



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 06:04 AM UTC

PDB ID : 8JKE / pdb_00008jke
EMDB ID : EMD-36370
Title : AfsR(T337A) transcription activation complex
Authors : Wang, Y.; Zheng, J.
Deposited on : 2023-06-01
Resolution : 3.67 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:

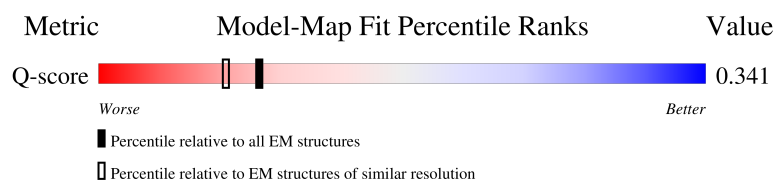
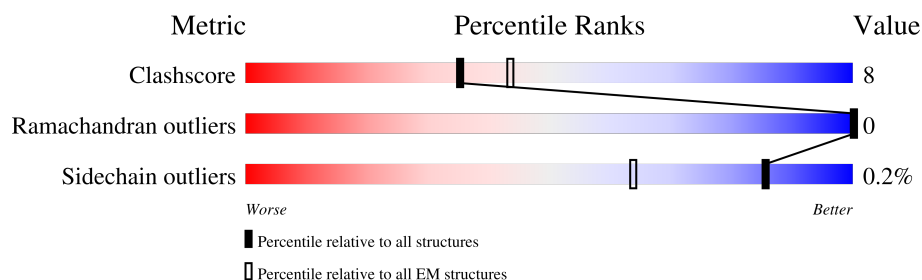
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 3.67 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.



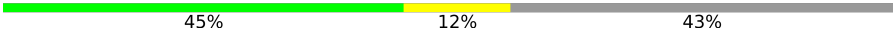
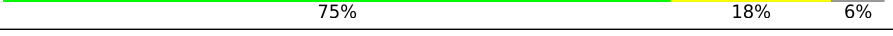
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	11424 (3.17 - 4.17)

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

Mol	Chain	Length	Quality of chain
1	A	340	 56% 10% 34%
1	B	340	 52% 16% 31%
1	K	340	 9% 20% 79%
2	C	1161	 75% 21%

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Mol	Chain	Length	Quality of chain
3	D	1307	 75%21%.
4	E	90	 63%22%14%
5	F	531	 45%12%43%
6	G	124	 64%10%26%
7	H	160	 27%87%11%..
8	I	1013	 20%5%75%
8	J	1013	 21%.75%
9	O	65	 71%23%6%
10	P	65	 75%18%6%

2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 33932 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-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	226	Total	C	N	O	S	0	0
			1742	1102	302	334	4		
1	B	233	Total	C	N	O	S	0	0
			1792	1131	309	347	5		
1	K	73	Total	C	N	O	S	0	0
			545	340	94	109	2		

- Molecule 2 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	1114	Total	C	N	O	S	0	0
			8675	5439	1511	1694	31		

- Molecule 3 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	1259	Total	C	N	O	S	0	0
			9846	6161	1787	1857	41		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	1300	HIS	-	expression tag	UNP Q8CJT1
D	1301	HIS	-	expression tag	UNP Q8CJT1
D	1302	HIS	-	expression tag	UNP Q8CJT1
D	1303	HIS	-	expression tag	UNP Q8CJT1
D	1304	HIS	-	expression tag	UNP Q8CJT1
D	1305	HIS	-	expression tag	UNP Q8CJT1
D	1306	HIS	-	expression tag	UNP Q8CJT1
D	1307	HIS	-	expression tag	UNP Q8CJT1

- Molecule 4 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	E	77	Total	C	N	O	0	0
			597	382	98	117		

- Molecule 5 is a protein called RNA polymerase principal sigma factor HrdB.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	301	Total	C	N	O	S	0	0
			2398	1510	426	455	7		

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	-19	MET	-	initiating methionine	UNP P18183
F	-18	GLY	-	expression tag	UNP P18183
F	-17	SER	-	expression tag	UNP P18183
F	-16	SER	-	expression tag	UNP P18183
F	-15	HIS	-	expression tag	UNP P18183
F	-14	HIS	-	expression tag	UNP P18183
F	-13	HIS	-	expression tag	UNP P18183
F	-12	HIS	-	expression tag	UNP P18183
F	-11	HIS	-	expression tag	UNP P18183
F	-10	HIS	-	expression tag	UNP P18183
F	-9	SER	-	expression tag	UNP P18183
F	-8	SER	-	expression tag	UNP P18183
F	-7	GLY	-	expression tag	UNP P18183
F	-6	LEU	-	expression tag	UNP P18183
F	-5	VAL	-	expression tag	UNP P18183
F	-4	PRO	-	expression tag	UNP P18183
F	-3	ARG	-	expression tag	UNP P18183
F	-2	GLY	-	expression tag	UNP P18183
F	-1	SER	-	expression tag	UNP P18183
F	0	HIS	-	expression tag	UNP P18183

- Molecule 6 is a protein called RNA polymerase-binding protein RbpA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	92	Total	C	N	O	S	0	0
			734	455	132	141	6		

- Molecule 7 is a protein called Putative transcriptional factor regulator.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	158	Total	C	N	O	S	0	0
			1241	779	225	236	1		

- Molecule 8 is a protein called Regulatory protein AfsR.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	254	Total	C	N	O	S	0	0
			1934	1199	363	368	4		
8	J	254	Total	C	N	O	S	0	0
			1934	1199	363	368	4		

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	-19	MET	-	initiating methionine	UNP P25941
I	-18	GLY	-	expression tag	UNP P25941
I	-17	SER	-	expression tag	UNP P25941
I	-16	SER	-	expression tag	UNP P25941
I	-15	HIS	-	expression tag	UNP P25941
I	-14	HIS	-	expression tag	UNP P25941
I	-13	HIS	-	expression tag	UNP P25941
I	-12	HIS	-	expression tag	UNP P25941
I	-11	HIS	-	expression tag	UNP P25941
I	-10	HIS	-	expression tag	UNP P25941
I	-9	SER	-	expression tag	UNP P25941
I	-8	SER	-	expression tag	UNP P25941
I	-7	GLY	-	expression tag	UNP P25941
I	-6	LEU	-	expression tag	UNP P25941
I	-5	VAL	-	expression tag	UNP P25941
I	-4	PRO	-	expression tag	UNP P25941
I	-3	ARG	-	expression tag	UNP P25941
I	-2	GLY	-	expression tag	UNP P25941
I	-1	SER	-	expression tag	UNP P25941
I	0	HIS	-	expression tag	UNP P25941
I	337	ALA	THR	engineered mutation	UNP P25941
J	-19	MET	-	initiating methionine	UNP P25941
J	-18	GLY	-	expression tag	UNP P25941
J	-17	SER	-	expression tag	UNP P25941
J	-16	SER	-	expression tag	UNP P25941
J	-15	HIS	-	expression tag	UNP P25941
J	-14	HIS	-	expression tag	UNP P25941
J	-13	HIS	-	expression tag	UNP P25941
J	-12	HIS	-	expression tag	UNP P25941

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Chain	Residue	Modelled	Actual	Comment	Reference
J	-11	HIS	-	expression tag	UNP P25941
J	-10	HIS	-	expression tag	UNP P25941
J	-9	SER	-	expression tag	UNP P25941
J	-8	SER	-	expression tag	UNP P25941
J	-7	GLY	-	expression tag	UNP P25941
J	-6	LEU	-	expression tag	UNP P25941
J	-5	VAL	-	expression tag	UNP P25941
J	-4	PRO	-	expression tag	UNP P25941
J	-3	ARG	-	expression tag	UNP P25941
J	-2	GLY	-	expression tag	UNP P25941
J	-1	SER	-	expression tag	UNP P25941
J	0	HIS	-	expression tag	UNP P25941
J	337	ALA	THR	engineered mutation	UNP P25941

- Molecule 9 is a DNA chain called DNA(65-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
9	O	61	Total	C	N	O	P	0	0
			1233	587	211	374	61		

- Molecule 10 is a DNA chain called DNA(65-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
10	P	61	Total	C	N	O	P	0	0
			1258	593	244	360	61		

- Molecule 11 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
11	D	1	Total	Mg	0
			1	1	

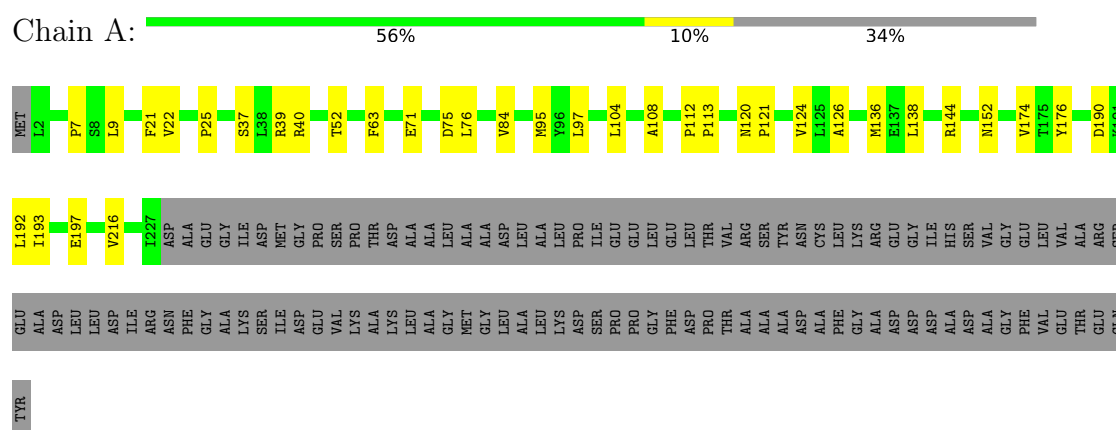
- Molecule 12 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
12	D	2	Total	Zn	0
			2	2	

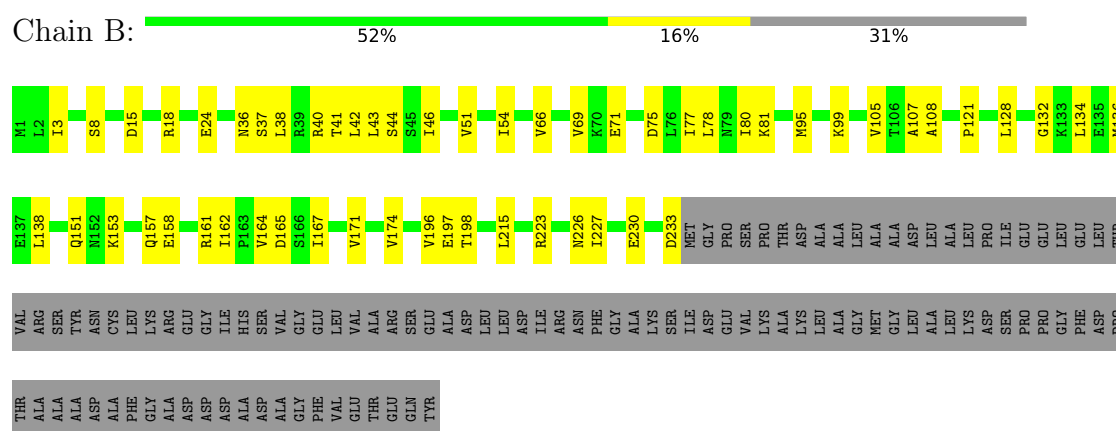
3 Residue-property plots

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.

