Full wwPDB EM Validation Report ⓘ

May 4, 2025 – 12:53 PM EDT

PDB ID	:	8DK2 / pdb_00008dk2
EMDB ID	:	EMD-27481
Title	:	CryoEM structure of Pseudomonas aeruginosa PA14 JetABC in an unclamped state trapped in ATP dependent dimeric form
Authors	:	Deep, A.; Gu, Y.; Gao, Y.; Ego, K.; Herzik, M.; Zhou, H.; Corbett, K.
Deposited on	:	2022-07-01
Resolution	:	4.10 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references ⓘ) were used in the production of this report:

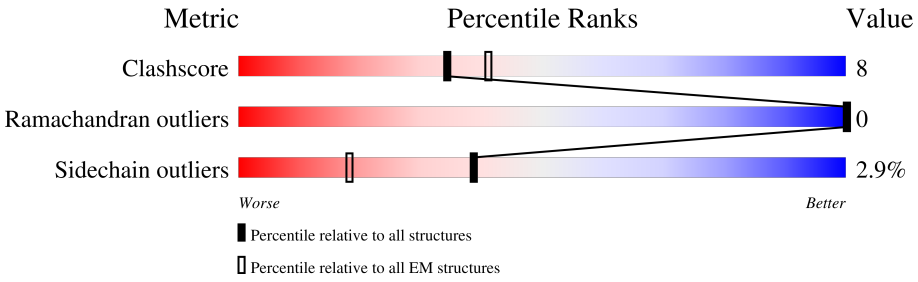
EMDB validation analysis	:	0.0.1.dev118
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.0rc1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.43.1

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 4.10 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	517	5% 69% 15% 15%
1	B	517	12% 57% 9% 34%
2	C	1119	48% 16% 35%
2	D	1119	50% 13% 36%
3	F	249	25% 23% 75%
3	G	249	57% 64% 12% 24%
3	H	249	54% 53% 17% 29%
3	I	249	23% 60% 16% 24%

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Mol	Chain	Length	Quality of chain
4	P	26	92% 8%
5	Q	26	73% 27%

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 23727 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 JetA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	441	Total	C	N	O	S	0	0
			3527	2197	668	654	8		
1	B	341	Total	C	N	O	S	0	0
			2738	1691	539	501	7		

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-17	MET	-	initiating methionine	UNP A0A0H2ZJP9
A	-16	LYS	-	expression tag	UNP A0A0H2ZJP9
A	-15	SER	-	expression tag	UNP A0A0H2ZJP9
A	-14	SER	-	expression tag	UNP A0A0H2ZJP9
A	-13	HIS	-	expression tag	UNP A0A0H2ZJP9
A	-12	HIS	-	expression tag	UNP A0A0H2ZJP9
A	-11	HIS	-	expression tag	UNP A0A0H2ZJP9
A	-10	HIS	-	expression tag	UNP A0A0H2ZJP9
A	-9	HIS	-	expression tag	UNP A0A0H2ZJP9
A	-8	HIS	-	expression tag	UNP A0A0H2ZJP9
A	-7	GLU	-	expression tag	UNP A0A0H2ZJP9
A	-6	ASN	-	expression tag	UNP A0A0H2ZJP9
A	-4	TYR	TRP	conflict	UNP A0A0H2ZJP9
A	-3	PHE	LYS	conflict	UNP A0A0H2ZJP9
A	-2	GLN	VAL	conflict	UNP A0A0H2ZJP9
A	-1	SER	ALA	conflict	UNP A0A0H2ZJP9
A	0	ASN	ALA	conflict	UNP A0A0H2ZJP9
A	1	ALA	MET	conflict	UNP A0A0H2ZJP9
B	-17	MET	-	initiating methionine	UNP A0A0H2ZJP9
B	-16	LYS	-	expression tag	UNP A0A0H2ZJP9
B	-15	SER	-	expression tag	UNP A0A0H2ZJP9
B	-14	SER	-	expression tag	UNP A0A0H2ZJP9
B	-13	HIS	-	expression tag	UNP A0A0H2ZJP9
B	-12	HIS	-	expression tag	UNP A0A0H2ZJP9
B	-11	HIS	-	expression tag	UNP A0A0H2ZJP9
B	-10	HIS	-	expression tag	UNP A0A0H2ZJP9

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-9	HIS	-	expression tag	UNP A0A0H2ZJP9
B	-8	HIS	-	expression tag	UNP A0A0H2ZJP9
B	-7	GLU	-	expression tag	UNP A0A0H2ZJP9
B	-6	ASN	-	expression tag	UNP A0A0H2ZJP9
B	-4	TYR	TRP	conflict	UNP A0A0H2ZJP9
B	-3	PHE	LYS	conflict	UNP A0A0H2ZJP9
B	-2	GLN	VAL	conflict	UNP A0A0H2ZJP9
B	-1	SER	ALA	conflict	UNP A0A0H2ZJP9
B	0	ASN	ALA	conflict	UNP A0A0H2ZJP9
B	1	ALA	MET	conflict	UNP A0A0H2ZJP9

- Molecule 2 is a protein called JetC.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	723	Total	C	N	O	S	0	0
			5720	3559	1052	1096	13		
2	D	718	Total	C	N	O	S	0	0
			5680	3535	1045	1087	13		

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-17	MET	-	initiating methionine	UNP A0A8G4Z850
C	-16	LYS	-	expression tag	UNP A0A8G4Z850
C	-15	SER	-	expression tag	UNP A0A8G4Z850
C	-14	SER	-	expression tag	UNP A0A8G4Z850
C	-13	HIS	-	expression tag	UNP A0A8G4Z850
C	-12	HIS	-	expression tag	UNP A0A8G4Z850
C	-11	HIS	-	expression tag	UNP A0A8G4Z850
C	-10	HIS	-	expression tag	UNP A0A8G4Z850
C	-9	HIS	-	expression tag	UNP A0A8G4Z850
C	-8	HIS	-	expression tag	UNP A0A8G4Z850
C	-7	GLU	-	expression tag	UNP A0A8G4Z850
C	-6	ASN	-	expression tag	UNP A0A8G4Z850
C	-5	LEU	-	expression tag	UNP A0A8G4Z850
C	-4	TYR	-	expression tag	UNP A0A8G4Z850
C	-3	PHE	-	expression tag	UNP A0A8G4Z850
C	-2	GLN	-	expression tag	UNP A0A8G4Z850
C	-1	SER	-	expression tag	UNP A0A8G4Z850
C	0	ASN	-	expression tag	UNP A0A8G4Z850
C	1	ALA	-	expression tag	UNP A0A8G4Z850
C	1022	GLN	GLU	conflict	UNP A0A8G4Z850

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-17	MET	-	initiating methionine	UNP A0A8G4Z850
D	-16	LYS	-	expression tag	UNP A0A8G4Z850
D	-15	SER	-	expression tag	UNP A0A8G4Z850
D	-14	SER	-	expression tag	UNP A0A8G4Z850
D	-13	HIS	-	expression tag	UNP A0A8G4Z850
D	-12	HIS	-	expression tag	UNP A0A8G4Z850
D	-11	HIS	-	expression tag	UNP A0A8G4Z850
D	-10	HIS	-	expression tag	UNP A0A8G4Z850
D	-9	HIS	-	expression tag	UNP A0A8G4Z850
D	-8	HIS	-	expression tag	UNP A0A8G4Z850
D	-7	GLU	-	expression tag	UNP A0A8G4Z850
D	-6	ASN	-	expression tag	UNP A0A8G4Z850
D	-5	LEU	-	expression tag	UNP A0A8G4Z850
D	-4	TYR	-	expression tag	UNP A0A8G4Z850
D	-3	PHE	-	expression tag	UNP A0A8G4Z850
D	-2	GLN	-	expression tag	UNP A0A8G4Z850
D	-1	SER	-	expression tag	UNP A0A8G4Z850
D	0	ASN	-	expression tag	UNP A0A8G4Z850
D	1	ALA	-	expression tag	UNP A0A8G4Z850
D	1022	GLN	GLU	conflict	UNP A0A8G4Z850

- Molecule 3 is a protein called JetB.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	F	63	Total	C	N	O	S	0	0
			507	320	90	95	2		
3	G	189	Total	C	N	O	S	0	0
			1506	949	272	283	2		
3	H	176	Total	C	N	O	S	0	0
			1413	894	257	260	2		
3	I	189	Total	C	N	O	S	0	0
			1506	949	272	283	2		

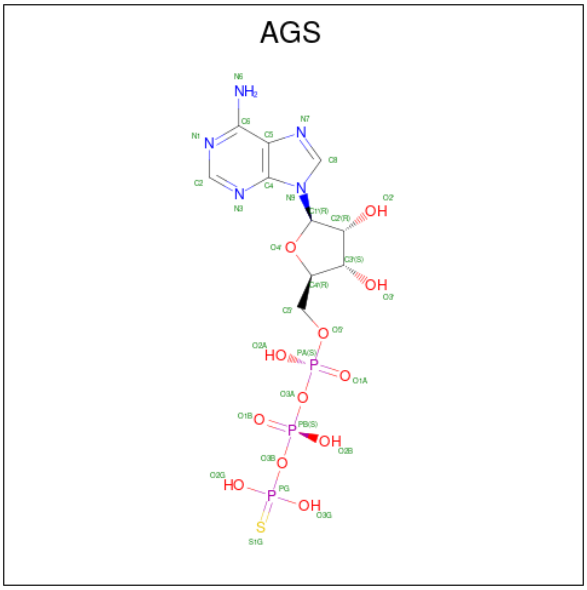
- Molecule 4 is a DNA chain called DNA (26-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
4	P	26	Total	C	N	O	P	0	0
			520	260	52	182	26		

- Molecule 5 is a DNA chain called DNA (26-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	Q	26	Total	C	N	O	P	0	0
			546	260	130	130	26		

- Molecule 6 is PHOSPHOTHIOPHOSPHORIC ACID-ADENYLATE ESTER (CCD ID: AGS) (formula: $C_{10}H_{16}N_5O_{12}P_3S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						AltConf
6	C	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	
6	D	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	

- Molecule 7 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

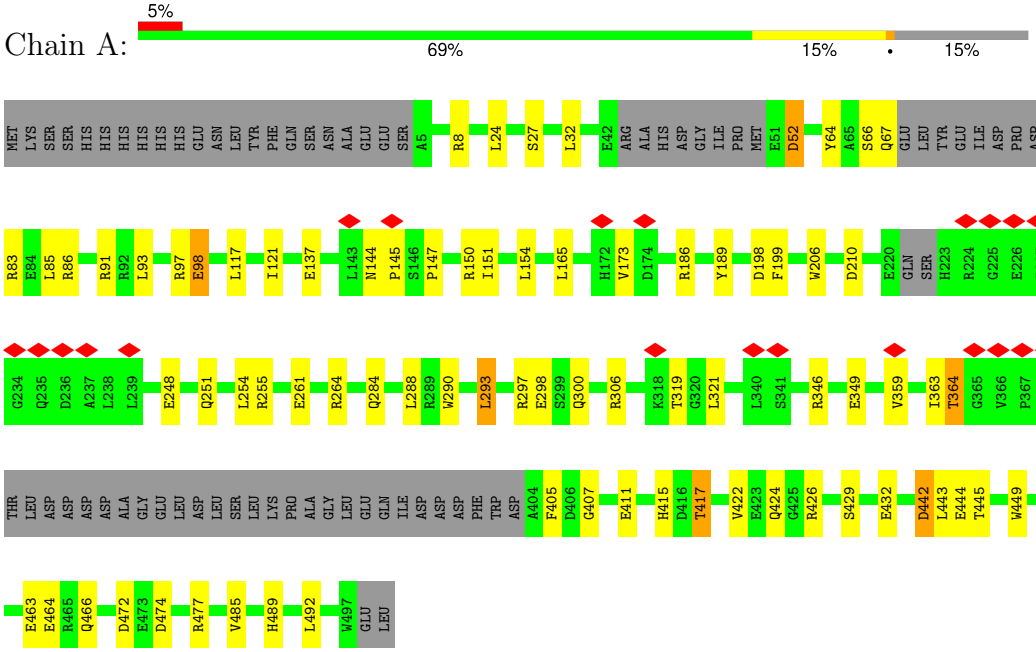
Mol	Chain	Residues	Atoms		AltConf
7	C	1	Total	Mg	0
			1	1	
7	D	1	Total	Mg	0
			1	1	

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

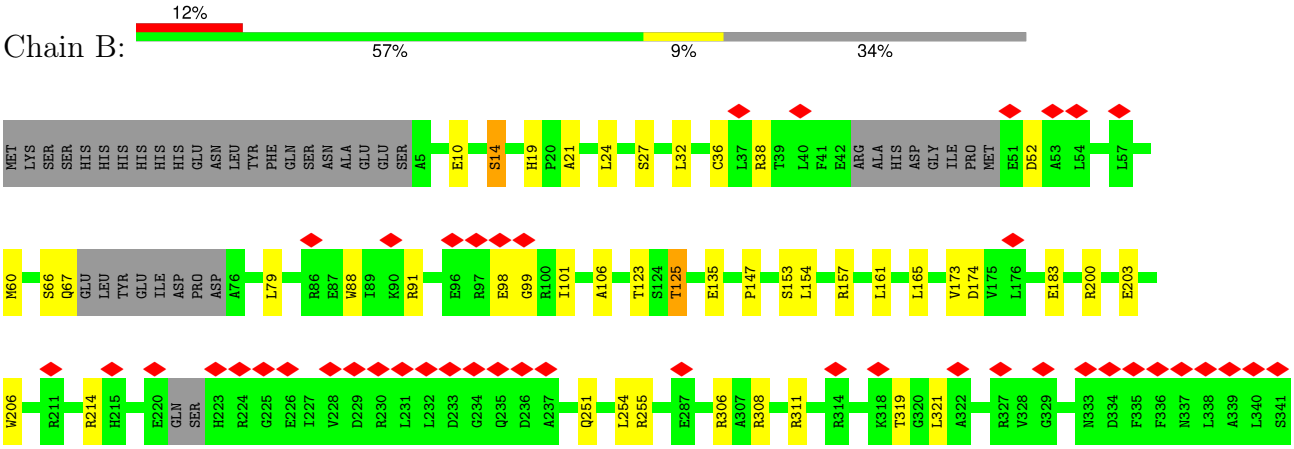
• Molecule 1: JetA

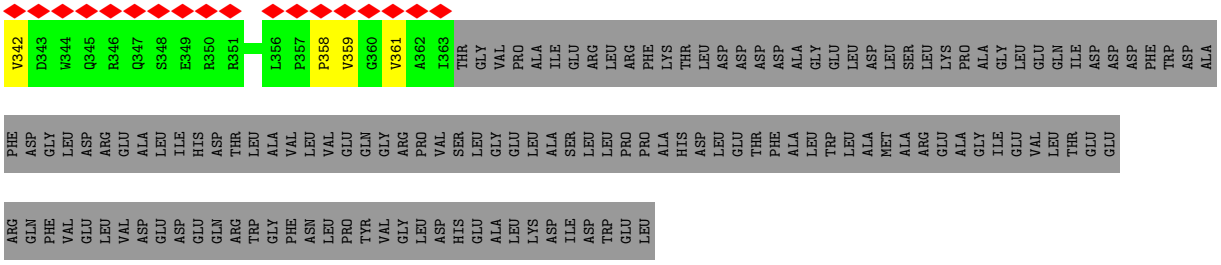
Chain A:



