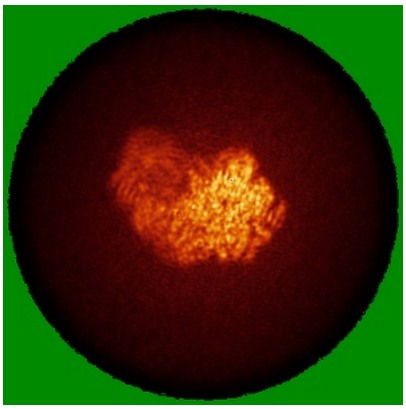

Z Index: 0

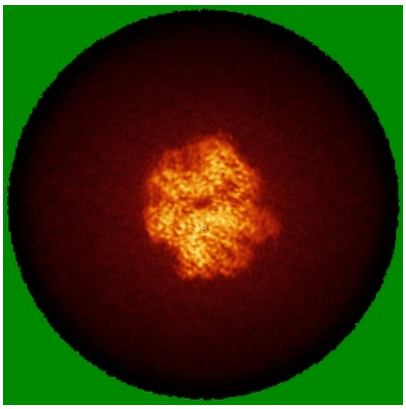
The images above show the largest variance slices of the map in three orthogonal directions.

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

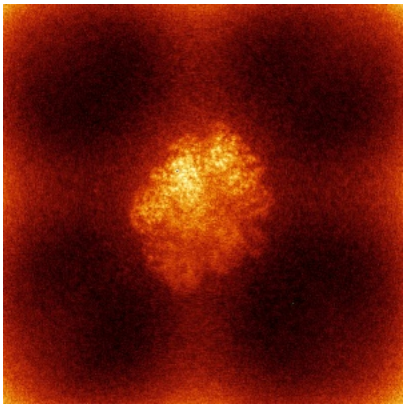
6.4.1 Primary map

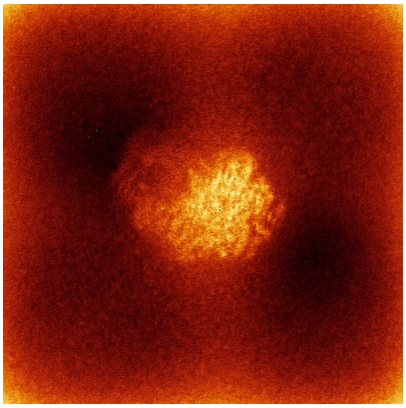

X

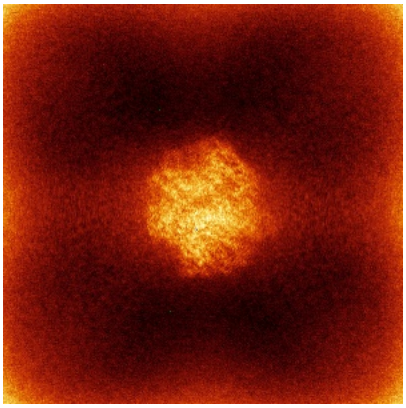

Y


Z

6.4.2 Raw map


X


Y


Z

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

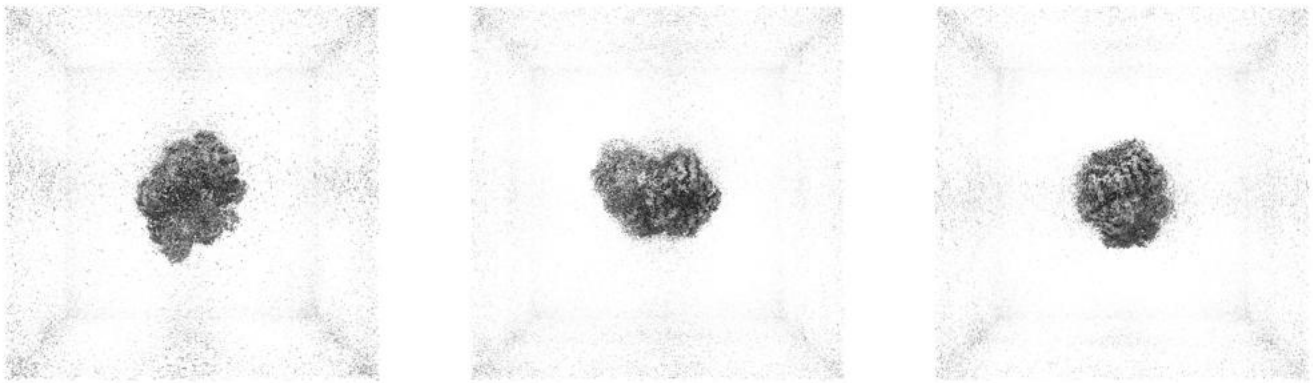
6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.09. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