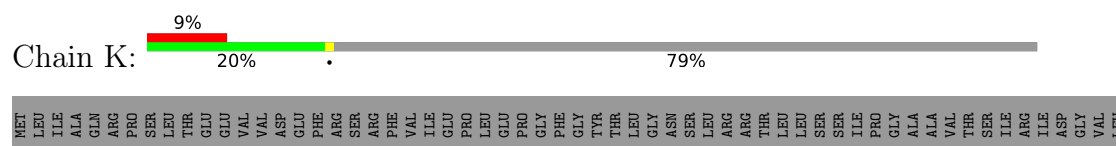
- Molecule 1: DNA-directed RNA polymerase subunit alpha



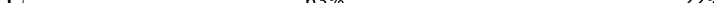
- Molecule 1: DNA-directed RNA polymerase subunit alpha

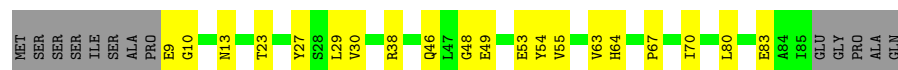


- Molecule 1: DNA-directed RNA polymerase subunit alpha

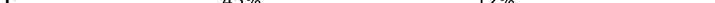


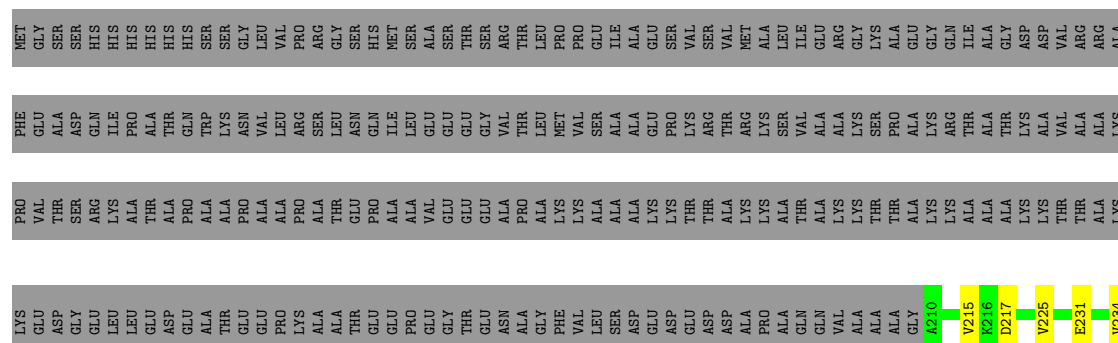
- Molecule 4: DNA-directed RNA polymerase subunit omega

Chain E:  63% 22% 14%



- Molecule 5: RNA polymerase principal sigma factor HrdB

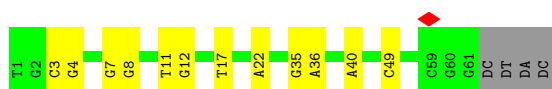
Chain F:  45% 12% 43%



- Molecule 8: Regulatory protein AfsR



ALA	ASN	GLY	ASP	PRO	PHE	ARG	ASP	TYR	THR	A232	E68	MET
ASN	SER	LEU	GLY	ALA	LEU	GLN	ALA	ASP	GLY	L233	Q81	GLY
HIS	GLN	TYR	PRO	ARG	TYR	ALA	VAL	GLN	ALA	A234	A84	SER
GLU	TYR	THR	THR	PHE	GLY	ASP	PRO	GLY	PHE	A237	S91	HIS
ALA	ALA	TYR	ASP	VAL	GLN	VAL	LEU	ALA	ARG	D238	R92	HIS
THR	THR	PRO	GLY	GLY	GLY	PRO	LEU	ALA	GLU	R241	R93	HIS
ALA	ALA	GLY	VAL	PRO	ALA	ALA	PRO	ALA	LEU	L242	R94	HIS
ARG	ARG	LEU	ARG	GLY	ALA	CYS	GLY	PRO	SER	L243	K95	SER
ALA	ALA	THR	THR	LEU	GLN	GLY	THR	ALA	ASP	L247	V96	SER
MET	PHE	THR	PHE	ASP	PHE	THR	ASP	GLY	VAL	G248	L102	GLY
CYS	ASP	THR	ARG	GLY	ARG	PRO	GLY	PRO	LEU	V249	L109	LEU
ASP	GLU	THR	GLY	ALA	PHE	LEU	CYS	GLU	SER	D250	Y109	VAL
ALA	ALA	THR	ALA	LEU	ALA	ALA	ALA	THR	ALA	P251	A150	PRO
THR	THR	GLY	ALA	LEU	LEU	ILE	LEU	GLY	SER	R252	L127	ARG
GLY	ALA	SER	ALA	GLU	GLY	ILE	VAL	SER	GLY	P253	L146	GLY
ALA	ALA	THR	THR	ARG	GLY	ALA	THR	PHE	GLU	G254	L147	SER
ALA	ALA	ASP	ALA	LEU	LEU	ALA	ALA	LEU	SER	E257	A150	MET
ASP	TRP	GLU	TRP	GLU	ALA	SER	VAL	LEU	ALA	L258	D155	ASP
THR	THR	ARG	TYR	ASP	GLY	THR	ARG	ALA	GLY	Q259	L158	GLY
GLU	GLU	THR	THR	ASN	ASP	LEU	MET	GLY	ARG	R261	L159	PRO
ALA	ALA	ALA	ALA	ALA	ILE	ALA	ASP	THR	MET	Q260	V162	ARG
ARG	ARG	PRO	PRO	PRO	SER	ARG	LEU	ALA	VAL	L262	L184	VAL
GLY	GLY	GLY	GLY	GLY	ALA	THR	GLY	ILE	LEU	Q264	R185	PRO
VAL	LEU	ALA	ALA	ALA	ALA	VAL	LEU	PRO	ALA	A265	Q168	ARG
SER	ASP	VAL	VAL	VAL	VAL	SER	ASP	SER	GLY	D266	T169	GLY
LEU	LEU	LEU	LEU	LEU	ASP	ALA	ASP	GLU	ILE	P267	Q170	PHE
VAL	VAL	VAL	GLY	LEU	PRO	LYS	MET	ARG	GLY	L269	R171	PRO
SER	SER	THR	THR	ASP	ALA	LEU	ALA	ALA	LYS	A270	T184	A17
GLY	GLY	ALA	PHE	PHE	GLN	LEU	PRO	ALA	ALA	GLU	R186	G31
ARG	ARG	TYR	ARG	TYR	ASP	ASP	GLY	LEU	THR	LEU	P32	G31
ILE	ILE	LEU	LEU	LEU	THR	GLU	GLU	TYR	SER	SER	R34	V33
GLU	GLU	ARG	ARG	ALA	GLU	ARG	ALA	ARG	ALA	ALA	A204	A35
HIS	HIS	ARG	THR	THR	ASP	ARG	LEU	SER	VAL	THR	A207	L42
GLU	GLU	VAL	VAL	ALA	LEU	LEU	LEU	VAL	HIS	ALA	A208	A43
GLU	GLU	ASP	GLY	GLY	GLU	GLU	PHE	ASP	VAL	ALA	T44	A43
GLU	GLU	VAL	VAL	THR	SER	LEU	THR	GLY	ALA	GLU	R212	T44
ALA	ALA	LEU	LEU	TYR	LEU	GLY	THR	GLY	HIS	THR	R216	Q49
ARG	ARG	TRP	TRP	TRP	VAL	GLN	ILE	ARG	ALA	THR	R216	R50
LEU	LEU	ALA	ALA	ILE	ASP	ALA	GLY	VAL	ARG	ALA	M220	A54
ALA	ALA	ALA	ALA	GLU	THR	GLY	GLY	LEU	ALA	THR	A54	A54
MET	MET	LYS	LYS	ARG	SER	GLN	GLU	VAL	PHE	LEU	Y224	L58
ARG	ARG	ASP	ASP	PRO	LEU	GLN	GLU	LEU	ARG	ALA	R225	R59
LEU	LEU	GLY	GLY	GLY	LEU	ALA	ARG	LEU	PRO	PRO	S226	R62
ALA	ALA	THR	THR	ASP	GLU	VAL	VAL	ASP	ALA	ALA	G227	R62
GLY	GLY	ARG	GLU	ARG	SER	ALA	ALA	ASN	GLN	GLN	R228	T65
SER	SER	LEU	LEU	LEU	ALA	ALA	SER	ALA	GLN	LEU	Q229	T65
ALA	ALA	GLY	GLY	VAL	ALA	THR	GLU	ARG	LEU	THR	A230	A230
											E231	E231



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	45208	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	130000	Depositor
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	1.588	Depositor
Minimum map value	-0.813	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.022	Depositor
Recommended contour level	0.025	Depositor
Map size (Å)	436.8, 436.8, 436.8	wwPDB
Map dimensions	416, 416, 416	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.05, 1.05, 1.05	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.18	0/1768	0.35	0/2400
1	B	0.17	0/1818	0.38	0/2467
1	K	0.19	0/548	0.38	0/737
2	C	0.23	0/8831	0.42	0/11959
3	D	0.26	0/9998	0.48	3/13490 (0.0%)
4	E	0.17	0/607	0.46	0/826
5	F	0.27	0/2433	0.50	0/3280
6	G	0.50	0/748	0.72	0/1007
7	H	0.50	0/1257	0.73	1/1700 (0.1%)
8	I	0.27	0/1961	0.52	0/2660
8	J	0.12	0/1961	0.34	0/2660
9	O	0.19	0/1376	0.36	0/2118
10	P	0.19	0/1414	0.32	0/2181
All	All	0.26	0/34720	0.46	4/47485 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	533	ASN	N-CA-C	-6.68	104.28	113.56
3	D	1078	ALA	N-CA-C	5.64	117.51	111.36
3	D	1079	ARG	N-CA-C	5.54	117.55	108.52
7	H	107	GLU	N-CA-CB	5.00	118.04	110.28