• Molecule 1: JetA

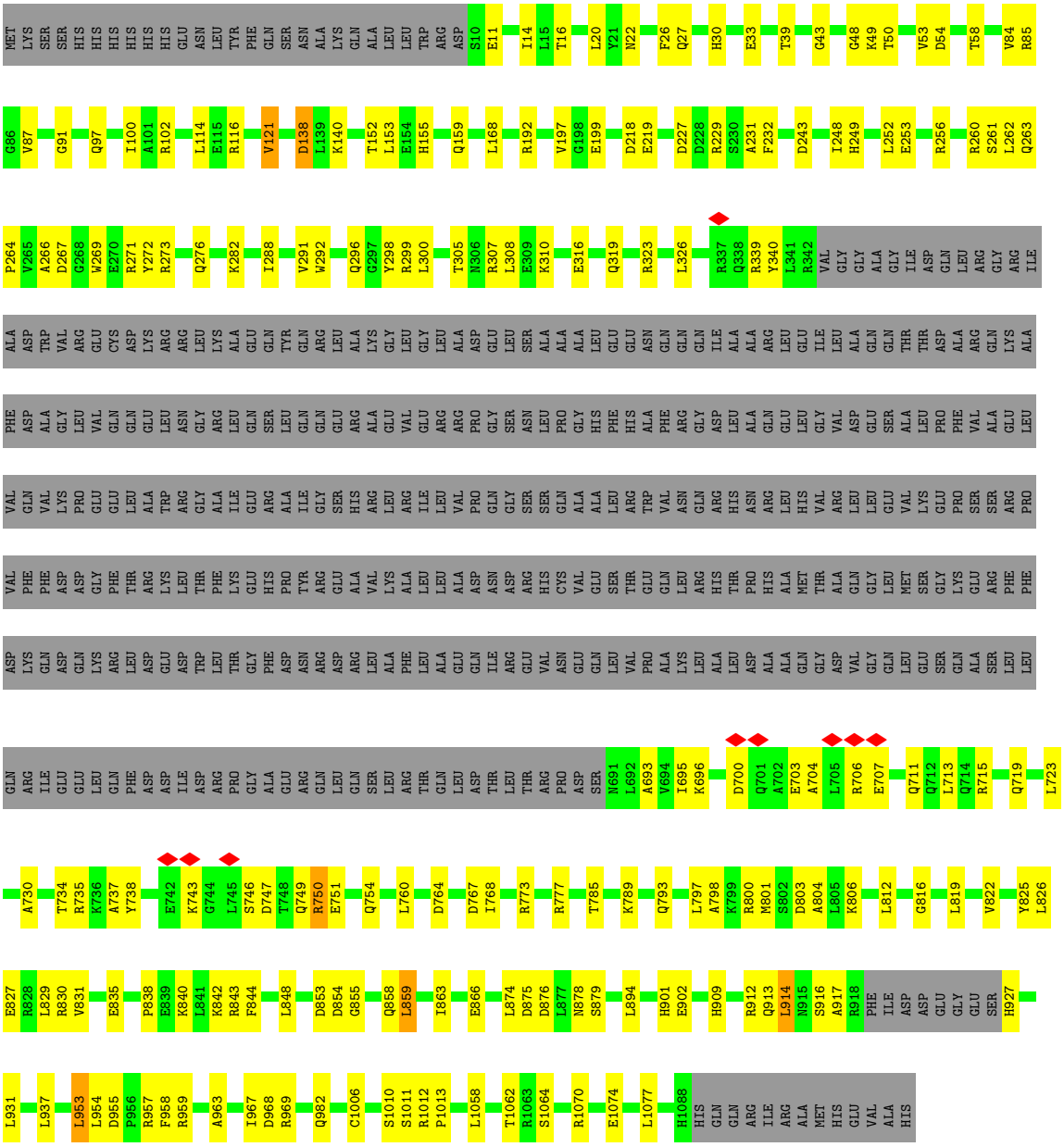
Chain B:





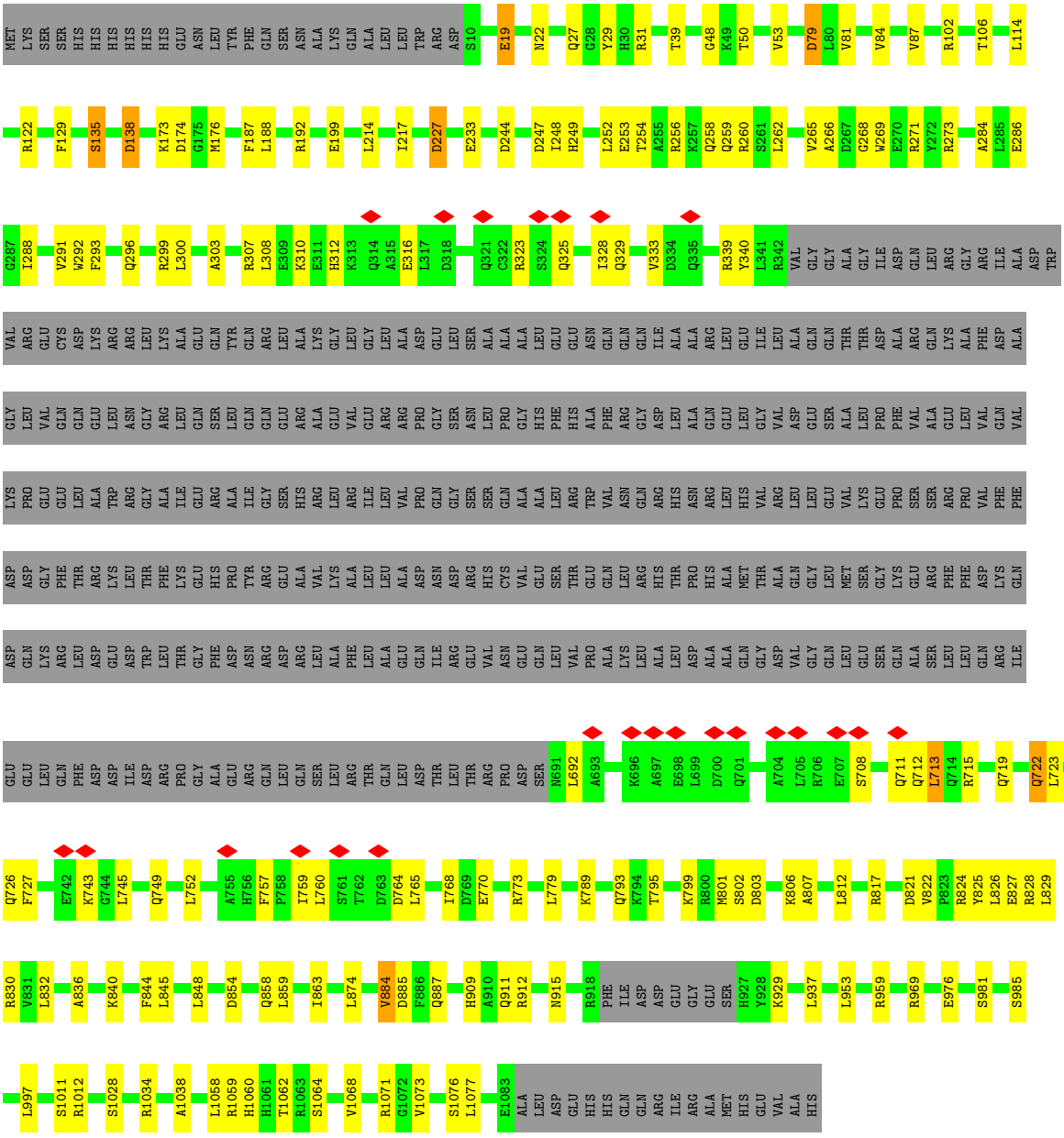
• Molecule 2: JetC

Chain C:



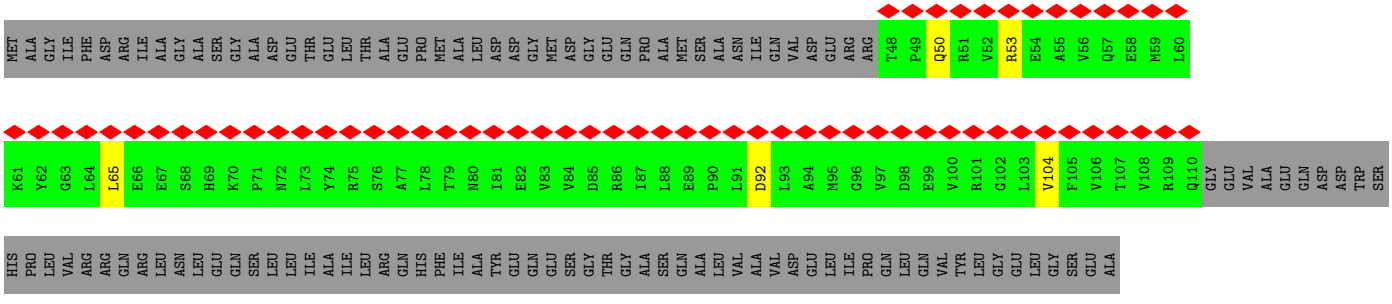
• Molecule 2: JetC

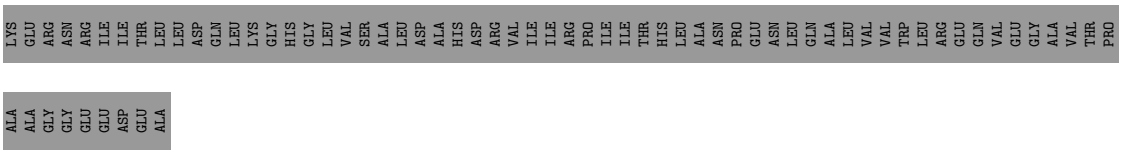
Chain D:



• Molecule 3: JetB

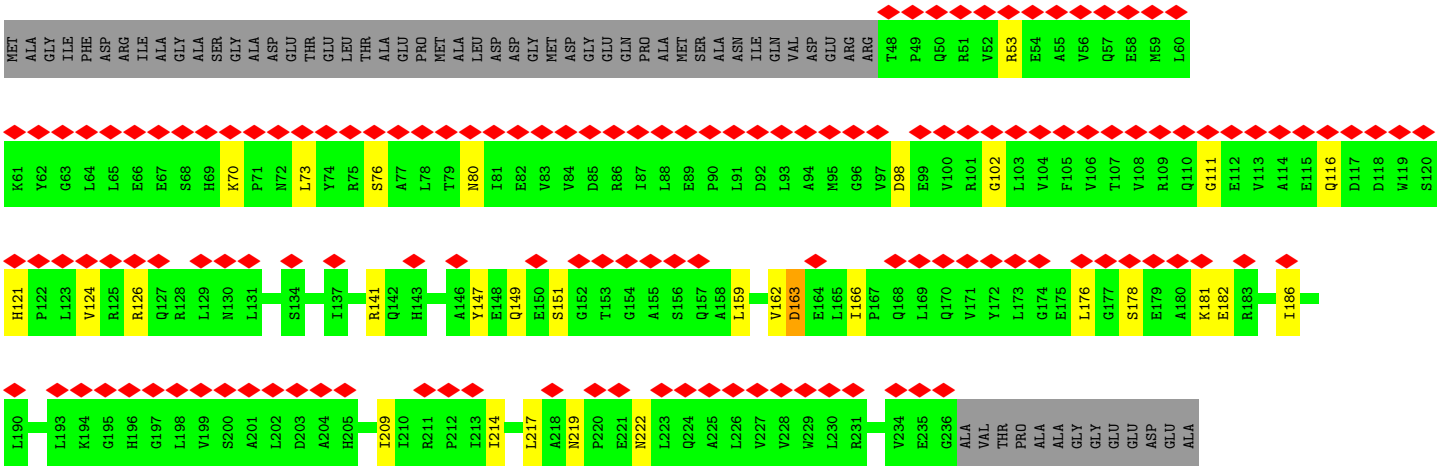
Chain F:





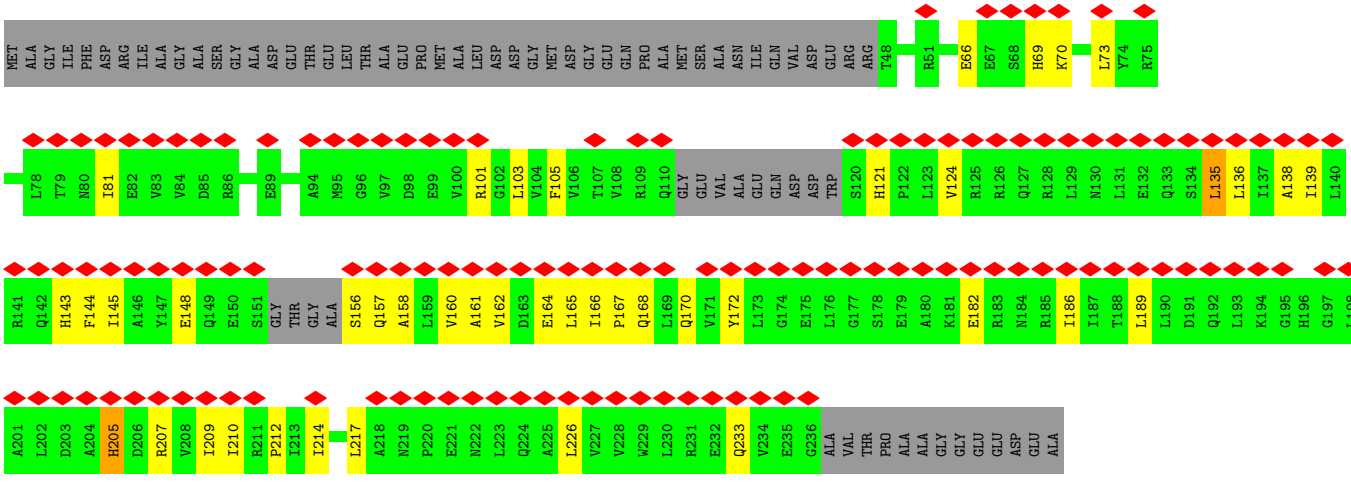
• Molecule 3: JetB

Chain G:



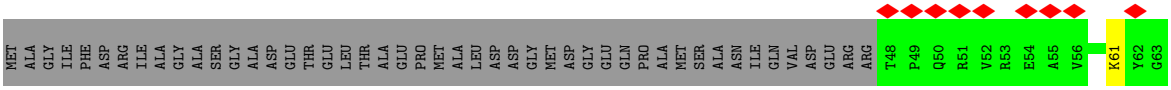
• Molecule 3: JetB

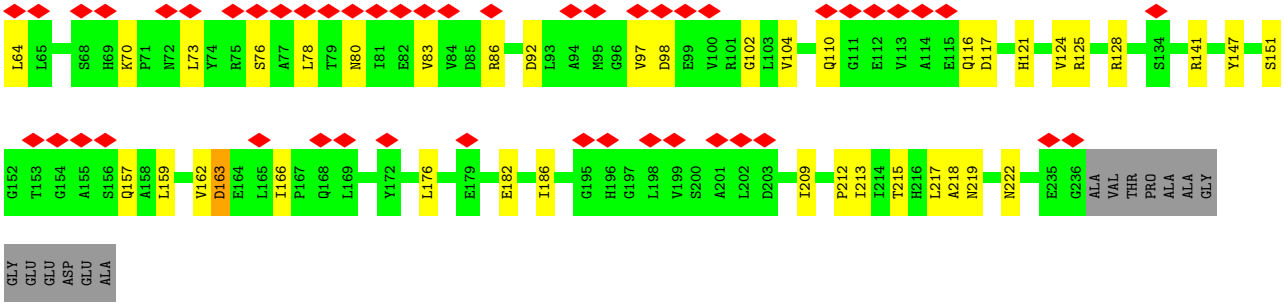
Chain H:



• Molecule 3: JetB

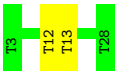
Chain I:





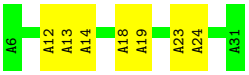
• Molecule 4: DNA (26-MER)

Chain P:



• Molecule 5: DNA (26-MER)

Chain Q:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	56600	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 ($e^-/Å^2$)	50.1	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	130000	Depositor
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	1.185	Depositor
Minimum map value	-0.382	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.020	Depositor
Recommended contour level	0.2	Depositor
Map size (Å)	563.21277, 563.21277, 563.21277	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.4667, 1.4667, 1.4667	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
1	A	0.10	0/3582	0.24	0/4843
1	B	0.09	0/2775	0.23	0/3741
2	C	0.14	0/5811	0.29	0/7837
2	D	0.14	0/5770	0.29	0/7781
3	F	0.06	0/513	0.19	0/694
3	G	0.08	0/1528	0.21	0/2074
3	H	0.09	0/1431	0.21	0/1938
3	I	0.08	0/1528	0.22	0/2074
4	P	0.22	0/571	0.51	0/880
5	Q	0.18	0/623	0.24	0/958
All	All	0.12	0/24132	0.27	0/32820

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	3527	0	3521	64	0
1	B	2738	0	2760	33	0
2	C	5720	0	5687	114	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	5680	0	5655	107	0
3	F	507	0	523	3	0
3	G	1506	0	1534	20	0
3	H	1413	0	1459	26	0
3	I	1506	0	1534	25	0
4	P	520	0	313	1	0
5	Q	546	0	287	5	0
6	C	31	0	12	4	0
6	D	31	0	12	2	0
7	C	1	0	0	0	0
7	D	1	0	0	0	0
All	All	23727	0	23297	370	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