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

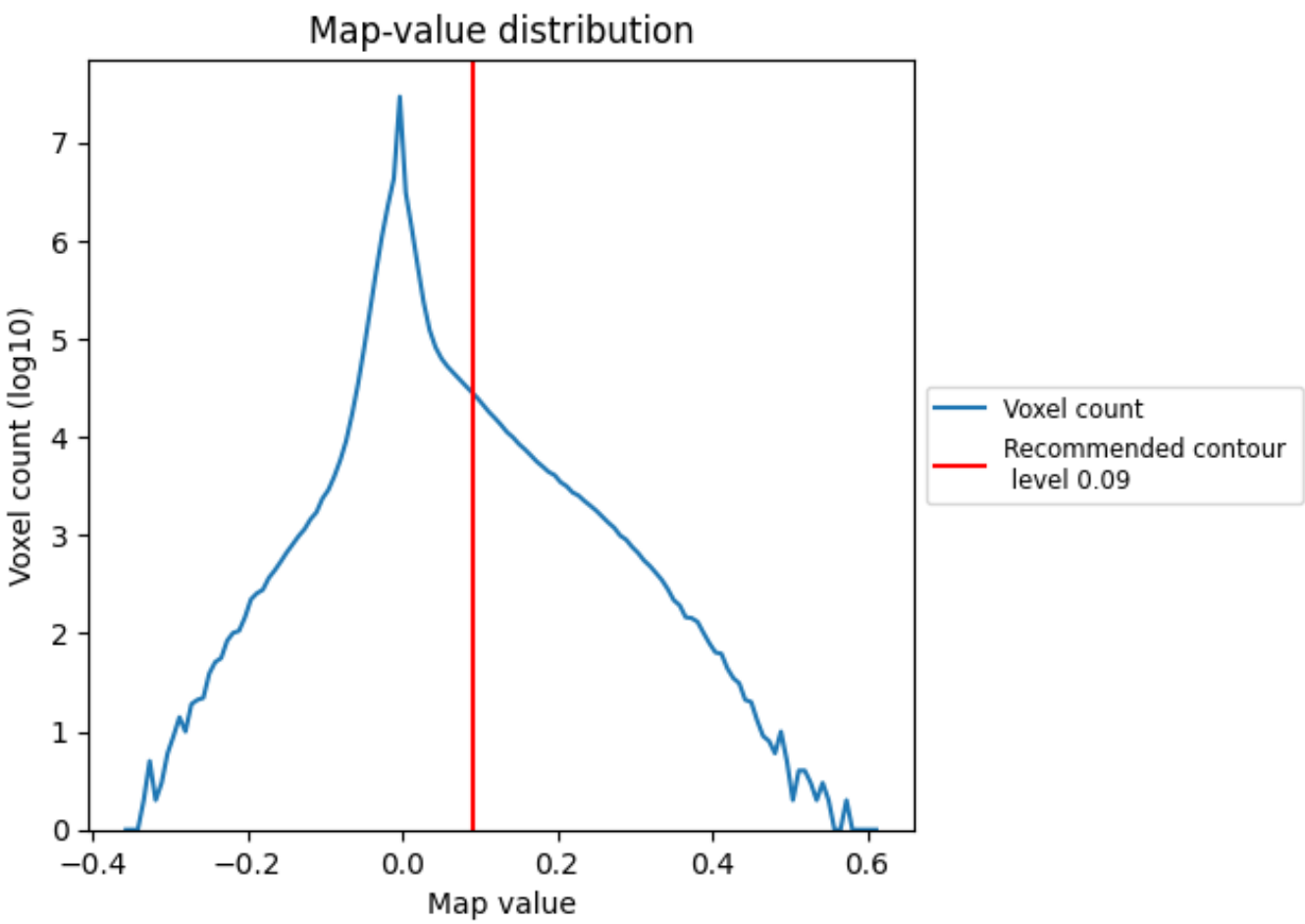
6.6 Mask visualisation (i)