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	1742	0	1796	22	0
1	B	1792	0	1841	37	0
1	K	545	0	561	3	0
2	C	8675	0	8615	162	0
3	D	9846	0	10017	184	0
4	E	597	0	604	13	0
5	F	2398	0	2458	43	0
6	G	734	0	714	10	0
7	H	1241	0	1263	11	0
8	I	1934	0	1950	40	0
8	J	1934	0	1950	29	0
9	O	1233	0	688	13	0
10	P	1258	0	681	11	0
11	D	1	0	0	0	0
12	D	2	0	0	0	0
All	All	33932	0	33138	519	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 (519) 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:243:TYR:H	2:C:247:ARG:HH21	1.32	0.77
8:I:74:TRP:HE3	8:I:78:PRO:HB3	1.50	0.77
2:C:862:LYS:HZ1	2:C:864:LYS:HE2	1.52	0.74
2:C:699:MET:HE2	2:C:701:LEU:HD11	1.75	0.69
2:C:173:VAL:HG12	2:C:192:ILE:HG12	1.75	0.68
3:D:461:VAL:HG21	3:D:469:ILE:HD13	1.75	0.68
3:D:434:PRO:O	3:D:712:LYS:NZ	2.25	0.68
2:C:723:LEU:HD12	2:C:727:LEU:HD12	1.75	0.68
3:D:1047:ARG:HH21	3:D:1087:HIS:HA	1.59	0.68
7:H:68:LEU:HB3	7:H:144:GLU:HG2	1.75	0.67
3:D:1105:LEU:HD21	3:D:1188:PRO:HB2	1.76	0.67
2:C:190:ALA:HB3	2:C:202:MET:HB2	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:228:ARG:HD3	8:J:212:ARG:HD2	1.75	0.67
1:A:40:ARG:NH1	2:C:889:ASP:OD1	2.28	0.67
8:I:121:LEU:HG	8:I:125:GLN:HE22	1.59	0.67
3:D:826:THR:OG1	3:D:1010:HIS:NE2	2.28	0.66
3:D:372:ARG:HH12	5:F:217:ASP:HB3	1.59	0.66
8:I:212:ARG:HG2	8:I:215:LEU:HD23	1.77	0.66
1:B:36:ASN:ND2	2:C:1000:SER:O	2.28	0.66
5:F:484:GLU:OE1	5:F:487:ARG:NH2	2.28	0.66
3:D:1063:PRO:HB2	3:D:1067:SER:HB2	1.78	0.66
3:D:214:ARG:HB3	3:D:218:ARG:HH21	1.61	0.65
3:D:173:ARG:HD2	3:D:205:MET:HE1	1.77	0.65
2:C:817:GLU:HB3	2:C:819:ARG:HH22	1.62	0.65
2:C:22:ARG:HG2	2:C:958:ALA:HB2	1.79	0.65
2:C:275:PRO:HB2	2:C:277:ARG:HH22	1.62	0.65
7:H:68:LEU:H	7:H:68:LEU:HD13	1.61	0.64
7:H:58:GLY:O	7:H:60:ARG:NH1	2.30	0.64
3:D:190:LYS:HB2	3:D:193:VAL:HB	1.78	0.64
2:C:196:ARG:HD3	2:C:295:ASP:HB3	1.79	0.64
3:D:527:LEU:HD21	3:D:708:LEU:HB3	1.80	0.64
8:I:176:GLU:O	8:I:180:GLN:NE2	2.31	0.64
2:C:364:ILE:HD11	2:C:492:ILE:HD12	1.79	0.64
3:D:128:VAL:HG13	3:D:129:ILE:HG23	1.80	0.64
3:D:162:ILE:HD13	3:D:165:ARG:HE	1.63	0.63
8:I:59:ARG:HB3	8:I:62:ARG:HG2	1.78	0.63
2:C:286:ASN:HA	2:C:290:ASN:HB2	1.80	0.63
2:C:795:LYS:NZ	2:C:796:GLY:O	2.30	0.63
2:C:1077:LYS:NZ	3:D:545:LEU:O	2.32	0.63
3:D:651:TRP:CE3	3:D:653:GLN:HB3	2.34	0.63
1:B:128:LEU:HD21	1:B:134:LEU:HD22	1.81	0.63
2:C:305:ASN:HB3	2:C:313:PRO:HG3	1.81	0.63
5:F:267:ILE:HD11	6:G:106:LEU:HD11	1.79	0.63
3:D:1234:ASN:HD22	3:D:1242:PRO:HD3	1.63	0.62
8:I:110:ALA:HB1	8:I:112:ARG:HE	1.63	0.62
2:C:151:LYS:HG3	2:C:625:GLY:HA3	1.81	0.62
3:D:1147:ARG:NH2	3:D:1199:ALA:O	2.32	0.62
3:D:500:ARG:HE	3:D:539:ASP:CG	2.08	0.62
3:D:1169:PHE:O	3:D:1173:ASN:ND2	2.30	0.62
3:D:583:LEU:HD21	3:D:724:VAL:HG11	1.80	0.62
3:D:717:PHE:O	3:D:721:ARG:NH1	2.33	0.62
8:I:47:PRO:HA	8:I:50:ARG:HD2	1.82	0.61
2:C:342:VAL:HA	2:C:348:GLU:HA	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:637:GLN:HG2	2:C:638:GLU:HG2	1.83	0.61
2:C:603:PRO:HB3	2:C:693:ALA:HB2	1.81	0.61
2:C:507:GLU:O	2:C:539:ARG:NH1	2.33	0.61
8:I:216:ARG:NH1	8:I:239:THR:OG1	2.33	0.61
2:C:753:GLU:HG3	2:C:791:LYS:HD2	1.82	0.61
1:B:77:ILE:HG23	1:B:164:VAL:HG23	1.81	0.61
3:D:453:LYS:HG3	3:D:476:VAL:HG11	1.83	0.60
2:C:24:SER:HA	2:C:958:ALA:HB3	1.83	0.60
3:D:891:GLY:HA2	3:D:961:THR:HG21	1.83	0.60
8:J:59:ARG:HB3	8:J:62:ARG:HB2	1.82	0.60
3:D:150:SER:O	3:D:154:HIS:ND1	2.31	0.60
2:C:432:LEU:HB2	2:C:699:MET:HE1	1.84	0.60
2:C:806:LEU:HD11	5:F:443:LEU:HD21	1.83	0.60
3:D:749:GLU:OE1	3:D:753:LYS:NZ	2.35	0.60
3:D:898:THR:HG22	3:D:899:ARG:HG3	1.84	0.60
2:C:885:ASN:HB2	2:C:890:MET:HE2	1.84	0.60
8:I:121:LEU:O	8:I:125:GLN:NE2	2.35	0.59
2:C:773:ARG:HG3	2:C:775:ILE:HG12	1.83	0.59
2:C:212:VAL:HG23	2:C:222:VAL:HG22	1.83	0.59
3:D:417:LEU:HD13	3:D:1236:ILE:HG23	1.84	0.59
2:C:333:LYS:HD3	2:C:341:THR:HG21	1.83	0.59
2:C:127:PHE:HB3	2:C:136:LYS:HB2	1.83	0.58
2:C:201:GLU:HB2	2:C:213:ARG:HB2	1.85	0.58
2:C:920:ILE:HG22	2:C:1013:MET:HB2	1.84	0.58
3:D:769:LEU:HD12	3:D:772:ILE:HD11	1.84	0.58
8:I:233:LEU:HD21	8:J:247:LEU:HD11	1.83	0.58
8:J:158:VAL:HG12	8:J:159:LEU:HG	1.84	0.58
2:C:1076:ILE:HG23	2:C:1087:VAL:HG21	1.84	0.58
3:D:401:SER:OG	3:D:402:LEU:N	2.33	0.58
3:D:568:PRO:HB3	3:D:978:ALA:HB2	1.85	0.58
2:C:579:MET:HB2	2:C:598:MET:HE1	1.86	0.58
2:C:1061:LEU:HD22	3:D:559:MET:HE1	1.86	0.58
2:C:27:LYS:HG3	2:C:946:ILE:HD11	1.86	0.58
8:J:91:SER:OG	8:J:95:LYS:NZ	2.36	0.58
3:D:64:LYS:NZ	3:D:76:GLU:OE2	2.38	0.57
3:D:899:ARG:HH22	3:D:909:GLU:HB2	1.69	0.57
3:D:115:GLY:HA3	3:D:298:VAL:HG11	1.85	0.57
3:D:845:PHE:O	3:D:848:THR:OG1	2.22	0.57
1:A:9:LEU:HD21	1:A:21:PHE:HD2	1.70	0.57
2:C:877:ASN:ND2	2:C:916:GLN:OE1	2.38	0.57
3:D:143:ARG:NH1	3:D:250:THR:O	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:J:31:GLY:HA3	8:J:155:ASP:HB3	1.86	0.56
3:D:550:GLU:OE1	4:E:38:ARG:NH2	2.35	0.56
1:B:153:LYS:O	1:B:157:GLN:NE2	2.39	0.56
5:F:472:LEU:O	5:F:483:ARG:NH2	2.38	0.56
1:B:167:ILE:HG23	3:D:612:MET:HE1	1.86	0.56
3:D:69:ARG:HH12	6:G:25:ALA:HB2	1.70	0.56
1:B:134:LEU:HG	1:B:136:MET:HE1	1.87	0.56
2:C:140:VAL:HG21	2:C:404:ILE:HD11	1.87	0.56
3:D:1157:GLU:OE2	3:D:1175:ARG:NH1	2.39	0.56
8:I:92:ARG:NH2	10:P:40:DA:N7	2.52	0.56
1:B:51:VAL:HG21	1:B:80:ILE:HG22	1.88	0.56
3:D:421:ARG:NH1	10:P:17:DT:OP1	2.38	0.56
3:D:920:LEU:HG	3:D:938:LEU:HD21	1.88	0.56
3:D:795:SER:HA	3:D:798:VAL:HG12	1.87	0.55
8:J:94:ARG:HG3	8:J:102:LEU:HD23	1.87	0.55
6:G:103:LEU:HD13	6:G:106:LEU:HD12	1.88	0.55
8:I:221:LEU:HD21	8:I:261:ARG:HH22	1.72	0.55
1:B:77:ILE:HD11	1:B:162:ILE:HD12	1.89	0.55
5:F:451:SER:HB2	5:F:454:GLU:HG2	1.88	0.55
2:C:502:TYR:OH	2:C:522:GLU:OE2	2.22	0.55
2:C:737:HIS:CD2	2:C:863:ARG:HE	2.25	0.55
5:F:280:GLU:HA	5:F:283:LEU:HG	1.87	0.55
2:C:110:CYS:HA	2:C:115:PHE:HB2	1.88	0.55
2:C:548:ARG:HD3	3:D:842:LEU:HD21	1.88	0.55
3:D:1254:ARG:NH2	4:E:83:GLU:OE2	2.39	0.55
8:J:59:ARG:NH2	8:J:68:GLU:OE1	2.40	0.55
3:D:1104:VAL:O	3:D:1108:LEU:HB2	2.06	0.55
2:C:676:VAL:HG11	2:C:688:LEU:HD13	1.89	0.55
3:D:1079:ARG:HH12	3:D:1096:VAL:HB	1.72	0.55
3:D:25:HIS:CD2	3:D:91:ARG:HE	2.24	0.55
3:D:1046:GLY:HA3	3:D:1063:PRO:HA	1.89	0.55
5:F:450:LEU:HD11	5:F:502:ARG:HH22	1.72	0.55
2:C:816:ARG:HB2	8:I:62:ARG:HH12	1.72	0.54
1:A:63:PHE:HE1	2:C:736:ILE:HD12	1.72	0.54
2:C:85:GLU:HB3	2:C:89:GLY:HA2	1.90	0.54
2:C:493:ASN:ND2	2:C:499:GLU:OE1	2.41	0.54
2:C:722:ILE:HB	2:C:902:ILE:HB	1.88	0.54
3:D:1105:LEU:HD12	3:D:1113:VAL:HG11	1.90	0.54
2:C:213:ARG:HH22	2:C:219:LYS:HA	1.73	0.53
3:D:765:ARG:NH2	3:D:766:THR:OG1	2.41	0.53
1:A:22:VAL:HG22	1:A:193:ILE:HG12	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:20:ILE:HG12	3:D:318:PRO:HG3	1.89	0.53
8:I:236:TYR:OH	8:I:240:ARG:NH1	2.41	0.53
2:C:55:LYS:HA	2:C:58:VAL:HG12	1.90	0.53
2:C:116:THR:HG23	2:C:156:ILE:HG22	1.89	0.53
2:C:509:GLN:HE21	2:C:538:MET:HE2	1.73	0.53
2:C:574:SER:OG	2:C:575:VAL:N	2.41	0.53
4:E:46:GLN:HB2	4:E:49:GLU:HG2	1.91	0.53
2:C:459:ARG:NH1	2:C:480:ILE:O	2.40	0.53
3:D:343:LEU:HD13	3:D:381:LEU:HA	1.91	0.53
2:C:156:ILE:HD13	2:C:417:PHE:HB3	1.91	0.53
3:D:71:LYS:O	6:G:27:ARG:NH2	2.41	0.53
5:F:378:THR:HG23	5:F:381:GLU:H	1.73	0.53
3:D:110:VAL:HG12	3:D:112:SER:H	1.74	0.53
3:D:582:VAL:HG22	3:D:688:LEU:HD23	1.91	0.53
2:C:148:MET:HE1	2:C:367:VAL:HG11	1.89	0.53
2:C:444:LEU:HD21	2:C:482:LEU:HD13	1.91	0.53
9:O:56:DG:H2"	9:O:57:DA:H5"	1.91	0.53
1:A:52:THR:OG1	1:A:152:ASN:OD1	2.26	0.53
3:D:1104:VAL:HG13	3:D:1108:LEU:HD12	1.91	0.53
2:C:505:VAL:HG22	2:C:510:VAL:HG12	1.92	0.53
2:C:794:PRO:O	8:I:62:ARG:NH2	2.42	0.53
3:D:827:ILE:HG22	3:D:829:ARG:H	1.73	0.53
2:C:299:VAL:HG12	2:C:495:PHE:HB3	1.91	0.52
2:C:572:MET:HG3	2:C:573:VAL:HG13	1.91	0.52
5:F:241:GLU:HG3	5:F:320:TYR:HE2	1.75	0.52
8:J:44:THR:O	8:J:49:GLN:NE2	2.43	0.52
3:D:350:ARG:NH1	3:D:373:MET:O	2.38	0.52
7:H:140:LEU:HD13	7:H:144:GLU:OE1	2.09	0.52
3:D:36:TYR:OH	3:D:37:ARG:NH2	2.33	0.52
3:D:1058:LYS:NZ	3:D:1059:ILE:O	2.42	0.52
8:I:145:ASP:OD2	8:I:149:ARG:NH1	2.42	0.52
8:J:33:VAL:HG11	8:J:54:ALA:HB2	1.91	0.52
1:B:81:LYS:NZ	1:B:165:ASP:OD2	2.36	0.52
2:C:987:VAL:HG22	2:C:993:ALA:HB2	1.91	0.52
3:D:871:ARG:NH1	3:D:1031:GLU:OE2	2.43	0.52
5:F:279:LEU:HD21	5:F:312:ILE:HD13	1.91	0.52
1:A:76:LEU:HD21	1:A:126:ALA:HB2	1.92	0.52
2:C:240:PHE:O	2:C:247:ARG:NH2	2.35	0.52
3:D:104:ILE:HD12	3:D:379:ASP:HB3	1.91	0.52