All (370) 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:764:ASP:HB3	2:C:767:ASP:HB2	1.70	0.73
1:B:361:VAL:HA	3:G:126:ARG:HE	1.54	0.73
2:D:765:LEU:O	2:D:768:ILE:HB	1.91	0.71
1:A:144:ASN:O	1:A:150:ARG:NH1	2.18	0.71
2:D:801:MET:HG2	2:D:817:ARG:HA	1.73	0.70
2:C:22:ASN:OD1	2:C:102:ARG:NH1	2.21	0.70
2:C:264:PRO:HB2	2:C:800:ARG:HE	1.58	0.68
2:C:305:THR:HG1	2:C:734:THR:HG1	1.40	0.67
2:D:745:LEU:HB3	2:D:749:GLN:HB2	1.76	0.67
3:H:214:ILE:HA	3:H:217:LEU:HG	1.77	0.67
1:A:443:LEU:H	2:D:1059:ARG:HH12	1.43	0.65
2:C:300:LEU:HD12	2:C:768:ILE:HD11	1.78	0.65
1:A:411:GLU:O	1:A:415:HIS:ND1	2.29	0.65
2:C:339:ARG:HG3	2:C:695:ILE:HD13	1.79	0.64
1:A:97:ARG:NH1	1:A:98:GLU:OE2	2.31	0.64
2:D:293:PHE:HE1	2:D:757:PHE:HB3	1.63	0.63
2:C:252:LEU:HD13	2:C:840:LYS:HD3	1.78	0.63
2:D:258:GLN:NE2	2:D:807:ALA:O	2.30	0.63
1:B:153:SER:OG	1:B:157:ARG:NH1	2.32	0.63
2:C:229:ARG:NH1	2:C:866:GLU:OE2	2.31	0.63
2:C:760:LEU:HD13	2:C:768:ILE:HG12	1.80	0.62
2:D:312:HIS:HB2	2:D:727:PHE:HD2	1.65	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:125:THR:OG1	1:B:183:GLU:OE2	2.14	0.62
6:D:1201:AGS:S1G	6:D:1201:AGS:O2B	2.58	0.62
3:H:161:ALA:HB3	3:H:164:GLU:HG3	1.81	0.62
2:D:22:ASN:OD1	2:D:102:ARG:NE	2.30	0.61
2:D:192:ARG:NH2	2:D:199:GLU:OE2	2.32	0.61
2:D:312:HIS:HB2	2:D:727:PHE:CD2	2.35	0.61
3:H:172:TYR:O	3:H:233:GLN:NE2	2.33	0.61
2:D:760:LEU:HB3	2:D:764:ASP:HB2	1.82	0.61
2:D:340:TYR:HE1	2:D:692:LEU:HB2	1.64	0.61
2:D:286:GLU:HA	2:D:779:LEU:HD13	1.82	0.60
3:I:117:ASP:OD2	3:I:128:ARG:NH2	2.34	0.60
1:A:154:LEU:HD13	1:B:165:LEU:HA	1.83	0.60
1:A:364:THR:HA	3:I:125:ARG:HD3	1.83	0.60
2:D:308:LEU:HB3	2:D:727:PHE:CD1	2.36	0.60
2:D:859:LEU:HD12	2:D:863:ILE:HD12	1.83	0.60
2:C:703:GLU:HB2	2:C:706:ARG:HH21	1.66	0.60
1:A:165:LEU:HA	1:B:154:LEU:HD13	1.83	0.59
2:D:803:ASP:HA	2:D:806:LYS:HD2	1.84	0.59
2:C:914:LEU:HD11	2:C:931:LEU:HD23	1.85	0.59
3:H:200:SER:HB2	3:H:209:ILE:HB	1.84	0.59
2:C:734:THR:O	2:C:738:TYR:N	2.31	0.59
2:C:152:THR:HG23	2:C:155:HIS:H	1.67	0.59
3:G:219:ASN:OD1	3:G:222:ASN:ND2	2.36	0.59
2:C:326:LEU:HD11	2:C:713:LEU:HB2	1.85	0.59
1:A:442:ASP:OD1	1:A:442:ASP:N	2.31	0.58
2:D:79:ASP:N	2:D:79:ASP:OD1	2.35	0.58
1:A:151:ILE:HG23	1:B:165:LEU:HD11	1.86	0.58
2:D:214:LEU:O	2:D:981:SER:OG	2.20	0.58
2:D:292:TRP:HZ2	2:D:759:ILE:HG12	1.68	0.58
2:D:138:ASP:OD1	2:D:138:ASP:N	2.36	0.58
2:C:39:THR:HG22	2:C:1064:SER:HB3	1.84	0.58
2:C:803:ASP:HA	2:C:806:LYS:HD2	1.85	0.57
2:D:795:THR:HG22	2:D:799:LYS:HE3	1.86	0.57
1:A:198:ASP:OD2	1:B:123:THR:N	2.36	0.57
6:C:1201:AGS:S1G	2:D:985:SER:OG	2.61	0.57
2:D:712:GLN:HG2	2:D:715:ARG:HH21	1.70	0.57
1:A:363:ILE:HB	3:I:61:LYS:HA	1.86	0.57
2:C:11:GLU:HA	2:C:116:ARG:HD3	1.87	0.57
2:C:874:LEU:O	2:C:878:ASN:ND2	2.38	0.57
3:H:170:GLN:NE2	3:H:182:GLU:OE2	2.37	0.57
3:H:138:ALA:HB2	3:H:226:LEU:HD11	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:27:GLN:O	2:C:30:HIS:NE2	2.34	0.57
1:B:98:GLU:N	1:B:98:GLU:OE1	2.37	0.56
2:C:296:GLN:O	2:C:300:LEU:HG	2.05	0.56
2:C:271:ARG:NH1	2:C:793:GLN:OE1	2.39	0.56
2:D:227:ASP:OD1	2:D:227:ASP:N	2.38	0.56
1:A:460:VAL:HG22	1:A:485:VAL:HG13	1.87	0.56
2:D:256:ARG:O	2:D:260:ARG:HG2	2.06	0.56
3:G:214:ILE:HA	3:G:217:LEU:HB3	1.89	0.55
3:G:159:LEU:HG	3:G:209:ILE:HG12	1.87	0.55
2:C:746:SER:HB3	2:C:750:ARG:HB2	1.88	0.55
2:C:291:VAL:HG13	2:C:743:LYS:HE3	1.88	0.55
3:I:219:ASN:OD1	3:I:222:ASN:ND2	2.39	0.55
1:A:293:LEU:HD21	2:C:1011:SER:HB2	1.87	0.55
2:D:953:LEU:O	2:D:959:ARG:NH2	2.39	0.55
3:F:65:LEU:HB2	3:F:104:VAL:HB	1.88	0.55
2:C:261:SER:O	2:C:800:ARG:NH2	2.40	0.55
3:G:76:SER:O	3:G:80:ASN:ND2	2.40	0.55
1:B:32:LEU:H	1:B:32:LEU:HD23	1.72	0.55
2:D:885:ASP:OD1	2:D:969:ARG:NH2	2.38	0.54
2:C:253:GLU:OE2	2:C:256:ARG:NH2	2.36	0.54
3:H:103:LEU:HG	3:H:105:PHE:HD1	1.72	0.54
3:I:70:LYS:HD3	3:I:73:LEU:HD12	1.89	0.54
2:C:305:THR:OG1	2:C:734:THR:OG1	2.16	0.54
5:Q:23:DA:H2"	5:Q:24:DA:C8	2.43	0.54
1:A:429:SER:OG	1:A:432:GLU:OE1	2.19	0.54
2:D:708:SER:O	2:D:711:GLN:HG2	2.08	0.54
1:A:290:TRP:CG	2:C:1010:SER:HG	2.26	0.54
2:D:912:ARG:HA	2:D:915:ASN:HD21	1.73	0.53
1:A:319:THR:HG22	1:A:321:LEU:HG	1.90	0.53
2:C:876:ASP:O	2:C:879:SER:OG	2.24	0.53
2:D:84:VAL:O	2:D:102:ARG:NH1	2.42	0.53
2:D:262:LEU:HB2	2:D:829:LEU:HD13	1.91	0.53
1:A:52:ASP:N	1:A:52:ASP:OD1	2.39	0.53
1:A:443:LEU:HB2	2:D:1059:ARG:HH12	1.73	0.53
2:C:227:ASP:O	2:C:957:ARG:NH1	2.42	0.53
3:H:70:LYS:HD3	3:H:73:LEU:HD12	1.91	0.53
1:A:261:GLU:OE1	1:A:264:ARG:NH2	2.42	0.53
2:C:114:LEU:HB2	2:C:121:VAL:HG13	1.91	0.53
2:D:284:ALA:O	2:D:288:ILE:HG12	2.09	0.53
1:A:297:ARG:HH11	2:C:1011:SER:HA	1.74	0.52
2:C:323:ARG:HA	2:C:326:LEU:HD12	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:50:THR:HA	2:D:53:VAL:HG12	1.91	0.52
2:D:291:VAL:HG22	2:D:743:LYS:HD2	1.92	0.52
2:D:911:GLN:O	2:D:915:ASN:ND2	2.43	0.52
2:D:81:VAL:HA	2:D:84:VAL:HG22	1.91	0.52
2:C:746:SER:O	2:C:750:ARG:N	2.36	0.52
2:C:816:GLY:O	2:C:825:TYR:OH	2.27	0.52
2:D:296:GLN:OE1	2:D:299:ARG:NH2	2.40	0.52
3:I:159:LEU:HG	3:I:209:ILE:HG12	1.91	0.52
2:C:218:ASP:OD1	2:C:219:GLU:N	2.43	0.52
1:A:443:LEU:HB2	2:D:1059:ARG:NH1	2.26	0.51
1:A:464:GLU:HG2	1:A:466:GLN:HE22	1.75	0.51
2:C:704:ALA:O	2:C:707:GLU:HG2	2.09	0.51
2:D:265:VAL:HG12	2:D:822:VAL:HG13	1.92	0.51
2:D:19:GLU:OE2	2:D:122:ARG:NH2	2.43	0.51
2:C:43:GLY:O	2:C:49:LYS:NZ	2.35	0.51
2:C:812:LEU:HD13	2:C:825:TYR:HD1	1.74	0.51
2:D:1011:SER:OG	2:D:1012:ARG:NH1	2.44	0.51
3:I:163:ASP:OD1	3:I:163:ASP:N	2.42	0.51
1:B:21:ALA:HB2	1:B:106:ALA:HB1	1.92	0.51
6:C:1201:AGS:O2G	6:C:1201:AGS:O2B	2.29	0.51
1:A:460:VAL:HG13	1:A:485:VAL:HG22	1.93	0.51
3:G:147:TYR:O	3:G:151:SER:OG	2.29	0.51
2:C:262:LEU:HB3	2:C:829:LEU:HD22	1.93	0.51
2:C:263:GLN:NE2	2:C:267:ASP:OD1	2.43	0.51
2:D:692:LEU:HD23	2:D:692:LEU:H	1.75	0.51
2:C:859:LEU:HD12	2:C:863:ILE:HD12	1.91	0.51
2:D:789:LYS:NZ	2:D:793:GLN:OE1	2.44	0.50
2:C:256:ARG:O	2:C:260:ARG:HG2	2.11	0.50
2:C:917:ALA:HB1	2:C:927:HIS:HA	1.92	0.50
3:G:70:LYS:HD3	3:G:73:LEU:HD12	1.93	0.50
1:A:199:PHE:HE2	1:A:298:GLU:HB3	1.76	0.50
2:D:244:ASP:OD1	2:D:244:ASP:N	2.45	0.50
2:C:308:LEU:HD12	2:C:730:ALA:HB2	1.94	0.50
2:D:802:SER:OG	2:D:817:ARG:NH1	2.45	0.50
3:I:176:LEU:HB2	3:I:182:GLU:HG3	1.93	0.50
2:D:288:ILE:HG13	2:D:752:LEU:HD11	1.94	0.50
1:B:358:PRO:HB2	1:B:361:VAL:HG22	1.94	0.50
3:I:121:HIS:HB3	3:I:124:VAL:HG23	1.93	0.50
3:I:147:TYR:O	3:I:151:SER:OG	2.29	0.50
2:C:85:ARG:C	2:C:102:ARG:HH21	2.19	0.50
2:D:292:TRP:CZ2	2:D:759:ILE:HG12	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:323:ARG:HA	2:D:713:LEU:HD11	1.93	0.50
2:C:751:GLU:O	2:C:754:GLN:HG2	2.12	0.49
2:C:269:TRP:HZ3	2:C:819:LEU:HD22	1.77	0.49
3:G:162:VAL:HG13	3:G:186:ILE:HG21	1.93	0.49
1:A:150:ARG:HD2	1:B:173:VAL:HG13	1.94	0.49
2:C:785:THR:HG22	2:C:789:LYS:HE3	1.95	0.49
2:D:827:GLU:HA	2:D:830:ARG:HD2	1.93	0.49
1:A:464:GLU:OE1	1:A:464:GLU:N	2.44	0.49
2:C:339:ARG:O	2:C:339:ARG:NE	2.46	0.49
2:D:288:ILE:HD12	2:D:749:GLN:HB3	1.94	0.49
2:C:316:GLU:O	2:C:319:GLN:HG2	2.13	0.49
3:F:92:ASP:OD1	3:G:53:ARG:NH1	2.45	0.49
3:I:98:ASP:O	3:I:102:GLY:N	2.46	0.49
1:A:472:ASP:OD1	1:A:474:ASP:N	2.46	0.49
1:A:297:ARG:NH1	2:C:1012:ARG:HG2	2.28	0.48
2:D:723:LEU:HB3	2:D:727:PHE:CE2	2.48	0.48
3:I:76:SER:O	3:I:80:ASN:ND2	2.46	0.48
1:A:248:GLU:OE2	1:A:306:ARG:NH1	2.38	0.48
1:B:200:ARG:NH1	1:B:203:GLU:OE2	2.46	0.48
2:C:291:VAL:HG22	2:C:743:LYS:HZ2	1.78	0.48
3:H:162:VAL:HG13	3:H:186:ILE:HG21	1.95	0.48
2:C:87:VAL:HG12	2:C:100:ILE:HG12	1.95	0.48
2:C:700:ASP:O	2:C:703:GLU:HG2	2.13	0.48
2:D:248:ILE:O	2:D:252:LEU:HG	2.13	0.48
1:A:66:SER:OG	1:A:67:GLN:N	2.46	0.48
2:C:835:GLU:C	2:C:838:PRO:HD2	2.39	0.48
3:H:205:HIS:CE1	3:H:207:ARG:HE	2.31	0.48
1:A:455:GLU:O	2:D:1071:ARG:NH1	2.47	0.48
1:B:319:THR:HG22	1:B:321:LEU:HG	1.96	0.48
1:A:189:TYR:CZ	1:A:284:GLN:HG2	2.48	0.48
3:G:178:SER:HB3	3:G:181:LYS:HG3	1.96	0.47
1:A:147:PRO:HA	1:B:173:VAL:HG21	1.96	0.47
2:C:231:ALA:HB3	2:C:954:LEU:HB3	1.96	0.47
3:H:101:ARG:HD3	3:H:212:PRO:HB3	1.96	0.47
2:C:838:PRO:O	2:C:842:LYS:HG2	2.14	0.47
2:D:135:SER:OG	2:D:138:ASP:OD1	2.22	0.47
2:C:288:ILE:HD12	2:C:749:GLN:HB3	1.97	0.47
2:C:822:VAL:HA	2:C:825:TYR:HD2	1.79	0.47
2:C:262:LEU:HD22	2:C:804:ALA:HB1	1.96	0.47
2:C:955:ASP:HB3	2:C:958:PHE:HD2	1.80	0.47
2:D:268:GLY:HA2	2:D:271:ARG:HH21	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:269:TRP:CD1	2:D:273:ARG:HE	2.33	0.47
1:A:417:THR:HG21	1:A:449:TRP:HE1	1.80	0.47
3:H:66:GLU:HB2	3:H:69:HIS:HD2	1.80	0.47
3:H:158:ALA:HB3	3:H:210:ILE:HB	1.96	0.47
2:C:298:TYR:HA	2:C:737:ALA:HB1	1.97	0.47
2:C:909:HIS:O	2:C:912:ARG:HG2	2.14	0.47
3:H:161:ALA:HA	3:H:207:ARG:HG2	1.96	0.47
2:C:901:HIS:CD2	2:C:902:GLU:HG2	2.50	0.46
3:I:162:VAL:O	3:I:166:ILE:HG13	2.15	0.46
3:I:212:PRO:O	3:I:215:THR:OG1	2.29	0.46
2:C:26:PHE:HE2	2:C:1077:LEU:HD21	1.81	0.46
1:A:346:ARG:NH1	1:A:349:GLU:OE2	2.48	0.46
2:D:48:GLY:N	6:D:1201:AGS:O1B	2.48	0.46
3:G:176:LEU:HB2	3:G:182:GLU:HG3	1.96	0.46
5:Q:18:DA:H2"	5:Q:19:DA:C8	2.51	0.46
2:C:693:ALA:O	2:C:696:LYS:HB3	2.16	0.46
2:D:293:PHE:CD2	2:D:768:ILE:HG23	2.51	0.46
2:C:22:ASN:O	2:C:102:ARG:NH1	2.48	0.46
2:C:711:GLN:O	2:C:715:ARG:HG3	2.15	0.46
1:A:24:LEU:O	1:A:27:SER:OG	2.23	0.46
2:D:249:HIS:O	2:D:253:GLU:HG2	2.15	0.46
2:D:854:ASP:OD1	2:D:854:ASP:N	2.46	0.45
2:D:884:VAL:HG11	2:D:1038:ALA:HA	1.98	0.45
3:I:110:GLN:HA	3:I:116:GLN:HE22	1.81	0.45
4:P:12:DT:H2'	4:P:13:DT:H71	1.98	0.45
1:A:117:LEU:HB3	1:B:19:HIS:CE1	2.51	0.45
3:H:205:HIS:CE1	3:H:207:ARG:HH21	2.34	0.45
2:C:292:TRP:O	2:C:296:GLN:HG2	2.16	0.45
2:D:296:GLN:O	2:D:300:LEU:HG	2.17	0.45
2:D:303:ALA:O	2:D:307:ARG:HG2	2.16	0.45
1:B:214:ARG:NH1	3:G:149:GLN:O	2.50	0.45
3:H:135:LEU:HD12	3:H:172:TYR:HD2	1.80	0.45
3:H:144:PHE:HB2	3:H:210:ILE:HG21	1.99	0.45
2:C:138:ASP:N	2:C:138:ASP:OD1	2.47	0.45
2:C:155:HIS:O	2:C:159:GLN:HG2	2.17	0.45
3:H:136:LEU:HD11	3:H:165:LEU:HD13	1.98	0.45
2:D:29:TYR:HE1	2:D:31:ARG:HG3	1.82	0.45
2:C:827:GLU:OE2	2:C:830:ARG:NH1	2.44	0.45
1:A:76:ALA:O	1:A:78:HIS:N	2.49	0.45
1:A:424:GLN:OE1	1:A:426:ARG:NH2	2.48	0.45
1:B:251:GLN:O	1:B:255:ARG:HG2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:929:LYS:HD3	2:D:929:LYS:HA	1.85	0.45
2:D:997:LEU:HD23	2:D:997:LEU:HA	1.85	0.45
3:H:157:GLN:HB3	3:H:209:ILE:HG23	1.98	0.44
1:A:8:ARG:HD3	1:B:38:ARG:HD3	1.98	0.44
2:C:307:ARG:HH12	2:C:310:LYS:HD2	1.81	0.44
2:C:340:TYR:HE1	2:C:693:ALA:HA	1.81	0.44
2:D:29:TYR:CE1	2:D:31:ARG:HG3	2.52	0.44
2:C:801:MET:HE3	2:C:801:MET:HB3	1.76	0.44
2:C:894:LEU:HD12	2:C:963:ALA:O	2.17	0.44
3:I:64:LEU:HA	3:I:104:VAL:O	2.16	0.44
2:D:39:THR:HG22	2:D:1064:SER:HB3	2.00	0.44
1:B:10:GLU:O	1:B:14:SER:OG	2.36	0.44
2:D:199:GLU:N	2:D:199:GLU:OE1	2.51	0.44
3:G:98:ASP:O	3:G:102:GLY:N	2.51	0.44
3:G:162:VAL:O	3:G:166:ILE:HG13	2.18	0.44
1:A:251:GLN:O	1:A:255:ARG:HG2	2.17	0.44
1:B:88:TRP:HA	1:B:91:ARG:HB2	2.00	0.44
2:C:793:GLN:HE21	2:C:797:LEU:HG	1.82	0.44
2:C:913:GLN:O	2:C:916:SER:OG	2.29	0.44
2:D:217:ILE:HD12	2:D:217:ILE:H	1.83	0.44
2:C:1006:CYS:HB3	2:C:1013:PRO:HA	1.99	0.43
2:C:875:ASP:HA	2:C:878:ASN:HD21	1.81	0.43
2:C:909:HIS:HA	2:C:912:ARG:NE	2.33	0.43
1:A:98:GLU:OE1	1:A:98:GLU:N	2.44	0.43
1:A:206:TRP:CZ3	1:A:306:ARG:HB2	2.53	0.43
1:A:121:ILE:HA	1:A:186:ARG:HH21	1.83	0.43
2:C:48:GLY:N	6:C:1201:AGS:O1A	2.48	0.43
2:D:722:GLN:HE21	2:D:726:GLN:NE2	2.17	0.43
3:G:111:GLY:H	3:G:116:GLN:HE22	1.64	0.43
3:G:121:HIS:HB3	3:G:124:VAL:HG23	1.99	0.43
3:G:163:ASP:OD1	3:G:163:ASP:N	2.52	0.43
2:D:912:ARG:HA	2:D:915:ASN:ND2	2.33	0.43
3:I:78:LEU:HD13	3:I:97:VAL:HG11	1.99	0.43
1:B:161:LEU:HD23	1:B:161:LEU:HA	1.87	0.43
2:D:715:ARG:O	2:D:719:GLN:HG2	2.19	0.43
3:I:83:VAL:HG13	3:I:86:ARG:NH2	2.33	0.43
2:D:325:GLN:O	2:D:328:ILE:HG22	2.18	0.43
1:A:8:ARG:HE	1:B:38:ARG:HE	1.66	0.43
2:C:1070:ARG:HG3	2:C:1074:GLU:O	2.19	0.43
2:D:812:LEU:HD13	2:D:825:TYR:CD2	2.54	0.43
3:F:50:GLN:HA	3:F:53:ARG:HE	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:255:ARG:HH22	1:A:300:GLN:HG2	1.83	0.43
1:A:359:VAL:HG21	3:I:217:LEU:HA	2.00	0.43
2:C:982:GLN:N	2:C:982:GLN:OE1	2.51	0.43
2:D:266:ALA:HB2	2:D:826:LEU:HD22	1.99	0.43
3:G:182:GLU:O	3:G:186:ILE:HG12	2.19	0.43
1:A:405:PHE:O	1:A:407:GLY:N	2.52	0.43
2:C:50:THR:OG1	6:C:1201:AGS:O2A	2.35	0.43
2:C:773:ARG:HB3	2:C:777:ARG:NH1	2.34	0.43
2:D:252:LEU:HD13	2:D:840:LYS:HD3	2.01	0.43
2:D:339:ARG:HD3	2:D:339:ARG:HA	1.81	0.43
3:H:121:HIS:HB3	3:H:124:VAL:HB	2.01	0.42
1:B:66:SER:OG	1:B:67:GLN:N	2.50	0.42
2:C:256:ARG:HB3	2:C:260:ARG:NH2	2.34	0.42
2:D:770:GLU:HA	2:D:773:ARG:HD2	2.00	0.42
2:D:828:ARG:O	2:D:832:LEU:N	2.30	0.42
2:C:307:ARG:NH1	2:C:307:ARG:HA	2.34	0.42
2:D:187:PHE:HD1	2:D:188:LEU:HD22	1.84	0.42
2:D:233:GLU:CD	2:D:233:GLU:H	2.27	0.42
1:A:173:VAL:HG21	1:B:147:PRO:HB3	2.00	0.42
2:D:812:LEU:HD11	2:D:828:ARG:HG2	2.00	0.42
5:Q:13:DA:H2"	5:Q:14:DA:H8	1.84	0.42
1:B:206:TRP:CZ3	1:B:306:ARG:HB2	2.54	0.42
2:C:822:VAL:O	2:C:826:LEU:HG	2.20	0.42
2:D:1068:VAL:HG22	2:D:1077:LEU:HG	2.00	0.42
2:C:269:TRP:CD1	2:C:273:ARG:HE	2.36	0.42
2:C:715:ARG:O	2:C:719:GLN:HG2	2.19	0.42
2:C:723:LEU:HD13	2:C:723:LEU:HA	1.93	0.42
3:I:219:ASN:OD1	3:I:219:ASN:N	2.49	0.42
1:A:32:LEU:HD21	1:A:64:TYR:CG	2.54	0.42
1:A:150:ARG:NH2	1:B:174:ASP:O	2.53	0.42
2:C:249:HIS:O	2:C:253:GLU:HG2	2.20	0.42
2:D:259:GLN:HG2	2:D:829:LEU:HD11	2.00	0.42
3:G:141:ARG:HD3	3:G:214:ILE:HG12	2.01	0.42
1:A:422:VAL:HG12	1:A:489:HIS:CG	2.54	0.42
1:A:154:LEU:HB2	1:B:165:LEU:HD13	2.02	0.42
2:C:266:ALA:HB2	2:C:826:LEU:HD22	2.01	0.42
2:D:909:HIS:HA	2:D:912:ARG:NE	2.35	0.42
1:B:98:GLU:HG2	1:B:99:GLY:N	2.35	0.42
2:D:252:LEU:HD22	2:D:840:LYS:HD3	2.02	0.42
1:A:288:LEU:HD23	1:A:288:LEU:HA	1.92	0.41
2:D:269:TRP:NE1	2:D:273:ARG:HE	2.18	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:292:TRP:O	2:D:296:GLN:HG2	2.20	0.41
3:H:139:ILE:HD13	3:H:168:GLN:HB3	2.02	0.41
1:A:91:ARG:HD3	1:A:91:ARG:HA	1.88	0.41
1:A:474:ASP:N	1:A:474:ASP:OD1	2.51	0.41
2:D:821:ASP:HA	2:D:824:ARG:HD3	2.01	0.41
1:B:359:VAL:HG21	3:G:217:LEU:HA	2.02	0.41
2:C:831:VAL:O	2:C:835:GLU:HG2	2.20	0.41
2:D:887:GLN:HA	2:D:1034:ARG:NH2	2.35	0.41
3:I:141:ARG:HD3	3:I:218:ALA:HB3	2.01	0.41
1:A:83:ARG:HA	1:A:86:ARG:NH1	2.35	0.41
2:C:272:TYR:O	2:C:276:GLN:HG3	2.20	0.41
1:A:24:LEU:HD22	1:A:93:LEU:HD21	2.02	0.41
2:D:307:ARG:HA	2:D:310:LYS:HE2	2.01	0.41
2:D:312:HIS:O	2:D:316:GLU:HG2	2.19	0.41
3:H:166:ILE:HB	3:H:167:PRO:HD3	2.02	0.41
3:I:92:ASP:HB2	3:I:121:HIS:HE2	1.85	0.41
2:C:296:GLN:OE1	2:C:299:ARG:NH2	2.42	0.41
2:C:844:PHE:O	2:C:848:LEU:HG	2.20	0.41
2:D:329:GLN:O	2:D:333:VAL:HG23	2.20	0.41
2:C:91:GLY:N	2:D:976:GLU:OE2	2.50	0.41
2:C:735:ARG:HA	2:C:738:TYR:HB3	2.02	0.41
2:C:798:ALA:HA	2:C:801:MET:HE3	2.03	0.41
2:D:254:THR:O	2:D:258:GLN:HG2	2.21	0.41
3:H:143:HIS:CE1	3:H:160:VAL:HG22	2.56	0.41
1:A:359:VAL:HG12	3:I:213:ILE:HD11	2.03	0.41
1:B:24:LEU:O	1:B:27:SER:OG	2.38	0.41
2:C:703:GLU:O	2:C:706:ARG:HB3	2.20	0.41
2:C:953:LEU:O	2:C:959:ARG:NH2	2.53	0.41
2:D:821:ASP:HB3	2:D:825:TYR:HE1	1.85	0.41
2:D:836:ALA:O	2:D:840:LYS:HG2	2.20	0.41
3:H:156:SER:OG	3:H:157:GLN:N	2.54	0.41
3:I:182:GLU:O	3:I:186:ILE:HG12	2.21	0.41
1:B:36:CYS:HB2	1:B:60:MET:SD	2.61	0.41
2:D:173:LYS:HE3	2:D:173:LYS:HB2	1.88	0.41
1:A:206:TRP:CH2	1:A:306:ARG:HD2	2.56	0.40
2:C:192:ARG:NH1	2:C:199:GLU:OE2	2.54	0.40
2:C:1058:LEU:O	2:C:1062:THR:OG1	2.22	0.40
2:D:858:GLN:OE1	2:D:859:LEU:N	2.54	0.40
2:D:1058:LEU:O	2:D:1062:THR:OG1	2.22	0.40
3:H:145:ILE:O	3:H:148:GLU:HG3	2.20	0.40
5:Q:12:DA:H2"	5:Q:13:DA:C8	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:Q:13:DA:H2"	5:Q:14:DA:C8	2.56	0.40
1:A:443:LEU:C	1:A:445:THR:H	2.29	0.40
1:A:463:GLU:OE1	1:A:463:GLU:N	2.46	0.40
2:C:854:ASP:OD1	2:C:855:GLY:N	2.54	0.40
2:C:84:VAL:O	2:C:102:ARG:NH2	2.55	0.40
2:C:232:PHE:CE2	2:C:954:LEU:HD12	2.57	0.40
2:C:282:LYS:HD3	2:C:282:LYS:HA	1.89	0.40
2:C:968:ASP:OD1	2:C:969:ARG:N	2.54	0.40
2:D:293:PHE:HD2	2:D:768:ILE:HG23	1.85	0.40
2:D:764:ASP:O	2:D:768:ILE:N	2.42	0.40
1:A:144:ASN:HA	1:A:145:PRO:HD3	1.96	0.40
2:C:20:LEU:HA	2:C:20:LEU:HD23	1.83	0.40
2:C:33:GLU:OE1	2:C:33:GLU:N	2.55	0.40
2:D:845:LEU:HD23	2:D:848:LEU:HD12	2.02	0.40
3:H:136:LEU:HD22	3:H:189:LEU:HB3	2.03	0.40
1:A:454:ARG:NH1	2:D:1076:SER:OG	2.55	0.40
1:B:308:ARG:HA	1:B:311:ARG:NH1	2.37	0.40
2:C:248:ILE:HG21	2:C:843:ARG:HB3	2.04	0.40
2:D:176:MET:HE3	2:D:176:MET:HB3	1.98	0.40
3:I:157:GLN:HE21	3:I:159:LEU:HD11	1.86	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	431/517 (83%)	410 (95%)	21 (5%)	0	100	100
1	B	333/517 (64%)	321 (96%)	12 (4%)	0	100	100
2	C	717/1119 (64%)	688 (96%)	29 (4%)	0	100	100
2	D	712/1119 (64%)	684 (96%)	28 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	F	61/249 (24%)	60 (98%)	1 (2%)	0	100	100
3	G	187/249 (75%)	182 (97%)	5 (3%)	0	100	100
3	H	170/249 (68%)	167 (98%)	3 (2%)	0	100	100
3	I	187/249 (75%)	182 (97%)	5 (3%)	0	100	100
All	All	2798/4268 (66%)	2694 (96%)	104 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	368/440 (84%)	355 (96%)	13 (4%)	31	53
1	B	286/440 (65%)	278 (97%)	8 (3%)	38	59
2	C	604/936 (64%)	582 (96%)	22 (4%)	30	53
2	D	600/936 (64%)	579 (96%)	21 (4%)	31	53
3	F	57/205 (28%)	57 (100%)	0	100	100
3	G	164/205 (80%)	163 (99%)	1 (1%)	84	88
3	H	156/205 (76%)	153 (98%)	3 (2%)	52	69
3	I	164/205 (80%)	163 (99%)	1 (1%)	84	88
All	All	2399/3572 (67%)	2330 (97%)	69 (3%)	39	58