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

7 Map analysis (i)

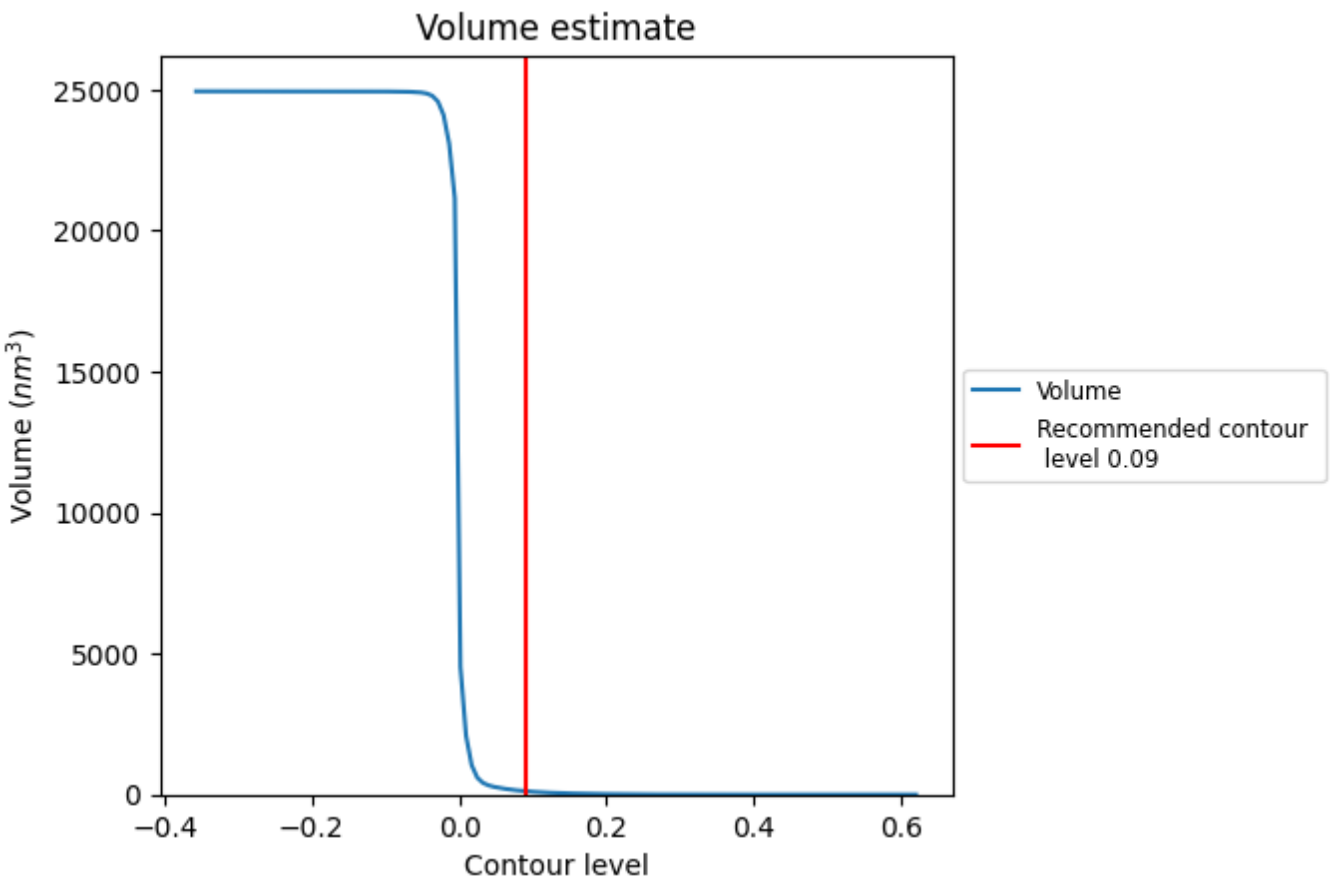
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