2:C:204:ILE:HG13	2:C:210:VAL:HB	1.92	0.52
2:C:301:ARG:O	2:C:305:ASN:ND2	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:156:ILE:HD11	2:C:161:ARG:HD3	1.92	0.52
3:D:1247:LEU:HB2	3:D:1250:TYR:HD2	1.75	0.52
1:A:39:ARG:HG3	1:A:174:VAL:HB	1.90	0.52
2:C:301:ARG:HH22	2:C:319:LEU:HA	1.75	0.52
2:C:815:ALA:H	8:I:173:ARG:NH1	2.08	0.52
3:D:498:LEU:HG	3:D:543:VAL:HG22	1.92	0.52
2:C:136:LYS:NZ	2:C:398:ILE:O	2.40	0.51
2:C:452:GLU:OE1	2:C:453:ARG:NH1	2.39	0.51
3:D:525:HIS:HD2	3:D:526:PRO:HD2	1.75	0.51
8:J:216:ARG:O	8:J:220:MET:HG2	2.10	0.51
2:C:186:ASP:OD1	2:C:186:ASP:N	2.42	0.51
3:D:325:ARG:NH1	3:D:341:ASN:OD1	2.35	0.51
3:D:1018:ASP:O	3:D:1036:LYS:NZ	2.41	0.51
2:C:23:ILE:O	2:C:958:ALA:N	2.42	0.51
3:D:640:GLU:HB2	3:D:641:PRO:HD3	1.91	0.51
8:I:87:ARG:NH1	8:I:109:TYR:OH	2.43	0.51
8:J:162:VAL:O	8:J:171:ARG:NH2	2.40	0.51
2:C:529:GLN:NE2	3:D:842:LEU:HD13	2.25	0.51
3:D:495:PRO:HG3	3:D:556:ARG:HG3	1.91	0.51
3:D:1059:ILE:HD13	3:D:1094:LEU:HD23	1.91	0.51
8:I:35:ALA:HB3	8:I:42:LEU:HB2	1.91	0.51
8:J:168:GLN:OE1	8:J:171:ARG:NH1	2.44	0.51
2:C:579:MET:HE1	2:C:617:GLU:HA	1.92	0.51
4:E:10:GLY:N	4:E:13:ASN:OD1	2.43	0.51
1:A:95:MET:HG2	1:A:112:PRO:HA	1.92	0.51
2:C:286:ASN:OD1	2:C:290:ASN:ND2	2.44	0.51
3:D:747:GLN:HE22	3:D:772:ILE:HD12	1.75	0.51
2:C:722:ILE:HG22	2:C:890:MET:HE1	1.93	0.51
8:I:57:LEU:HD22	8:I:119:LEU:HD13	1.93	0.51
2:C:202:MET:HE1	2:C:328:ILE:HD13	1.93	0.50
2:C:1087:VAL:HG13	2:C:1097:ILE:HD12	1.94	0.50
5:F:325:LYS:HB2	9:O:42:DT:H5'	1.93	0.50
2:C:746:ARG:HA	2:C:851:VAL:HA	1.94	0.50
8:I:243:LEU:HG	8:I:247:LEU:HD12	1.94	0.50
1:A:37:SER:OG	1:B:37:SER:OG	2.27	0.50
1:A:176:TYR:HB2	1:A:192:LEU:HD11	1.93	0.50
1:B:66:VAL:HG13	1:B:69:VAL:HB	1.94	0.50
2:C:192:ILE:HD12	2:C:200:LEU:HD11	1.93	0.50
3:D:102:THR:HG21	3:D:129:ILE:HD12	1.94	0.50
1:A:104:LEU:HD21	1:A:124:VAL:HG13	1.93	0.50
2:C:1022:VAL:HG22	3:D:520:LYS:HB2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:718:GLU:HG2	3:D:579:GLN:HG3	1.93	0.49
2:C:1064:TYR:HD2	3:D:559:MET:HE2	1.77	0.49
3:D:397:ARG:HH21	5:F:407:HIS:HB2	1.76	0.49
5:F:503:SER:O	5:F:507:ARG:N	2.43	0.49
2:C:468:ARG:NH2	2:C:518:THR:O	2.42	0.49
2:C:529:GLN:HE21	3:D:842:LEU:HD13	1.76	0.49
3:D:591:ASP:OD1	3:D:665:ARG:NH2	2.44	0.49
5:F:236:LEU:O	5:F:240:ILE:HG12	2.11	0.49
5:F:319:ASP:OD1	5:F:319:ASP:N	2.45	0.49
2:C:213:ARG:HH12	2:C:219:LYS:HD2	1.77	0.49
9:O:19:DG:H2''	9:O:20:DT:H5''	1.93	0.49
1:A:190:ASP:OD1	1:A:190:ASP:N	2.42	0.49
1:B:78:LEU:HD22	3:D:628:ARG:HH11	1.76	0.49
5:F:409:PRO:O	10:P:22:DA:N6	2.39	0.49
1:A:97:LEU:HB3	1:A:136:MET:HB3	1.94	0.49
5:F:476:GLY:HA3	5:F:483:ARG:HH22	1.77	0.49
1:B:107:ALA:HB3	1:B:121:PRO:HA	1.94	0.49
8:J:243:LEU:O	8:J:248:GLY:N	2.38	0.49
3:D:460:LEU:HD11	3:D:483:VAL:HG22	1.93	0.49
2:C:210:VAL:HG12	2:C:249:THR:HG21	1.95	0.49
9:O:57:DA:N6	10:P:8:DG:O6	2.45	0.49
3:D:766:THR:HG23	3:D:828:PRO:HG3	1.94	0.49
3:D:43:LYS:HE2	3:D:50:LYS:HD2	1.95	0.48
5:F:231:GLU:HA	5:F:234:VAL:HG22	1.95	0.48
5:F:245:PHE:HD1	6:G:95:LEU:HD13	1.77	0.48
5:F:424:ASP:OD1	5:F:424:ASP:N	2.45	0.48
5:F:486:ILE:HD12	5:F:489:ILE:HD11	1.95	0.48
1:A:144:ARG:NH1	1:B:230:GLU:OE2	2.45	0.48
1:B:136:MET:SD	1:B:136:MET:N	2.86	0.48
3:D:555:ALA:HA	3:D:559:MET:HB2	1.95	0.48
3:D:567:LYS:HG2	3:D:569:ALA:H	1.79	0.48
3:D:651:TRP:HE3	3:D:653:GLN:HB3	1.77	0.48
3:D:363:PRO:HD2	3:D:366:ILE:HD12	1.95	0.48
9:O:24:DT:H2''	9:O:25:DT:H5''	1.93	0.48
1:B:3:ILE:HD11	1:B:233:ASP:H	1.78	0.48
3:D:1081:LEU:HG	3:D:1096:VAL:HG23	1.96	0.48
3:D:1210:GLN:HG2	10:P:12:DG:H4'	1.95	0.48
1:A:71:GLU:HG3	1:A:75:ASP:HB3	1.96	0.48
1:B:171:VAL:HA	1:B:198:THR:HA	1.96	0.48
2:C:169:ARG:HD2	9:O:52:DG:C4	2.48	0.48
2:C:374:GLN:HG3	2:C:416:PHE:HB2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:710:MET:HE2	2:C:712:TRP:HD1	1.78	0.48
2:C:383:GLU:HA	2:C:386:VAL:HG12	1.95	0.48
3:D:570:ASP:OD2	3:D:1131:SER:OG	2.32	0.48
6:G:90:ARG:HG3	6:G:94:GLU:CG	2.43	0.48
2:C:1091:ILE:HD11	3:D:547:LEU:HD11	1.96	0.48
3:D:858:THR:OG1	3:D:861:ARG:NH2	2.47	0.48
8:I:33:VAL:HG21	8:I:50:ARG:HB3	1.95	0.48
3:D:125:LEU:HA	3:D:128:VAL:HG12	1.95	0.48
3:D:923:ASP:OD1	3:D:934:ALA:N	2.47	0.48
5:F:282:ASN:HB3	5:F:311:LEU:HD11	1.95	0.48
3:D:1006:MET:HG3	3:D:1128:GLN:HE21	1.78	0.47
4:E:23:THR:HG21	4:E:29:LEU:HB2	1.96	0.47
5:F:459:SER:HB2	5:F:465:THR:HG23	1.95	0.47
8:I:228:ARG:HH22	8:I:230:ALA:HB3	1.79	0.47
2:C:144:ASP:OD1	2:C:144:ASP:N	2.47	0.47
2:C:563:ASP:N	2:C:563:ASP:OD1	2.46	0.47
2:C:614:THR:HG23	2:C:960:PRO:HA	1.96	0.47
3:D:846:ILE:HA	3:D:849:HIS:ND1	2.28	0.47
8:J:109:TYR:OH	10:P:49:DC:OP2	2.32	0.47
2:C:1124:SER:N	2:C:1127:GLY:O	2.47	0.47
3:D:578:THR:OG1	3:D:801:GLY:O	2.32	0.47
8:J:127:LEU:HD22	8:J:146:LEU:HD22	1.96	0.47
1:K:291:ALA:HA	1:K:294:ILE:HD12	1.96	0.47
1:A:108:ALA:HB2	1:A:121:PRO:HB2	1.96	0.47
1:B:95:MET:HE2	1:B:138:LEU:HD11	1.96	0.47
3:D:98:ALA:HB2	3:D:355:LYS:HG3	1.96	0.47
3:D:147:ASP:OD2	3:D:251:TYR:OH	2.32	0.47
7:H:141:ALA:HA	7:H:146:THR:O	2.14	0.47
10:P:11:DT:H2'	10:P:12:DG:C8	2.50	0.47
1:B:54:ILE:HG13	1:B:138:LEU:HB3	1.97	0.47
2:C:746:ARG:NH1	3:D:331:ASP:OD1	2.40	0.47
3:D:964:SER:OG	3:D:967:GLY:O	2.33	0.47
3:D:1257:PRO:HA	4:E:80:LEU:HG	1.97	0.47
4:E:9:GLU:N	4:E:13:ASN:OD1	2.47	0.47
8:J:93:LEU:HA	8:J:96:VAL:HG12	1.96	0.47
8:J:102:LEU:HD11	8:J:109:TYR:HB3	1.97	0.47
3:D:896:ILE:HD13	3:D:915:VAL:HG11	1.97	0.47
8:I:148:ARG:HG3	8:I:185:ARG:HH12	1.79	0.47
2:C:69:PRO:HD3	2:C:494:PRO:HB3	1.96	0.47
3:D:381:LEU:O	3:D:401:SER:OG	2.22	0.47
3:D:780:VAL:HG11	3:D:815:MET:HG2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:1123:LEU:HA	2:C:1129:SER:H	1.79	0.47
3:D:1079:ARG:NH1	3:D:1096:VAL:HB	2.29	0.47
8:I:158:VAL:HB	8:I:178:ARG:HH22	1.80	0.47
8:J:65:THR:HG23	8:J:68:GLU:H	1.80	0.47
1:B:38:LEU:O	1:B:42:LEU:HB2	2.14	0.46
2:C:634:GLY:HA3	2:C:648:ASN:HA	1.95	0.46
6:G:53:GLU:OE1	6:G:62:GLN:NE2	2.47	0.46
1:B:71:GLU:HG3	1:B:75:ASP:HB3	1.98	0.46
2:C:233:THR:HG22	2:C:237:LEU:HD23	1.96	0.46
3:D:280:ILE:O	3:D:289:LYS:NZ	2.39	0.46
3:D:597:PRO:HA	3:D:620:THR:HG21	1.97	0.46
1:B:44:SER:O	1:B:44:SER:OG	2.29	0.46
2:C:756:THR:OG1	2:C:757:ARG:N	2.48	0.46
5:F:239:ARG:HD2	5:F:274:ALA:HB2	1.96	0.46
7:H:111:ASP:OD1	7:H:115:ARG:NH2	2.48	0.46
8:I:46:SER:HA	9:O:22:DC:H5'	1.97	0.46
2:C:207:ARG:HB3	2:C:209:MET:HE1	1.98	0.46
3:D:332:GLY:O	5:F:398:LYS:NZ	2.49	0.46
4:E:27:TYR:HA	4:E:30:VAL:HG12	1.97	0.46
2:C:439:ARG:NH2	2:C:487:ALA:O	2.46	0.46
5:F:241:GLU:HG3	5:F:320:TYR:CE2	2.51	0.46
1:B:128:LEU:HD12	1:B:132:GLY:HA2	1.98	0.46
2:C:123:VAL:HG21	2:C:142:MET:HE2	1.97	0.46
3:D:245:ARG:HH22	3:D:249:GLY:HA2	1.79	0.46
2:C:43:GLU:HA	2:C:57:ARG:HH22	1.81	0.46
3:D:438:LEU:HD13	3:D:527:LEU:HD23	1.97	0.46
1:B:108:ALA:HB2	1:B:121:PRO:HB2	1.98	0.46
2:C:77:ILE:HG13	2:C:376:ARG:CZ	2.46	0.46
2:C:635:VAL:HG12	2:C:681:ARG:HD2	1.98	0.46
3:D:208:LEU:HD12	3:D:211:ARG:HD3	1.98	0.46
3:D:225:ARG:O	3:D:225:ARG:NH1	2.48	0.46
3:D:407:LYS:HA	3:D:1212:THR:HG21	1.97	0.46
8:I:255:LEU:HD12	8:I:258:LEU:HD23	1.96	0.46
3:D:1257:PRO:HG2	4:E:55:VAL:HG11	1.98	0.46
5:F:264:LEU:HD23	5:F:267:ILE:HD12	1.98	0.46
8:I:92:ARG:HE	8:I:95:LYS:NZ	2.14	0.46
8:J:252:ARG:HG2	8:J:254:GLY:H	1.80	0.46
3:D:473:LYS:HB2	3:D:473:LYS:HE2	1.83	0.45
5:F:265:GLU:OE2	5:F:272:ARG:NH2	2.48	0.45
4:E:63:VAL:O	4:E:64:HIS:ND1	2.50	0.45
5:F:336:GLN:HB2	9:O:39:DC:H41	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:G:90:ARG:HG3	6:G:94:GLU:HG2	1.98	0.45
8:I:224:TYR:O	8:J:252:ARG:NH2	2.49	0.45
1:B:174:VAL:HG22	1:B:196:VAL:HG23	1.98	0.45
3:D:279:GLU:OE1	3:D:282:ARG:NH2	2.45	0.45
3:D:435:GLN:NE2	3:D:523:GLN:HE22	2.14	0.45
3:D:724:VAL:HA	3:D:793:PRO:HB3	1.97	0.45
8:I:147:LEU:HD23	8:I:150:ALA:HB3	1.96	0.45
3:D:897:ALA:HB3	3:D:952:GLU:HA	1.98	0.45
3:D:986:GLY:O	3:D:1244:GLY:N	2.49	0.45
2:C:518:THR:OG1	2:C:521:GLU:OE1	2.34	0.45
3:D:541:MET:HB2	3:D:541:MET:HE3	1.85	0.45
4:E:46:GLN:HG3	4:E:48:GLY:H	1.81	0.45
5:F:378:THR:OG1	5:F:380:GLU:OE1	2.33	0.45
8:I:263:LEU:HB3	1:K:266:ARG:HA	1.98	0.45
2:C:891:PRO:HB3	2:C:1004:PHE:HE2	1.82	0.45
1:B:18:ARG:NH1	1:B:197:GLU:OE2	2.50	0.45
3:D:96:GLU:O	3:D:351:ASN:ND2	2.40	0.45
3:D:136:ILE:HG21	3:D:229:LEU:HD21	1.98	0.45
3:D:586:PHE:CE2	3:D:796:MET:HG3	2.52	0.45
3:D:907:LYS:HE2	3:D:911:VAL:HG11	1.99	0.45