All (69) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	52	ASP
1	A	85	LEU
1	A	98	GLU
1	A	137	GLU
1	A	210	ASP
1	A	254	LEU

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Mol	Chain	Res	Type
1	A	293	LEU
1	A	364	THR
1	A	417	THR
1	A	442	ASP
1	A	444	GLU
1	A	477	ARG
1	A	492	LEU
1	B	14	SER
1	B	52	ASP
1	B	79	LEU
1	B	101	ILE
1	B	125	THR
1	B	135	GLU
1	B	254	LEU
1	B	342	VAL
2	C	14	ILE
2	C	16	THR
2	C	53	VAL
2	C	54	ASP
2	C	58	THR
2	C	97	GLN
2	C	121	VAL
2	C	138	ASP
2	C	140	LYS
2	C	153	LEU
2	C	168	LEU
2	C	197	VAL
2	C	243	ASP
2	C	747	ASP
2	C	750	ARG
2	C	853	ASP
2	C	858	GLN
2	C	859	LEU
2	C	914	LEU
2	C	937	LEU
2	C	953	LEU
2	C	967	ILE
2	D	19	GLU
2	D	27	GLN
2	D	79	ASP
2	D	87	VAL
2	D	106	THR

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Mol	Chain	Res	Type
2	D	114	LEU
2	D	129	PHE
2	D	135	SER
2	D	138	ASP
2	D	174	ASP
2	D	227	ASP
2	D	247	ASP
2	D	713	LEU
2	D	722	GLN
2	D	844	PHE
2	D	874	LEU
2	D	884	VAL
2	D	937	LEU
2	D	1028	SER
2	D	1060	HIS
2	D	1073	VAL
3	G	163	ASP
3	H	81	ILE
3	H	135	LEU
3	H	205	HIS
3	I	163	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (59) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	80	GLN
1	A	144	ASN
1	A	159	GLN
1	A	252	GLN
1	A	466	GLN
1	B	19	HIS
1	B	80	GLN
1	B	163	HIS
1	B	252	GLN
1	B	330	GLN
2	C	97	GLN
2	C	103	GLN
2	C	258	GLN
2	C	722	GLN
2	C	754	GLN
2	C	878	ASN
2	C	1060	HIS

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Mol	Chain	Res	Type
2	C	1069	HIS
2	D	155	HIS
2	D	712	GLN
2	D	722	GLN
2	D	915	ASN
2	D	973	ASN
2	D	1045	HIS
2	D	1061	HIS
3	F	57	GLN
3	F	69	HIS
3	F	110	GLN
3	G	57	GLN
3	G	80	ASN
3	G	110	GLN
3	G	116	GLN
3	G	127	GLN
3	G	142	GLN
3	G	149	GLN
3	G	157	GLN
3	G	168	GLN
3	G	196	HIS
3	G	205	HIS
3	G	216	HIS
3	G	222	ASN
3	G	224	GLN
3	H	57	GLN
3	H	69	HIS
3	H	110	GLN
3	H	149	GLN
3	H	233	GLN
3	I	57	GLN
3	I	69	HIS
3	I	80	ASN
3	I	110	GLN
3	I	116	GLN
3	I	127	GLN
3	I	142	GLN
3	I	149	GLN
3	I	157	GLN
3	I	168	GLN
3	I	222	ASN
3	I	224	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 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	$\#\|Z\| > 2$
6	AGS	D	1201	-	28,33,33	0.81	1 (3%)	31,52,52	0.95	2 (6%)
6	AGS	C	1201	-	28,33,33	0.89	1 (3%)	31,52,52	1.07	2 (6%)

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	AGS	D	1201	-	-	4/17/38/38	0/3/3/3
6	AGS	C	1201	-	-	4/17/38/38	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	D	1201	AGS	PG-S1G	2.09	1.95	1.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	C	1201	AGS	PG-S1G	2.07	1.95	1.90

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	C	1201	AGS	PB-O3B-PG	-4.65	116.14	133.17
6	D	1201	AGS	PB-O3B-PG	-3.72	119.55	133.17
6	C	1201	AGS	C5-C6-N6	2.28	123.79	120.31
6	D	1201	AGS	C5-C6-N6	2.28	123.78	120.31

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	C	1201	AGS	PB-O3B-PG-O2G
6	D	1201	AGS	PB-O3B-PG-O3G
6	D	1201	AGS	O4'-C4'-C5'-O5'
6	D	1201	AGS	C3'-C4'-C5'-O5'
6	C	1201	AGS	C5'-O5'-PA-O1A
6	C	1201	AGS	PA-O3A-PB-O1B
6	C	1201	AGS	C4'-C5'-O5'-PA
6	D	1201	AGS	C4'-C5'-O5'-PA

There are no ring outliers.