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

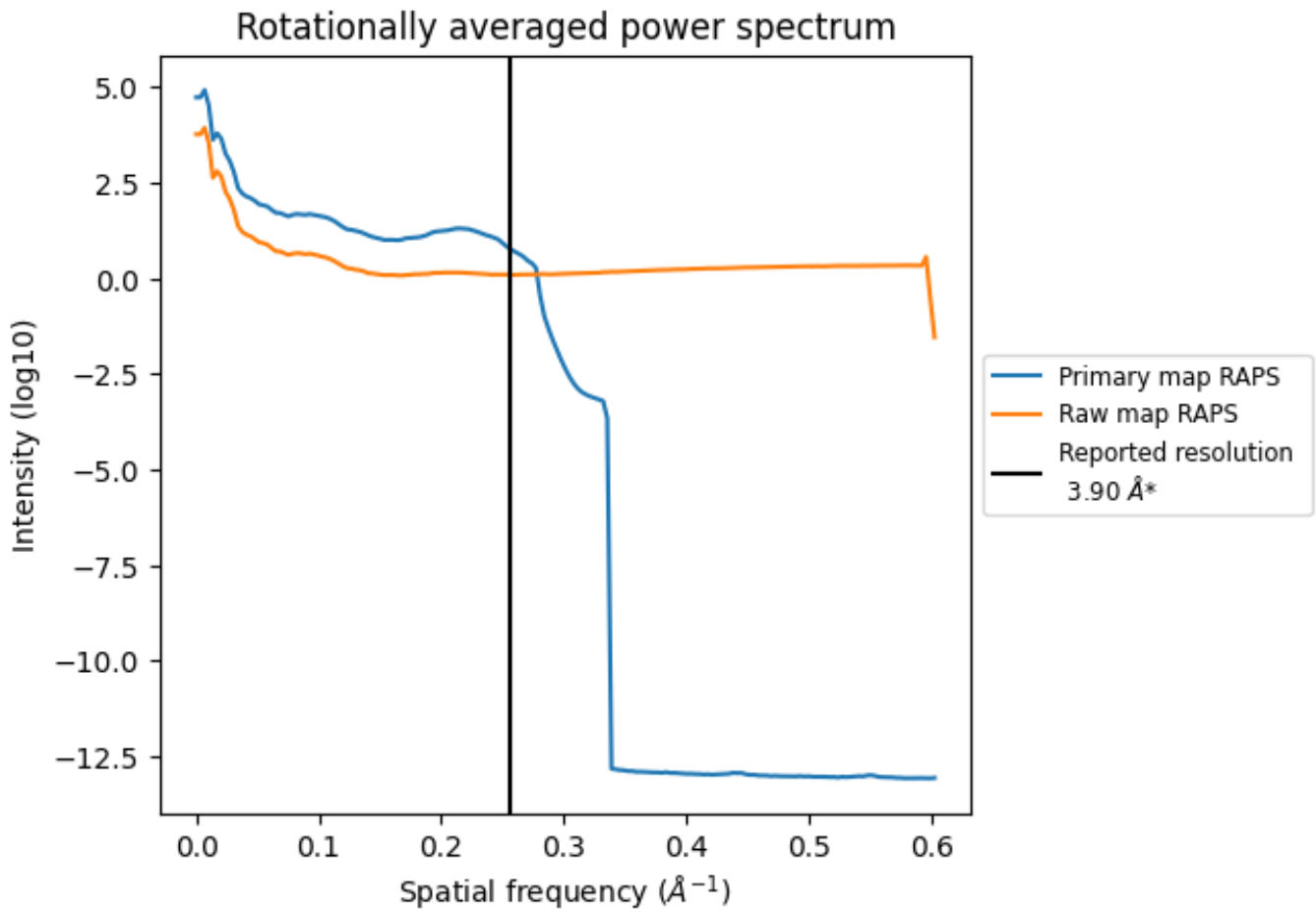
7.2 Volume estimate (i)



The volume at the recommended contour level is 120 nm^3; this corresponds to an approximate mass of 109 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)