5:F:286:VAL:HG23	5:F:334:ILE:HD12	1.99	0.45
3:D:500:ARG:HG2	3:D:502:PRO:HD2	1.98	0.45
3:D:1120:GLU:O	3:D:1124:VAL:HG23	2.16	0.45
5:F:381:GLU:HG2	5:F:384:LYS:HZ3	1.81	0.45
2:C:155:VAL:HG22	2:C:160:GLU:HG2	1.99	0.45
2:C:1027:HIS:CE1	2:C:1045:LYS:HA	2.52	0.45
3:D:125:LEU:O	3:D:129:ILE:HG12	2.17	0.45
9:O:59:DC:O2	10:P:7:DG:N2	2.35	0.45
2:C:246:MET:O	2:C:249:THR:OG1	2.25	0.44
2:C:1059:TRP:CE2	3:D:873:VAL:HG11	2.52	0.44
3:D:151:LEU:HD13	3:D:223:TRP:HH2	1.82	0.44
2:C:213:ARG:HH12	2:C:219:LYS:HA	1.82	0.44
2:C:324:VAL:O	2:C:328:ILE:HG12	2.18	0.44
2:C:428:GLN:HB2	2:C:664:SER:HB2	1.98	0.44
8:I:206:THR:HG21	8:I:219:LEU:HD11	1.98	0.44
2:C:167:LEU:HD13	2:C:362:ARG:HH21	1.83	0.44
2:C:1030:SER:HB3	3:D:450:GLU:O	2.17	0.44
3:D:342:ASP:OD1	3:D:345:ARG:NH1	2.50	0.44
2:C:526:VAL:HG13	2:C:562:VAL:HA	1.99	0.44
3:D:220:ASP:O	3:D:224:ASN:ND2	2.50	0.44
1:A:7:PRO:HA	1:A:25:PRO:HG2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:586:PHE:HE2	3:D:796:MET:HG3	1.83	0.44
5:F:225:VAL:HG11	5:F:280:GLU:HB3	1.99	0.44
5:F:311:LEU:HB2	5:F:334:ILE:HD11	2.00	0.44
1:K:274:GLU:O	1:K:278:ARG:HG2	2.18	0.44
3:D:1150:ILE:HA	3:D:1186:GLY:HA2	1.99	0.44
3:D:1240:LEU:HD22	3:D:1251:ARG:HD3	1.99	0.44
2:C:358:HIS:CD2	2:C:360:GLY:H	2.36	0.44
7:H:37:VAL:HG23	7:H:48:ARG:HG3	1.99	0.44
4:E:67:PRO:HA	4:E:70:ILE:HD13	2.00	0.44
2:C:173:VAL:HG13	2:C:304:VAL:HG22	2.00	0.44
3:D:143:ARG:HH12	3:D:250:THR:HG23	1.81	0.44
2:C:37:LEU:HD21	2:C:575:VAL:HG21	2.00	0.43
2:C:218:ARG:HD2	2:C:218:ARG:HA	1.85	0.43
2:C:649:ASP:N	2:C:649:ASP:OD1	2.48	0.43
2:C:1087:VAL:HG22	2:C:1097:ILE:HG23	2.00	0.43
2:C:1120:VAL:HG22	3:D:12:ILE:HG13	1.99	0.43
2:C:221:SER:OG	2:C:222:VAL:N	2.51	0.43
3:D:264:ARG:HA	3:D:264:ARG:HD2	1.77	0.43
3:D:414:ARG:HH12	3:D:870:ARG:HD2	1.82	0.43
3:D:576:MET:HE2	3:D:688:LEU:HD21	1.99	0.43
3:D:777:THR:HA	3:D:780:VAL:HG12	2.00	0.43
3:D:1048:VAL:HA	3:D:1061:VAL:HA	2.00	0.43
3:D:58:TRP:CD2	3:D:68:VAL:HG23	2.52	0.43
3:D:731:ILE:HG22	3:D:836:ARG:HD2	2.01	0.43
3:D:1024:PRO:HA	3:D:1027:VAL:HG12	2.00	0.43
4:E:53:GLU:HG3	4:E:54:TYR:CD1	2.53	0.43
1:B:42:LEU:HD12	1:B:46:ILE:HD11	2.01	0.43
2:C:210:VAL:H	2:C:249:THR:HG21	1.83	0.43
3:D:173:ARG:HD3	3:D:208:LEU:HD23	2.01	0.43
2:C:1058:VAL:HG13	2:C:1070:LEU:HD11	1.99	0.43
5:F:291:LYS:HD2	9:O:46:DA:H4'	2.00	0.43
8:I:53:LEU:HB2	8:I:93:LEU:HD11	2.00	0.43
2:C:737:HIS:CG	2:C:863:ARG:HH21	2.37	0.43
3:D:438:LEU:HA	3:D:525:HIS:HD1	1.81	0.43
1:B:43:LEU:HD23	1:B:171:VAL:HG23	2.00	0.43
2:C:690:ASP:OD2	2:C:696:ASN:N	2.51	0.43
9:O:59:DC:H2'	9:O:60:DG:C8	2.54	0.43
2:C:264:ASP:OD1	2:C:267:ARG:NH1	2.52	0.43
2:C:621:ALA:HB2	2:C:699:MET:HB2	2.01	0.43
3:D:195:ARG:HG3	3:D:198:ARG:HH12	1.82	0.43
5:F:490:GLU:O	5:F:493:THR:OG1	2.26	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:H:112:LEU:HD12	7:H:112:LEU:HA	1.92	0.43
2:C:92:SER:N	2:C:128:THR:O	2.43	0.43
8:J:81:GLN:HG3	8:J:84:ALA:HB3	2.01	0.43
8:J:184:THR:HA	8:J:187:ASP:OD2	2.19	0.43
2:C:838:VAL:HG22	2:C:855:VAL:HG12	2.01	0.43
3:D:296:LEU:HD23	3:D:1159:LEU:HD11	2.00	0.43
2:C:1006:GLU:HB3	2:C:1007:PRO:HD2	2.01	0.42
7:H:122:SER:OG	7:H:123:ALA:N	2.50	0.42
8:J:147:LEU:HD23	8:J:147:LEU:HA	1.84	0.42
3:D:175:LYS:HA	3:D:175:LYS:HD3	1.81	0.42
3:D:320:ILE:HG13	3:D:340:LEU:HD13	2.01	0.42
3:D:821:ASN:OD1	3:D:822:ALA:N	2.49	0.42
8:J:58:LEU:HD13	8:J:170:GLN:HG2	2.01	0.42
1:B:8:SER:H	1:B:24:GLU:HB2	1.84	0.42
1:B:226:ASN:OD1	1:B:227:ILE:N	2.52	0.42
2:C:816:ARG:HB2	8:I:62:ARG:NH1	2.35	0.42
3:D:145:THR:HA	3:D:148:LEU:HG	2.01	0.42
3:D:572:ARG:HH22	3:D:912:GLU:HG3	1.84	0.42
8:I:92:ARG:HH21	8:I:95:LYS:HZ3	1.65	0.42
2:C:91:MET:HA	2:C:129:ASN:HA	1.99	0.42
2:C:505:VAL:HB	2:C:563:ASP:HA	2.01	0.42
8:I:209:HIS:ND1	8:I:212:ARG:HB2	2.34	0.42
5:F:365:VAL:HG21	5:F:386:LEU:HD21	2.01	0.42
6:G:75:LYS:HE3	6:G:78:PRO:HG3	2.02	0.42
6:G:89:ARG:HB3	6:G:90:ARG:HE	1.84	0.42
2:C:1029:ARG:NH1	2:C:1048:PHE:O	2.53	0.42
2:C:1126:ASP:OD1	2:C:1126:ASP:N	2.47	0.42
1:B:41:THR:HG21	1:B:215:LEU:HG	2.01	0.42
1:B:158:GLU:OE2	1:B:161:ARG:NH2	2.52	0.42
2:C:39:ALA:O	2:C:43:GLU:HB2	2.20	0.42
2:C:47:TRP:HA	2:C:54:TRP:CD1	2.55	0.42
2:C:967:GLU:HG2	3:D:836:ARG:HH12	1.84	0.42
5:F:327:SER:O	5:F:331:THR:OG1	2.33	0.42
9:O:22:DC:H2"	9:O:23:DG:H8	1.85	0.42
2:C:730:ASP:HB3	2:C:732:VAL:HG23	2.02	0.42
3:D:582:VAL:HG11	3:D:685:LYS:HB2	2.02	0.42
3:D:785:ASN:HA	3:D:788:PHE:HE1	1.85	0.42
8:J:147:LEU:HD23	8:J:150:ALA:HB3	2.01	0.42
2:C:556:TYR:HD1	3:D:829:ARG:HH12	1.67	0.42
1:A:95:MET:N	1:A:138:LEU:O	2.45	0.41
1:A:112:PRO:HA	1:A:113:PRO:HD3	1.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:537:ASP:OD1	2:C:537:ASP:N	2.49	0.41
3:D:433:GLY:HA3	3:D:523:GLN:HE21	1.84	0.41
7:H:132:ALA:HA	7:H:135:ILE:HG12	2.01	0.41
8:J:147:LEU:HD12	8:J:185:ARG:NH2	2.34	0.41
1:B:151:GLN:OE1	1:B:151:GLN:N	2.53	0.41
3:D:166:ARG:NH2	3:D:169:ASP:OD2	2.52	0.41
3:D:430:ILE:HG12	3:D:539:ASP:O	2.19	0.41
3:D:580:ASP:HB3	3:D:716:PHE:HE1	1.85	0.41
3:D:728:ILE:HD12	3:D:728:ILE:HA	1.88	0.41
5:F:439:LEU:HD12	5:F:509:TYR:HD2	1.86	0.41
1:B:40:ARG:HD3	1:B:40:ARG:HA	1.89	0.41
2:C:906:LEU:HD12	3:D:803:ARG:HB3	2.02	0.41
3:D:438:LEU:HA	3:D:525:HIS:ND1	2.35	0.41
8:I:111:VAL:C	8:I:112:ARG:HD3	2.45	0.41
1:B:15:ASP:HB3	1:B:18:ARG:HB2	2.03	0.41
1:B:99:LYS:HD2	1:B:105:VAL:HB	2.02	0.41
2:C:52:ASP:OD1	2:C:53:ALA:N	2.54	0.41
2:C:557:VAL:HA	2:C:558:PRO:HD3	1.93	0.41
2:C:384:ARG:HH22	9:O:47:DT:H5"	1.85	0.41
2:C:470:CYS:HB2	2:C:574:SER:HB2	2.02	0.41
3:D:397:ARG:NH2	5:F:405:SER:OG	2.51	0.41
3:D:449:LEU:HD13	3:D:487:LEU:HD12	2.03	0.41
7:H:29:LYS:HD2	7:H:29:LYS:HA	1.95	0.41
2:C:227:LYS:HE2	2:C:227:LYS:HB3	1.85	0.41
2:C:276:THR:HB	2:C:279:ALA:HB3	2.02	0.41
3:D:487:LEU:HD22	3:D:516:LEU:HD11	2.02	0.41
1:A:197:GLU:OE1	2:C:981:ARG:NH2	2.50	0.41
1:A:216:VAL:HG11	1:B:223:ARG:HD2	2.03	0.41
8:I:74:TRP:CE3	8:I:78:PRO:HB3	2.41	0.41
8:J:35:ALA:HB3	8:J:42:LEU:HB2	2.01	0.41
1:A:84:VAL:HG12	1:A:120:ASN:ND2	2.36	0.41
3:D:525:HIS:NE2	3:D:712:LYS:HE2	2.35	0.41
3:D:527:LEU:HD13	3:D:712:LYS:HB2	2.01	0.41
3:D:911:VAL:HG23	3:D:915:VAL:HB	2.02	0.41
3:D:1042:SER:OG	3:D:1089:GLU:O	2.39	0.41
8:J:33:VAL:HG23	8:J:50:ARG:HD2	2.03	0.41
3:D:657:PHE:HE2	3:D:659:LEU:HD22	1.86	0.41
3:D:973:TYR:HD2	3:D:983:VAL:HG11	1.86	0.41
5:F:482:THR:HG23	5:F:485:ARG:HH21	1.85	0.41
2:C:227:LYS:NZ	2:C:257:GLY:H	2.18	0.40
3:D:30:LYS:HB3	3:D:32:GLU:OE2	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:774:THR:HA	3:D:777:THR:HG22	2.03	0.40
5:F:330:ALA:O	5:F:334:ILE:HG12	2.20	0.40
10:P:3:DC:H2'	10:P:4:DG:C8	2.56	0.40
10:P:35:DG:H2''	10:P:36:DA:C8	2.56	0.40
3:D:683:VAL:O	3:D:687:GLN:HB2	2.21	0.40
8:I:154:TRP:CG	8:I:178:ARG:HE	2.39	0.40
10:P:7:DG:H2'	10:P:8:DG:C8	2.56	0.40
3:D:916:TYR:O	3:D:1133:HIS:NE2	2.53	0.40
2:C:48:LEU:HA	2:C:73:GLY:HA3	2.03	0.40
2:C:753:GLU:HB3	2:C:794:PRO:HD3	2.04	0.40
3:D:320:ILE:HB	3:D:325:ARG:HD3	2.02	0.40
3:D:997:ILE:HD13	3:D:1132:ILE:HG21	2.02	0.40
2:C:23:ILE:HG13	2:C:951:VAL:HG22	2.02	0.40
2:C:236:ILE:O	2:C:240:PHE:HB2	2.22	0.40
3:D:959:ILE:HD13	3:D:1139:ILE:HG12	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	224/340 (66%)	213 (95%)	11 (5%)	0	100	100
1	B	231/340 (68%)	222 (96%)	9 (4%)	0	100	100
1	K	71/340 (21%)	71 (100%)	0	0	100	100
2	C	1112/1161 (96%)	1077 (97%)	35 (3%)	0	100	100
3	D	1257/1307 (96%)	1218 (97%)	39 (3%)	0	100	100
4	E	75/90 (83%)	75 (100%)	0	0	100	100
5	F	299/531 (56%)	294 (98%)	5 (2%)	0	100	100
6	G	90/124 (73%)	86 (96%)	4 (4%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	H	156/160 (98%)	147 (94%)	9 (6%)	0	100	100
8	I	252/1013 (25%)	244 (97%)	8 (3%)	0	100	100
8	J	252/1013 (25%)	249 (99%)	3 (1%)	0	100	100
All	All	4019/6419 (63%)	3896 (97%)	123 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	194/279 (70%)	194 (100%)	0	100	100
1	B	199/279 (71%)	199 (100%)	0	100	100
1	K	57/279 (20%)	57 (100%)	0	100	100
2	C	940/979 (96%)	940 (100%)	0	100	100
3	D	1054/1095 (96%)	1051 (100%)	3 (0%)	86	83
4	E	64/74 (86%)	64 (100%)	0	100	100
5	F	259/430 (60%)	258 (100%)	1 (0%)	84	81
6	G	76/104 (73%)	75 (99%)	1 (1%)	61	70
7	H	129/131 (98%)	127 (98%)	2 (2%)	55	67
8	I	190/738 (26%)	189 (100%)	1 (0%)	81	80
8	J	190/738 (26%)	190 (100%)	0	100	100
All	All	3352/5126 (65%)	3344 (100%)	8 (0%)	85	86