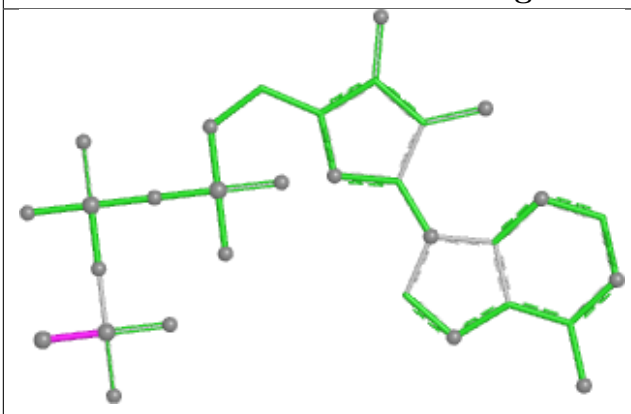
2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	D	1201	AGS	2	0
6	C	1201	AGS	4	0

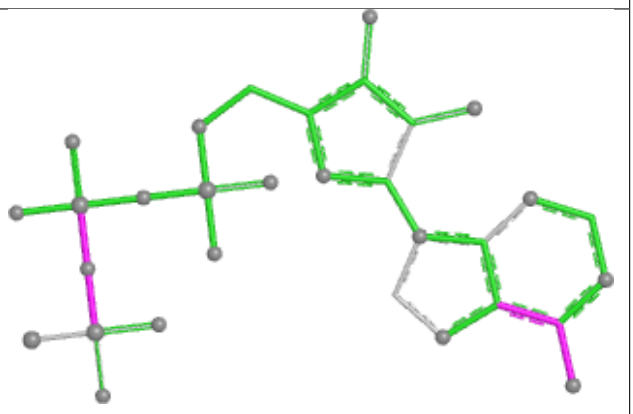
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

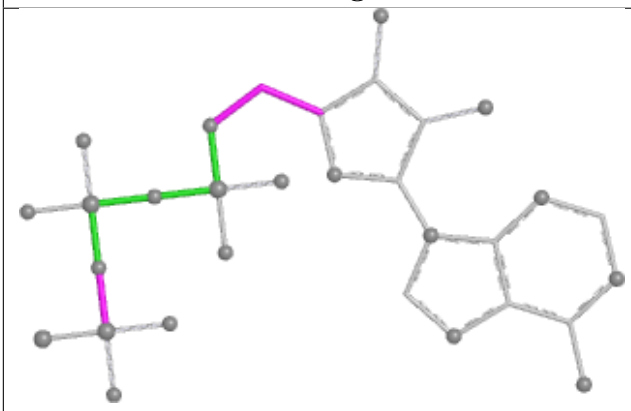
Ligand AGS D 1201



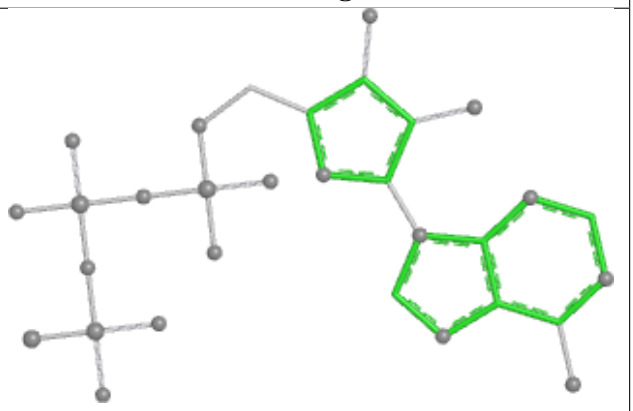
Bond lengths



Bond angles

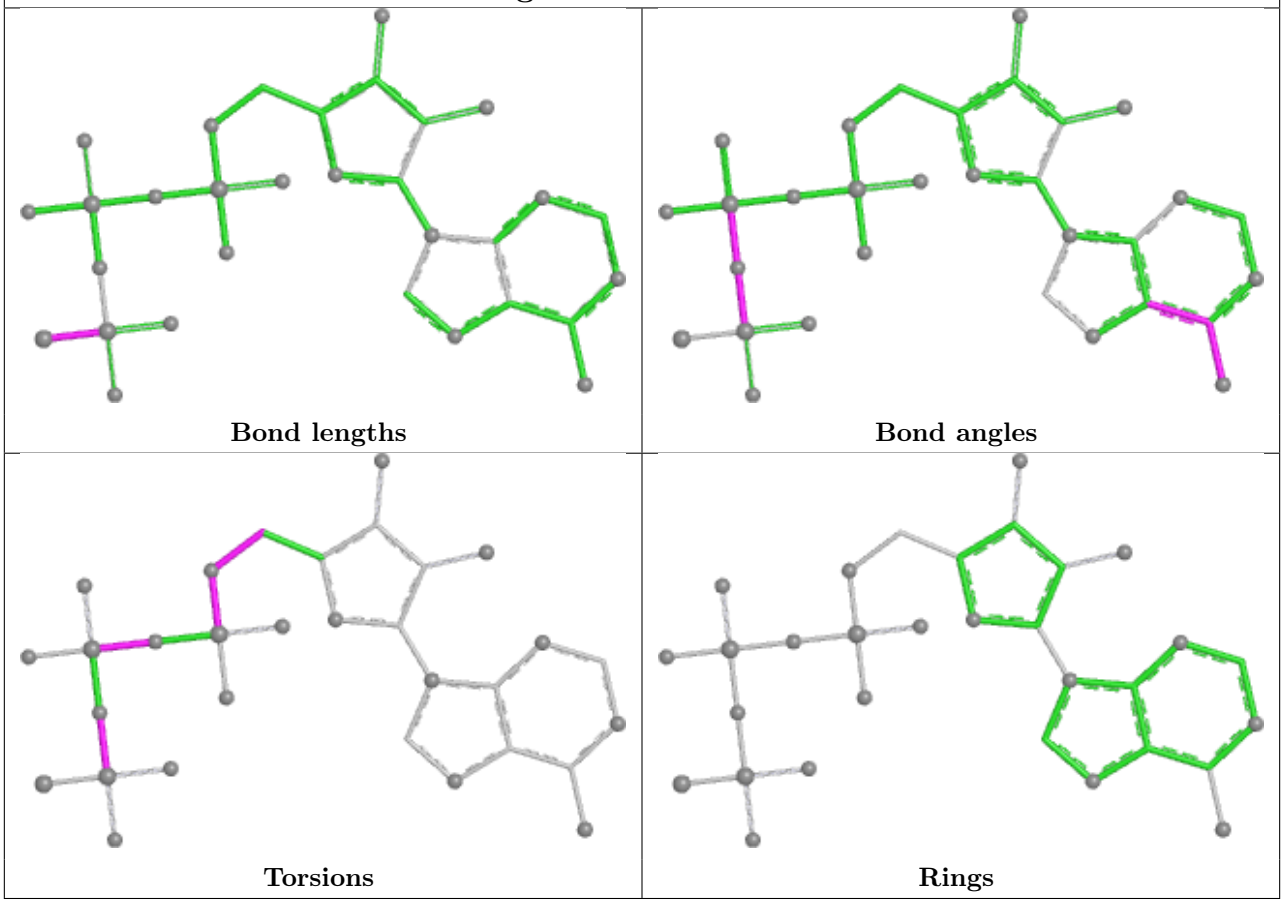


Torsions



Rings

Ligand AGS C 1201



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.

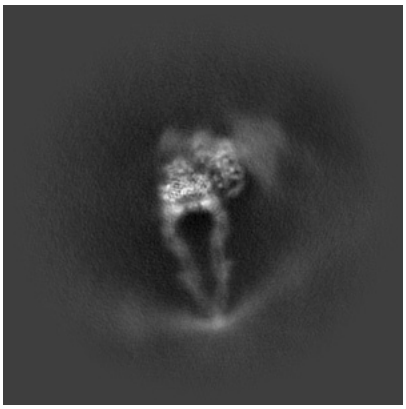
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-27481. These allow visual inspection of the internal detail of the map and identification of artifacts.

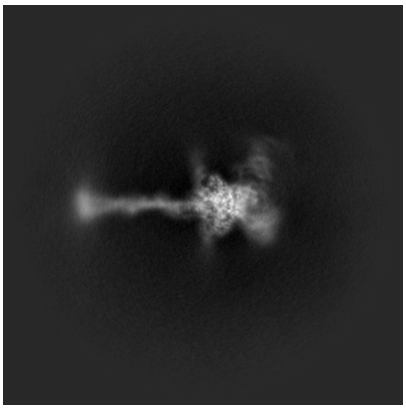
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

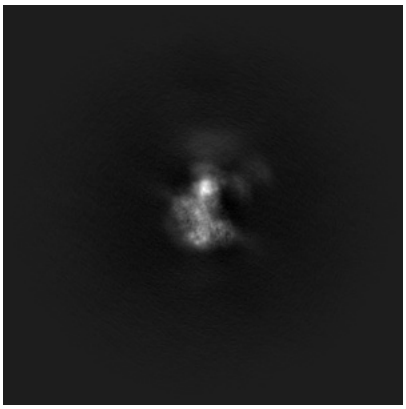
6.1.1 Primary map



X

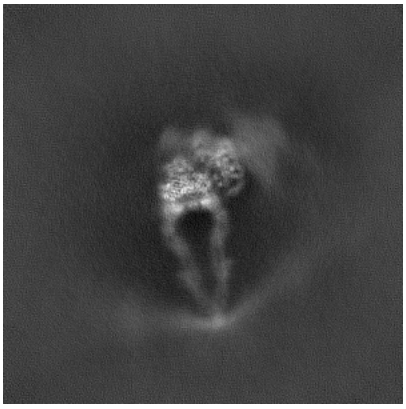


Y

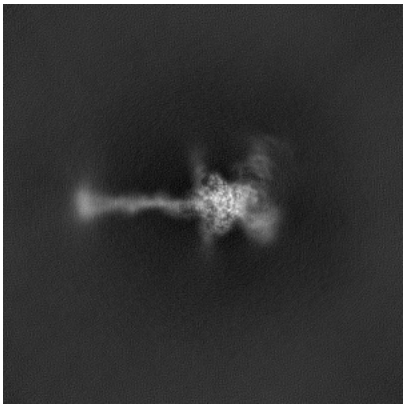


Z

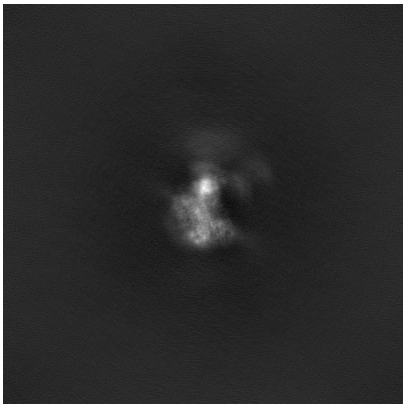
6.1.2 Raw map



X



Y

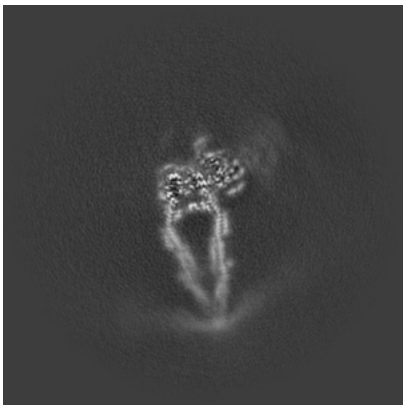


Z

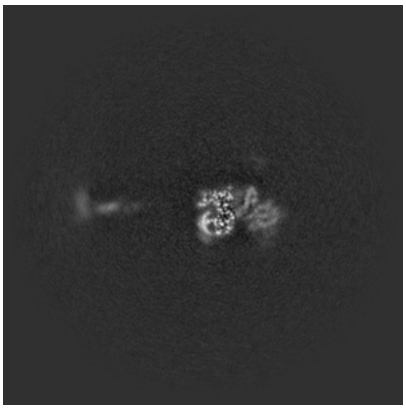
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

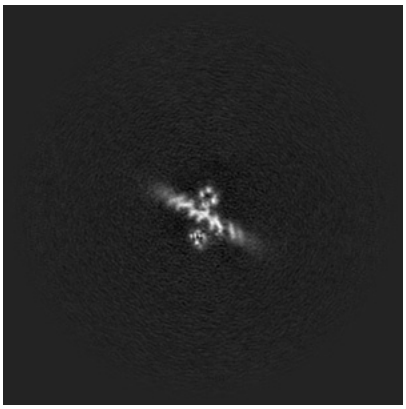
6.2.1 Primary map



X Index: 192



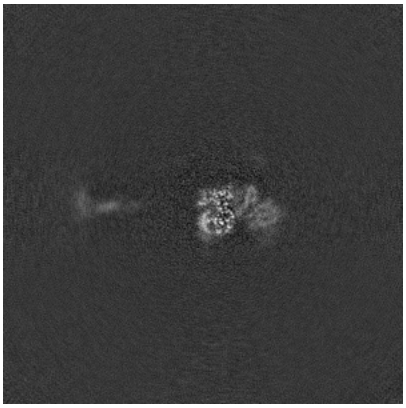
Y Index: 192



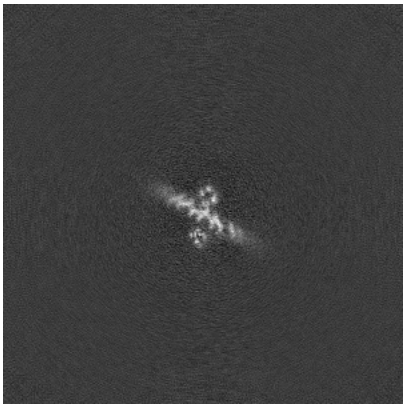
Z Index: 192

6.2.2 Raw map

X Index: 192



Y Index: 192

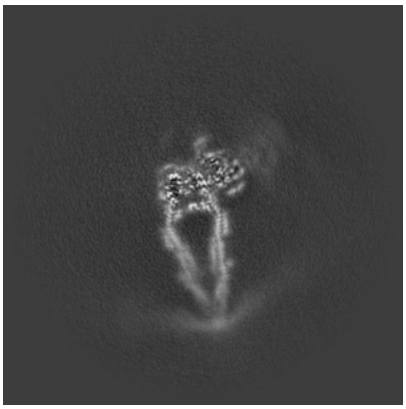


Z Index: 192

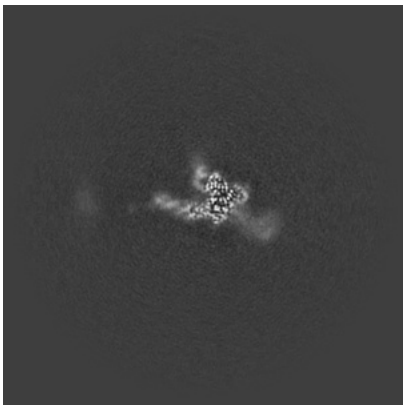
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

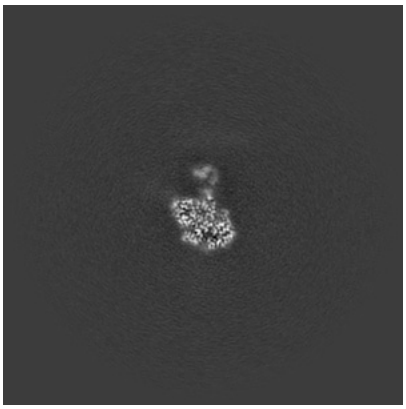
6.3.1 Primary map



X Index: 192

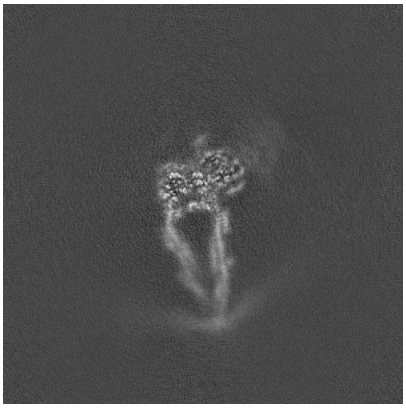


Y Index: 164

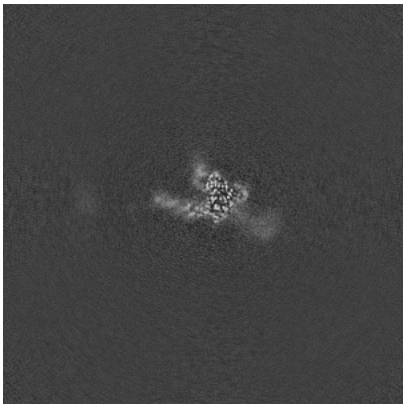


Z Index: 206

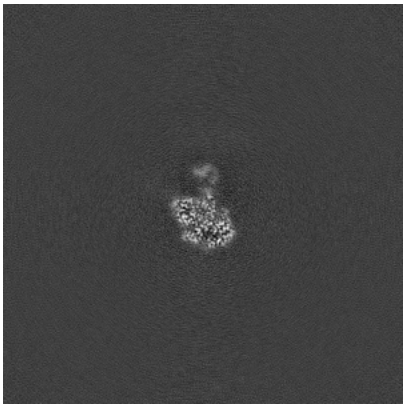
6.3.2 Raw map



X Index: 193



Y Index: 164

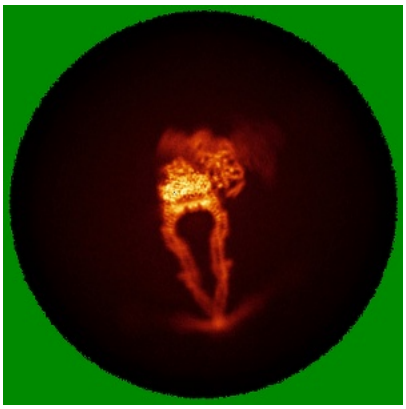


Z Index: 206

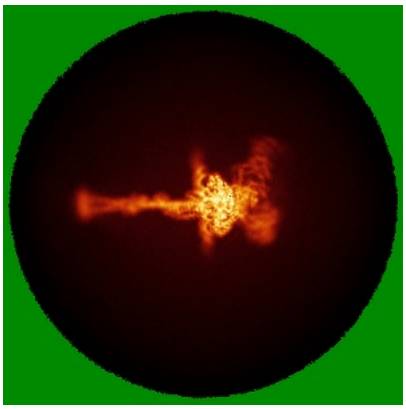
The images above show the largest variance slices of the map in three orthogonal directions.