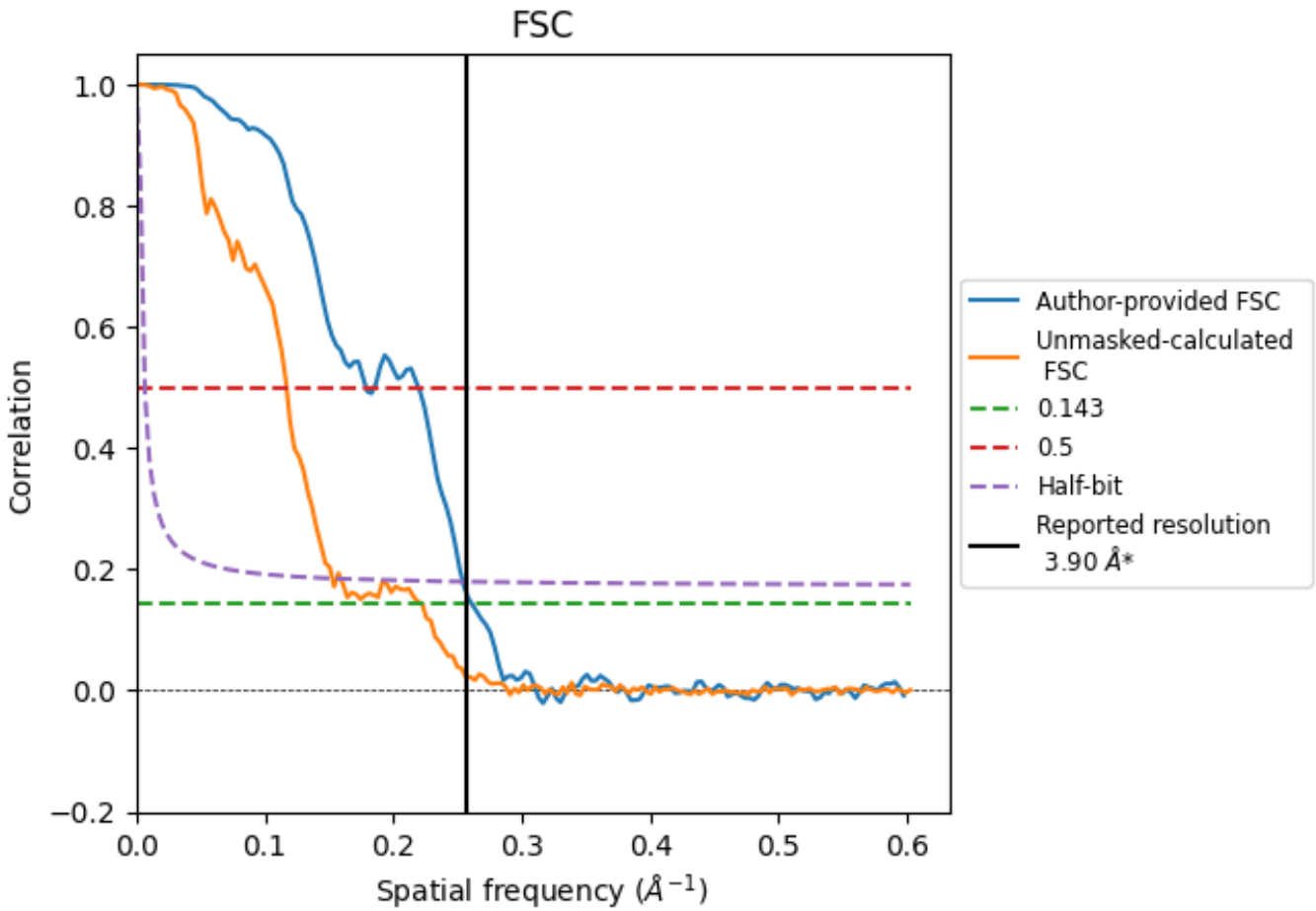


*Reported resolution corresponds to spatial frequency of 0.256 Å^{-1}

8 Fourier-Shell correlation (i)

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

8.1 FSC (i)



*Reported resolution corresponds to spatial frequency of 0.256 Å^{-1}

8.2 Resolution estimates (i)

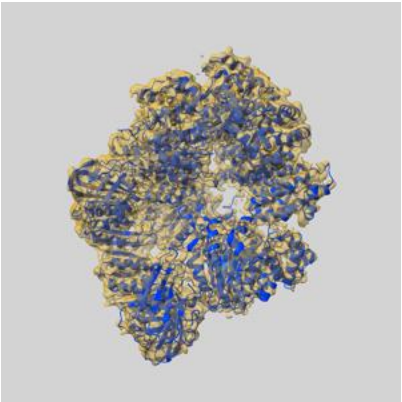
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	3.83	5.59	3.93
Unmasked-calculated*	4.49	8.55	6.55

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.49 differs from the reported value 3.9 by more than 10 %

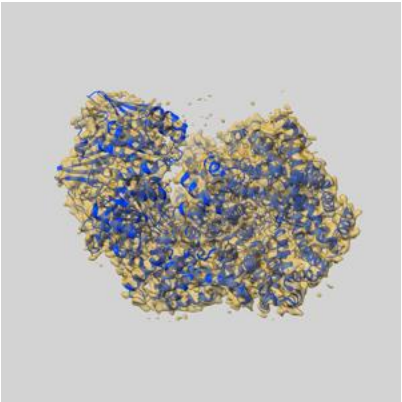
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-43095 and PDB model 8VAM. Per-residue inclusion information can be found in section 3 on page 8.