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	D	1080	LEU
3	D	1081	LEU
3	D	1082	VAL
5	F	215	VAL

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Mol	Chain	Res	Type
6	G	88	GLU
7	H	28	ILE
7	H	68	LEU
8	I	258	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (32) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	100	GLN
1	A	154	GLN
1	B	100	GLN
1	B	154	GLN
2	C	157	ASN
2	C	305	ASN
2	C	372	GLN
2	C	424	GLN
2	C	529	GLN
2	C	637	GLN
2	C	877	ASN
2	C	921	HIS
2	C	1027	HIS
2	C	1051	GLN
3	D	224	ASN
3	D	329	GLN
3	D	352	ASN
3	D	439	HIS
3	D	523	GLN
3	D	995	GLN
3	D	1128	GLN
3	D	1234	ASN
5	F	345	GLN
5	F	442	GLN
6	G	28	GLN
8	I	125	GLN
8	I	170	GLN
8	I	180	GLN
8	J	49	GLN
8	J	81	GLN
8	J	229	GLN
8	J	260	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 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

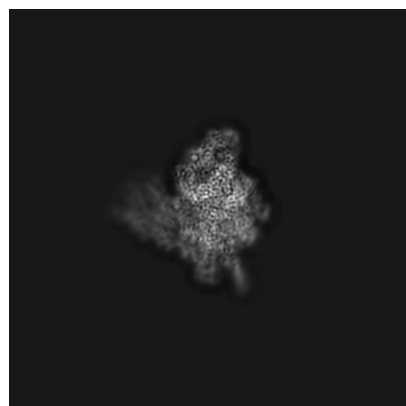
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-36370. These allow visual inspection of the internal detail of the map and identification of artifacts.