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

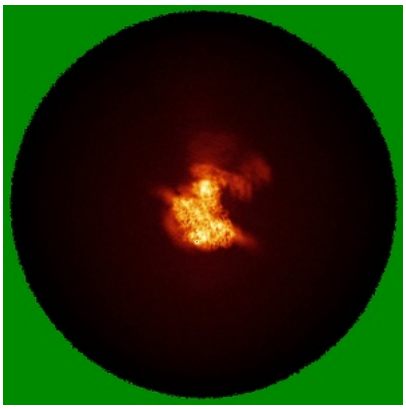
6.4.1 Primary map



X

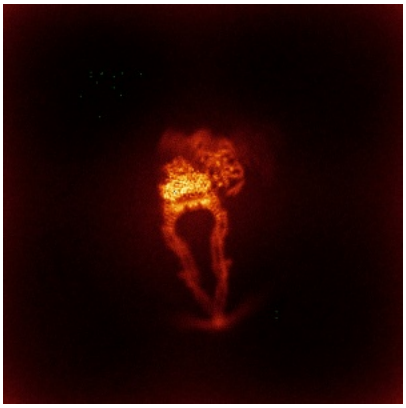


Y

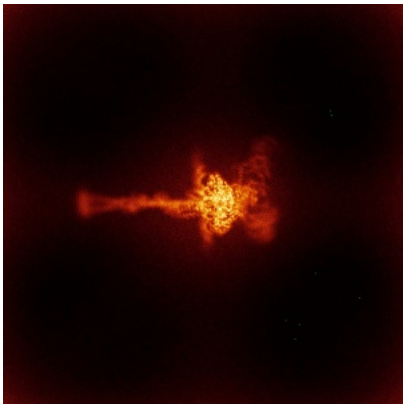


Z

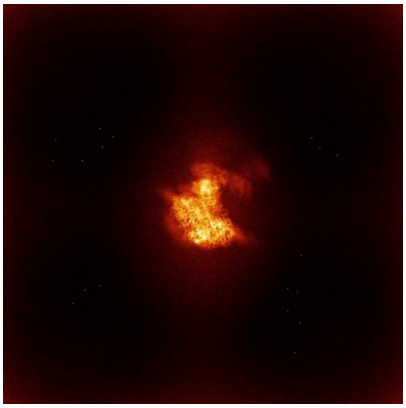
6.4.2 Raw map



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 0.2. 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.

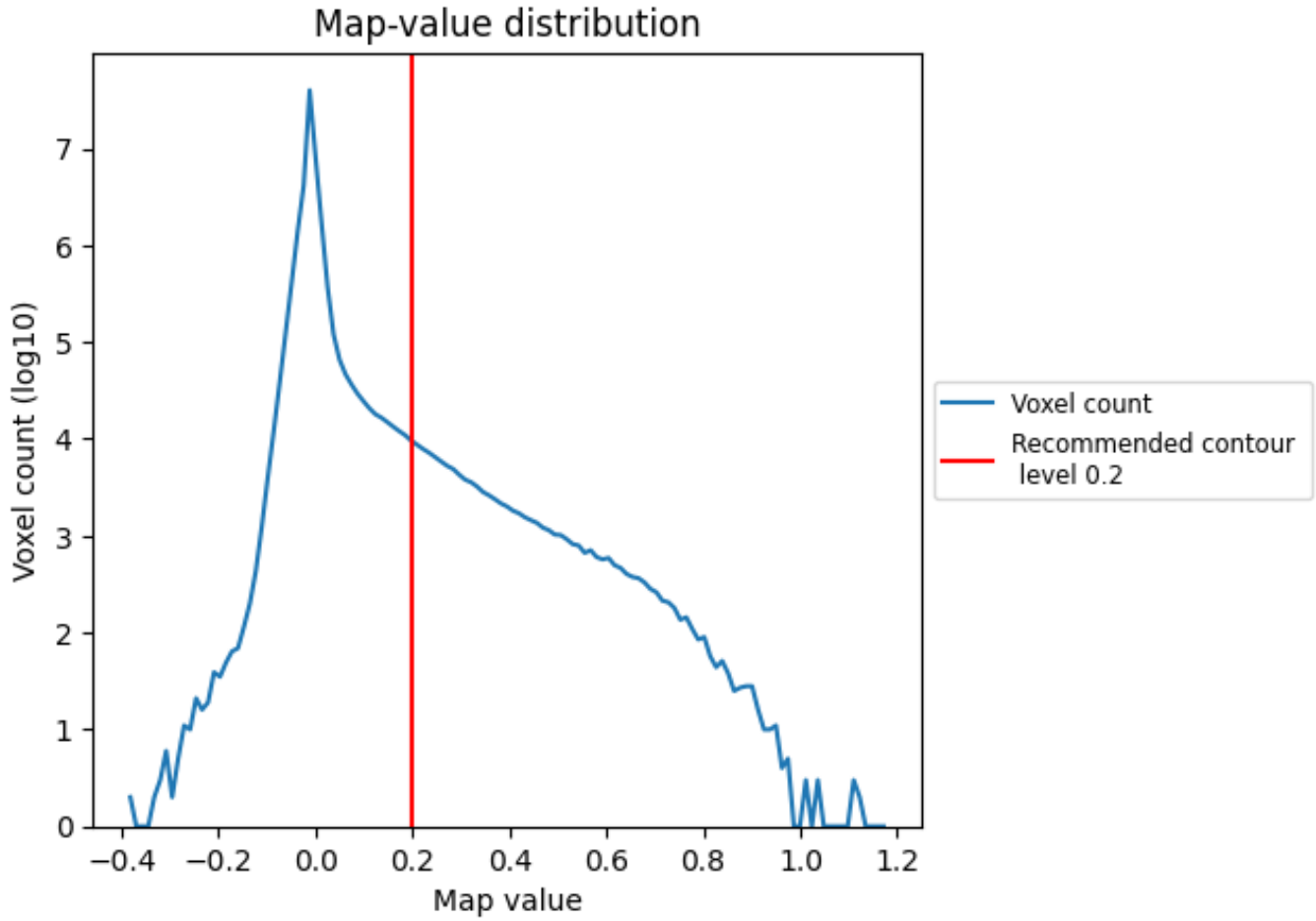
6.6 Mask visualisation (i)

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

7 Map analysis

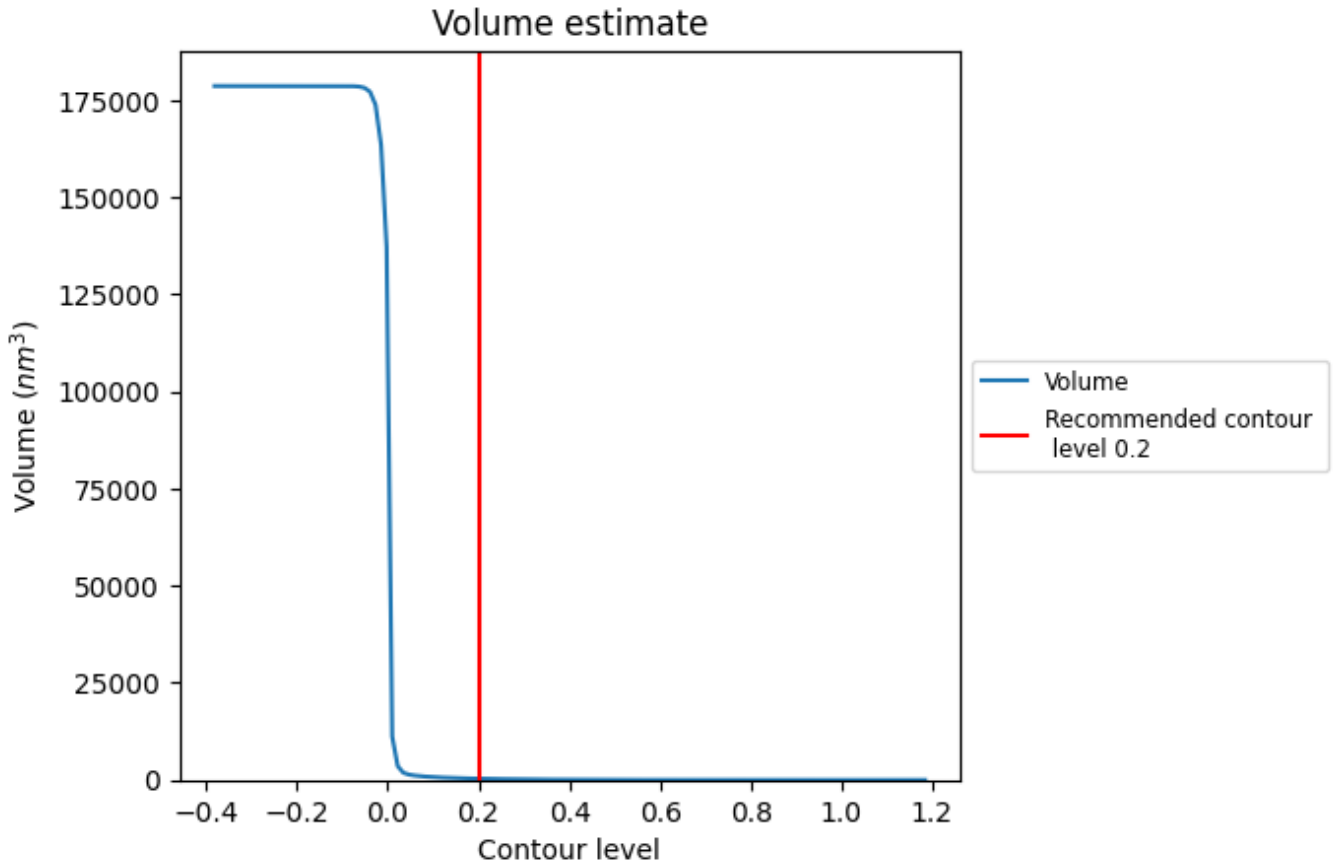
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

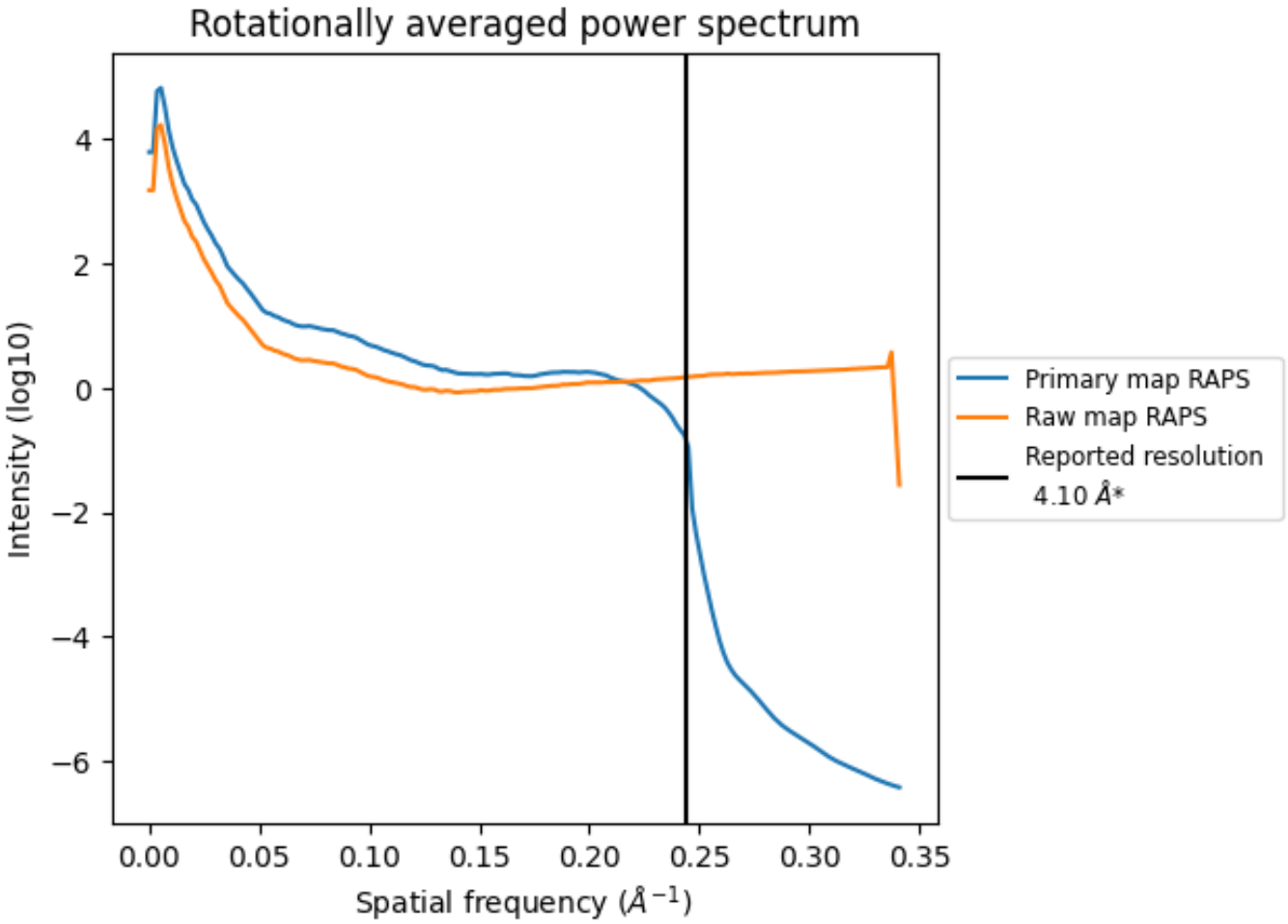
7.2 Volume estimate



The volume at the recommended contour level is 327 nm^3; this corresponds to an approximate mass of 295 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)