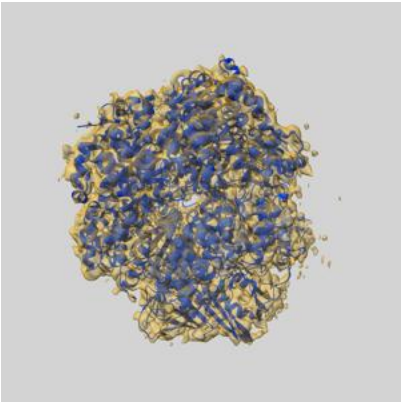
9.1 Map-model overlay (i)



X



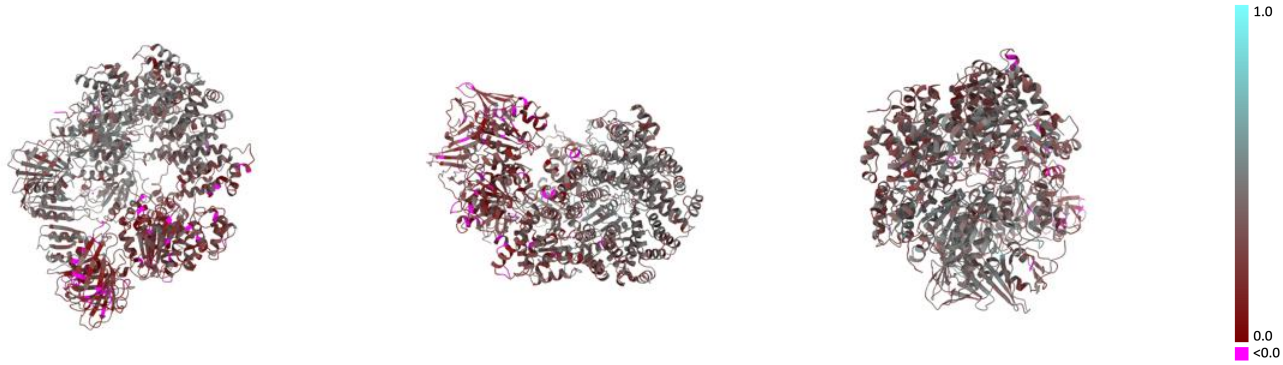
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.09 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

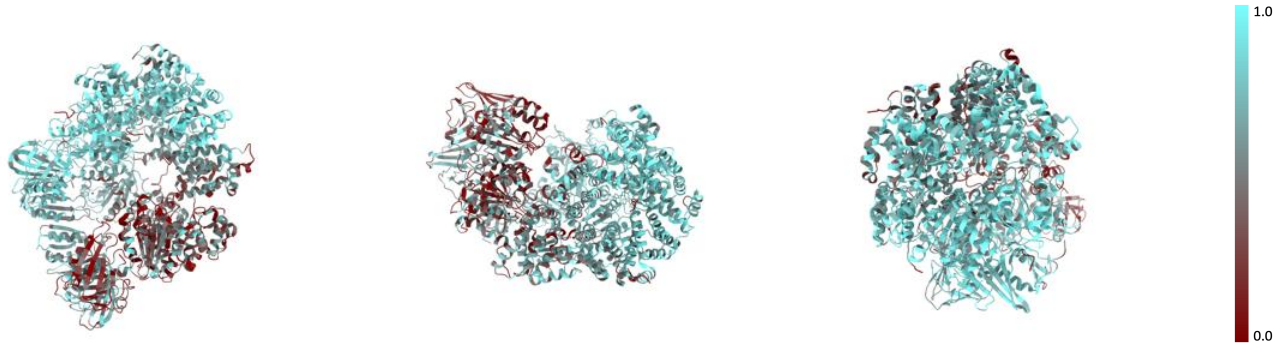
9.2 Q-score mapped to coordinate model (i)