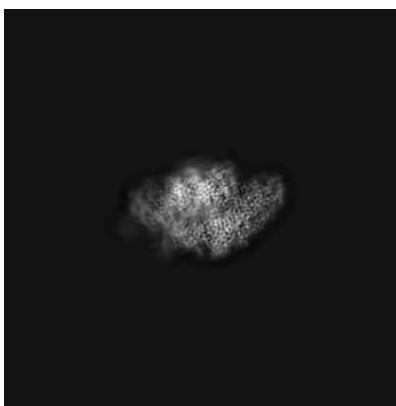
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

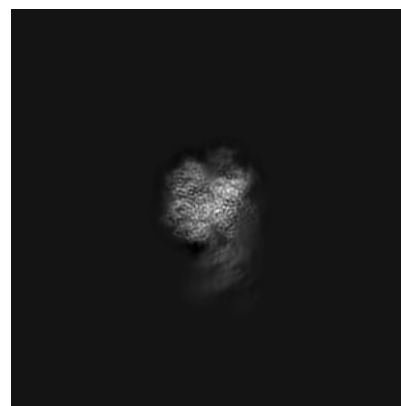
6.1.1 Primary map



X

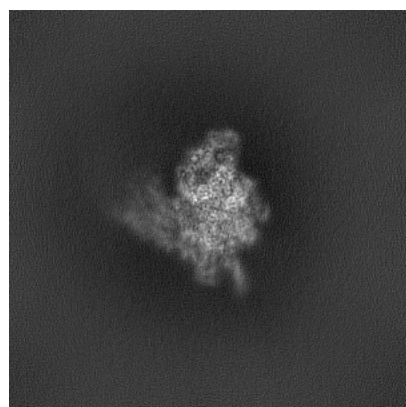


Y

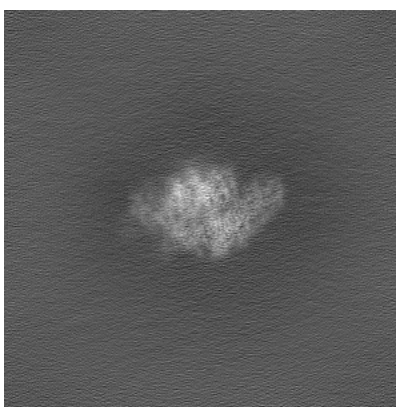


Z

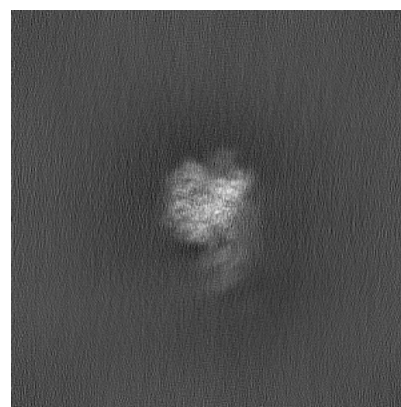
6.1.2 Raw map



X



Y

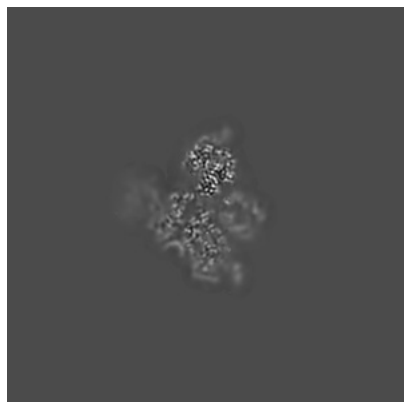


Z

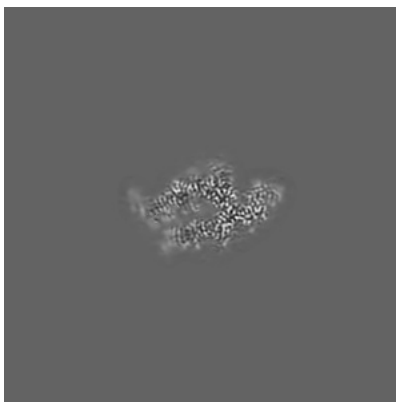
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

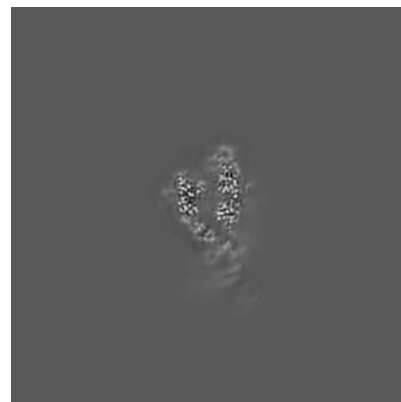
6.2.1 Primary map



X Index: 208

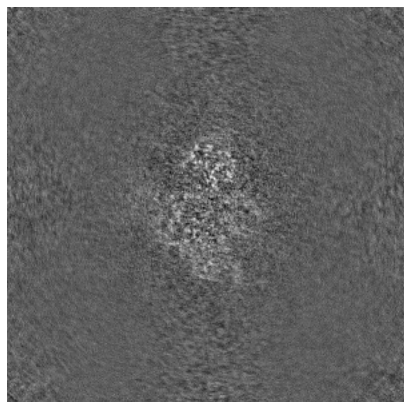


Y Index: 208

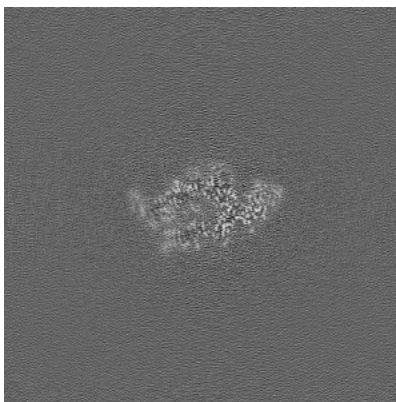


Z Index: 208

6.2.2 Raw map



X Index: 208



Y Index: 208

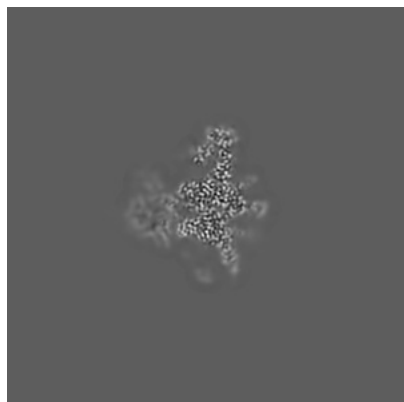


Z Index: 208

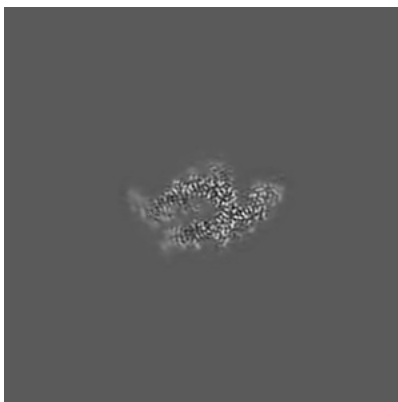
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