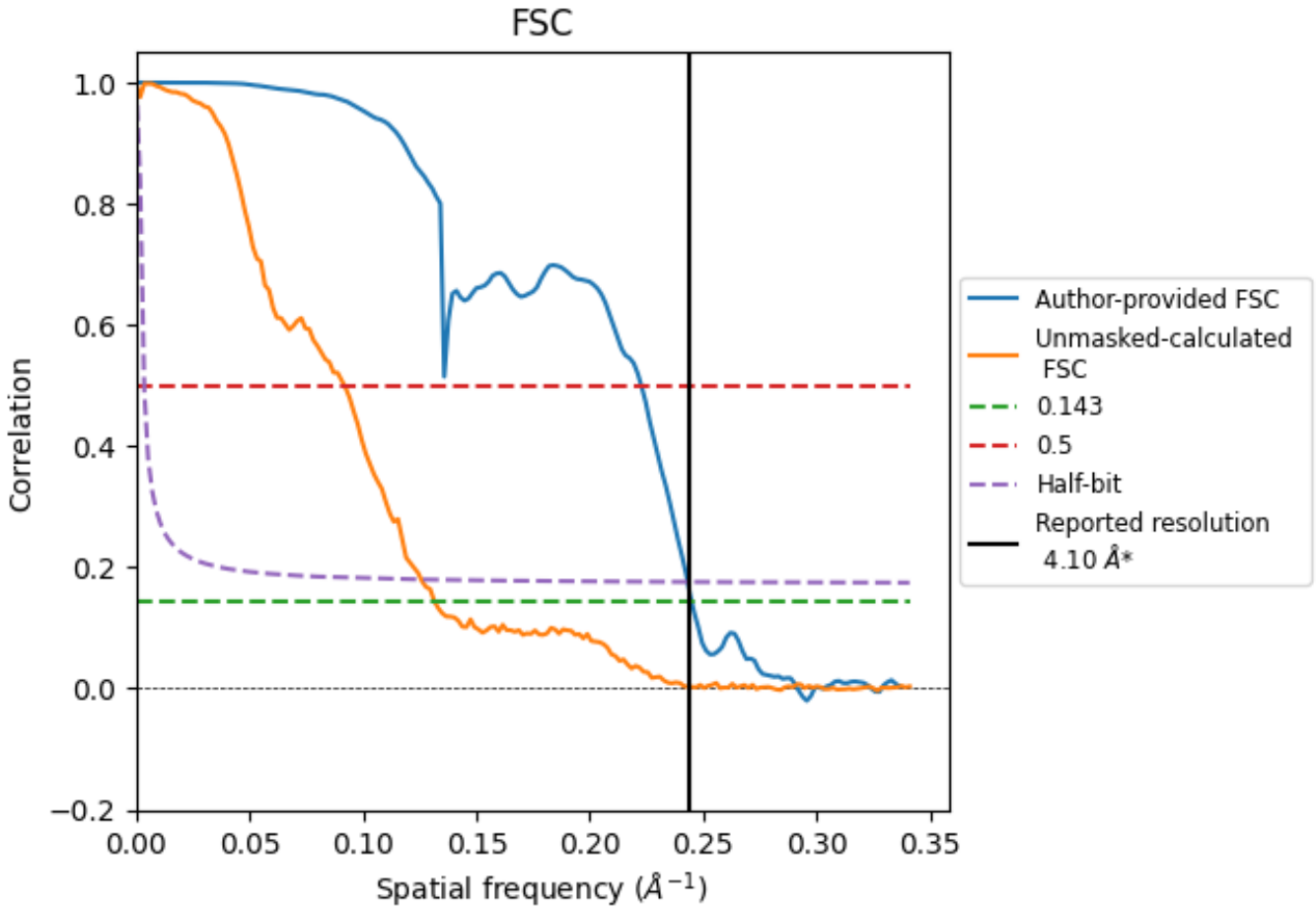


*Reported resolution corresponds to spatial frequency of 0.244 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.244 Å^{-1}

8.2 Resolution estimates (i)

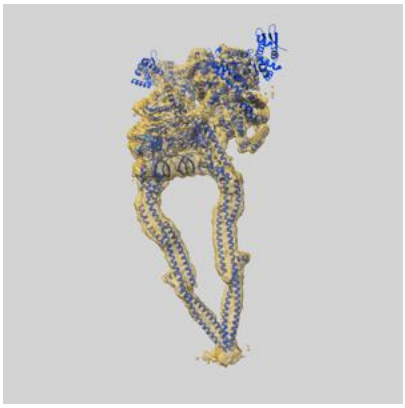
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.10	-	-
Author-provided FSC curve	4.08	4.49	4.11
Unmasked-calculated*	7.60	10.89	7.96

*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 7.60 differs from the reported value 4.1 by more than 10 %

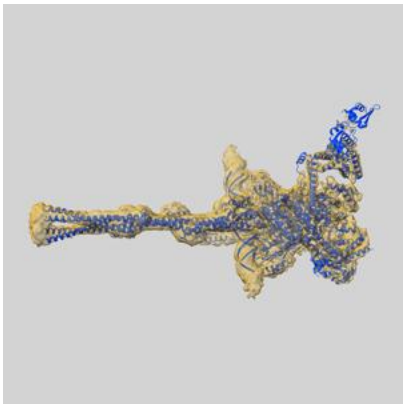
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-27481 and PDB model 8DK2. Per-residue inclusion information can be found in section 3 on page 8.

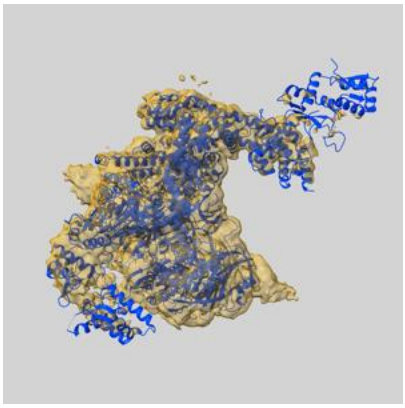
9.1 Map-model overlay



X



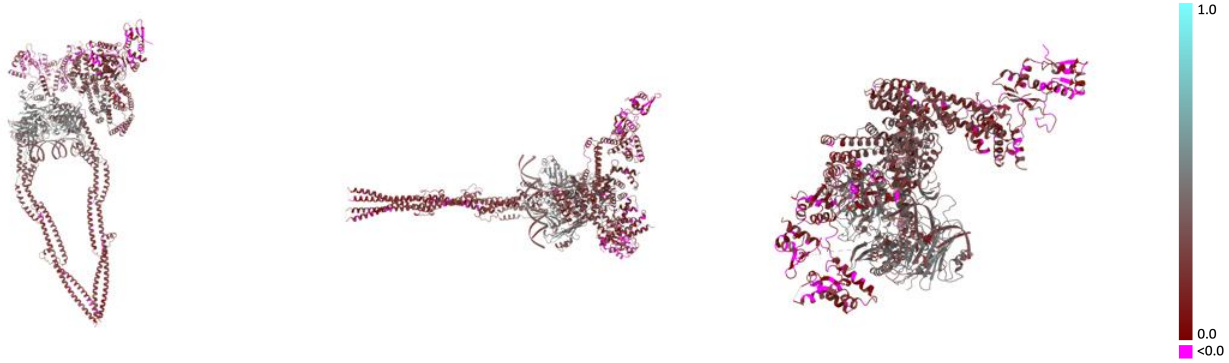
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.2 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.

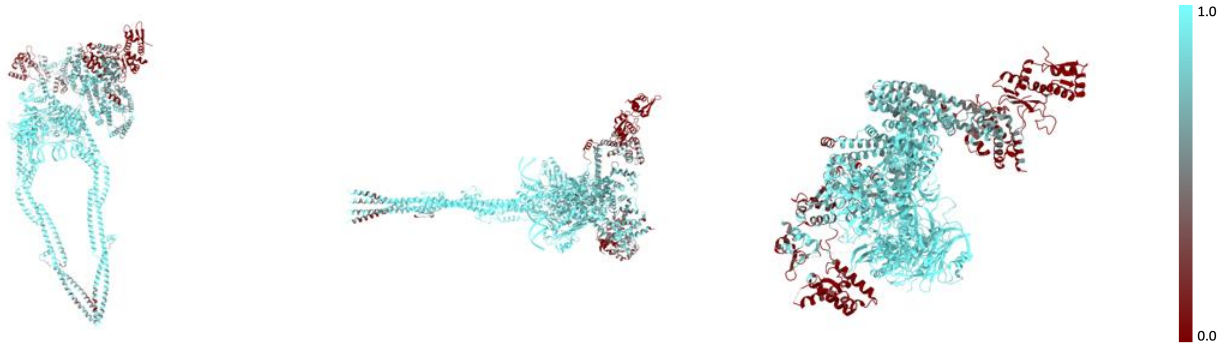
9.2 Q-score mapped to coordinate model (i)



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.

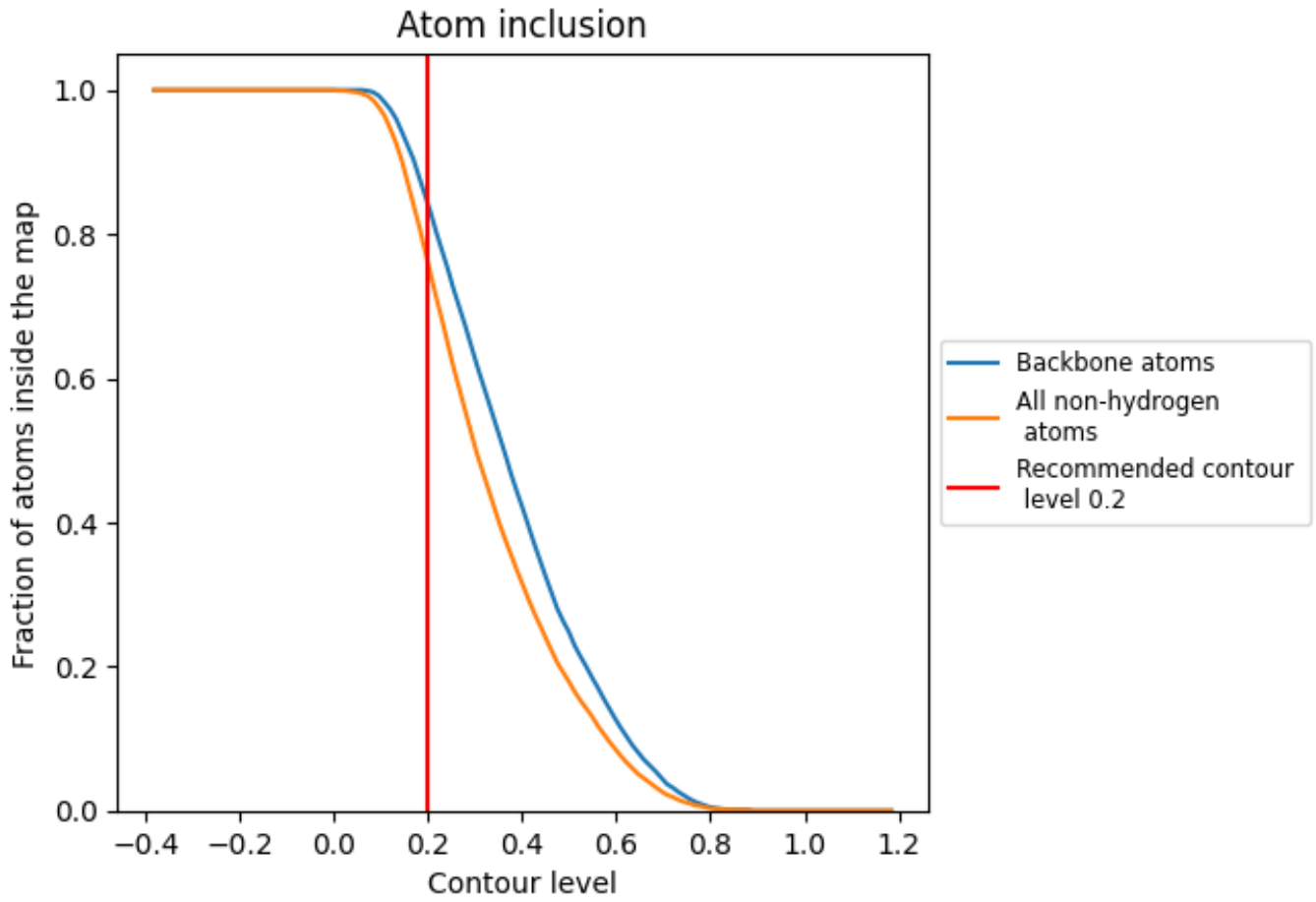
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.2).

9.4 Atom inclusion (i)



At the recommended contour level, 84% of all backbone atoms, 76% 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 (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7590	0.2690
A	0.8230	0.2880
B	0.6510	0.2410
C	0.9420	0.3290
D	0.9210	0.3300
F	0.0020	0.0580
G	0.2270	0.1510
H	0.2320	0.0750
I	0.5980	0.1460
P	1.0000	0.3170
Q	1.0000	0.3250