X Y Z

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

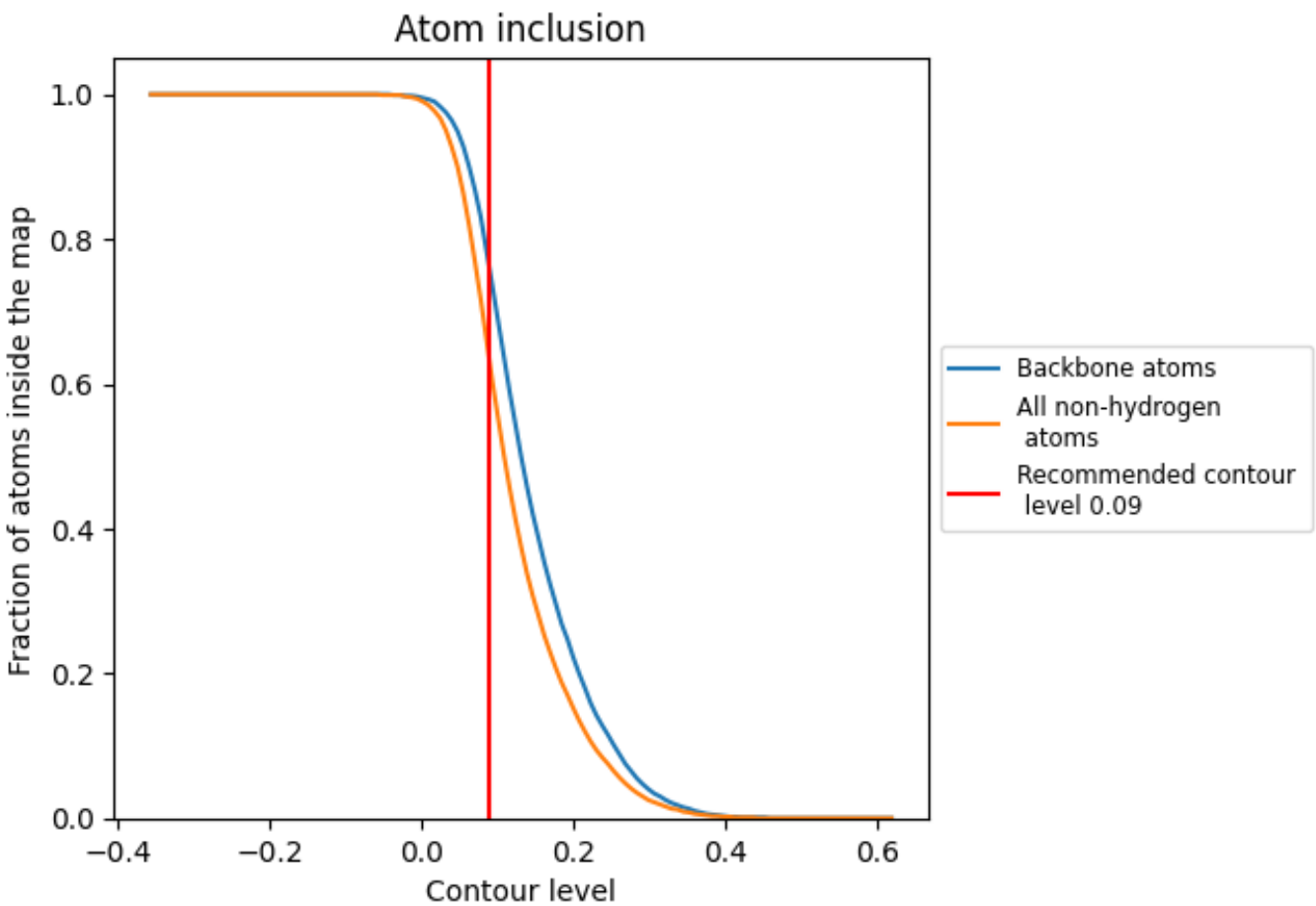
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.09).

9.4 Atom inclusion (i)



At the recommended contour level, 76% of all backbone atoms, 63% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.09) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6290	0.3390
A	0.4130	0.2470
B	0.4390	0.2620
C	0.7250	0.3730
D	0.8130	0.4350
E	0.8020	0.4220
F	0.4920	0.2560
G	0.7600	0.3960