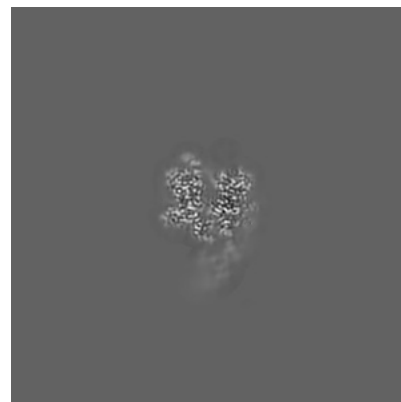
6.3.1 Primary map



X Index: 225

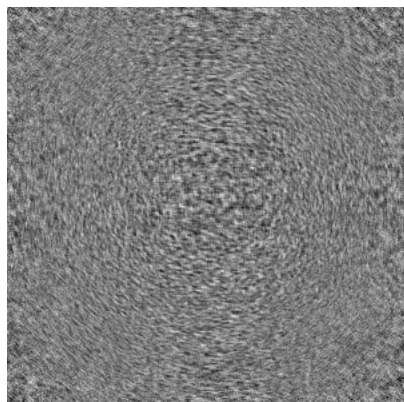


Y Index: 209

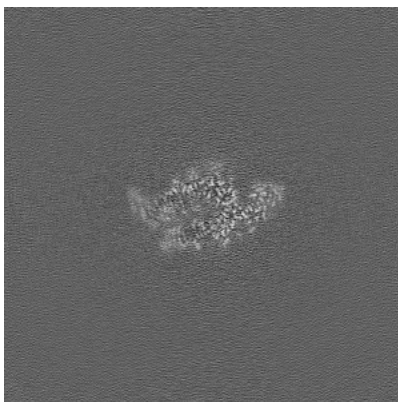


Z Index: 220

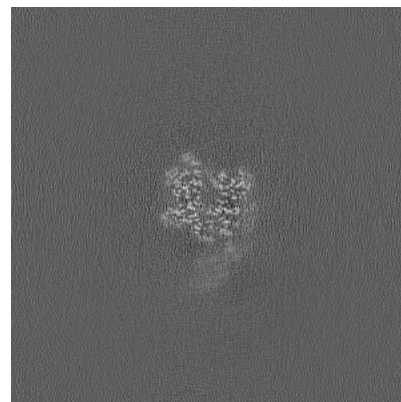
6.3.2 Raw map



X Index: 0



Y Index: 209

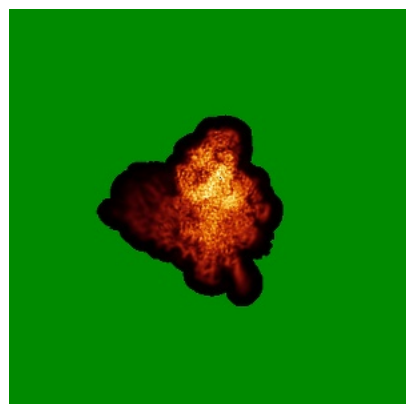


Z Index: 220

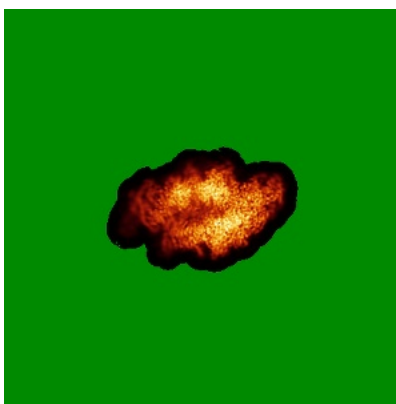
The images above show the largest variance slices of the map in three orthogonal directions.

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

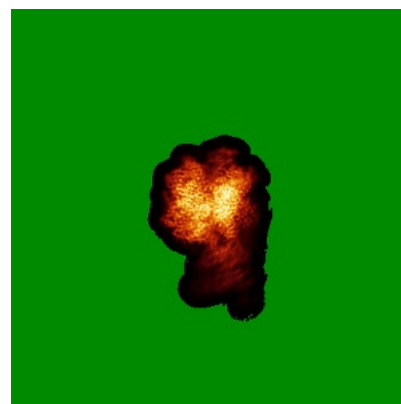
6.4.1 Primary map



X

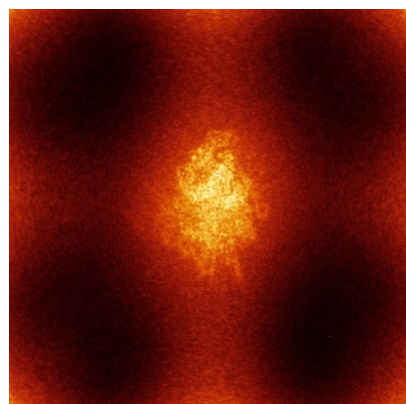


Y

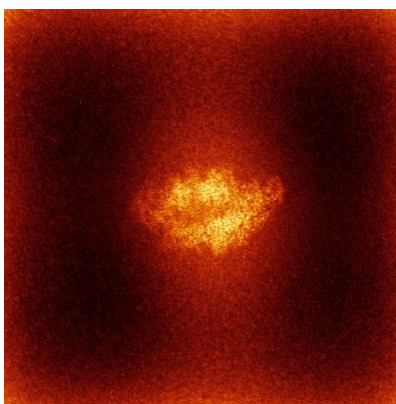


Z

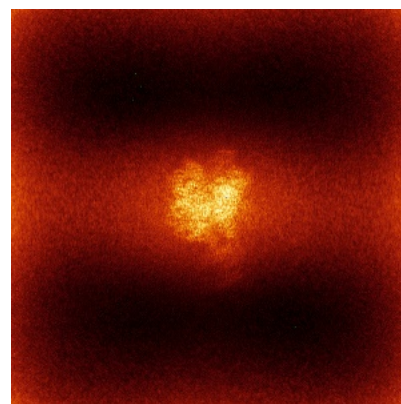
6.4.2 Raw map



X



Y

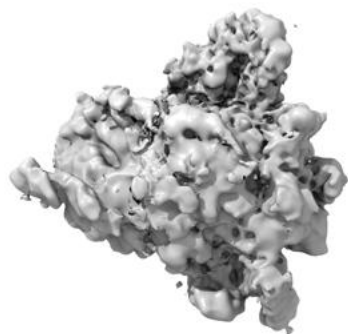


Z

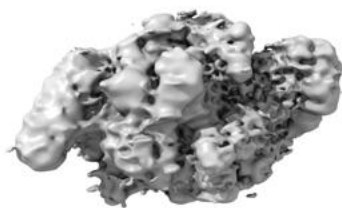
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



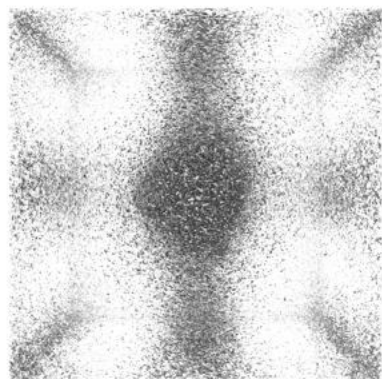
Y



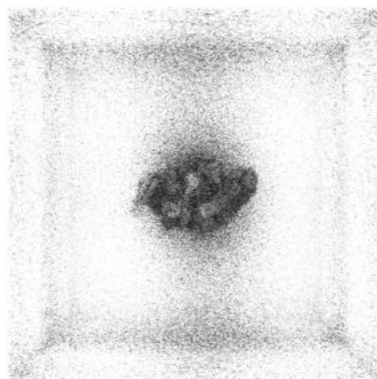
Z

The images above show the 3D surface view of the map at the recommended contour level 0.025. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

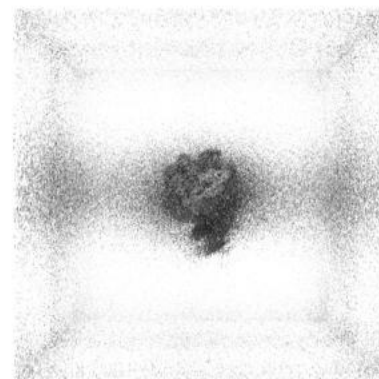
6.5.2 Raw map



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.

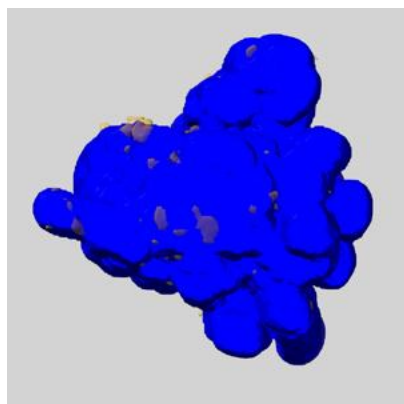
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

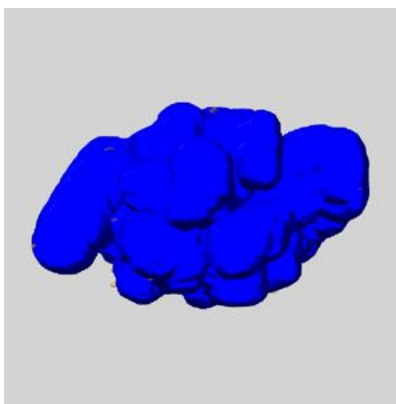
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

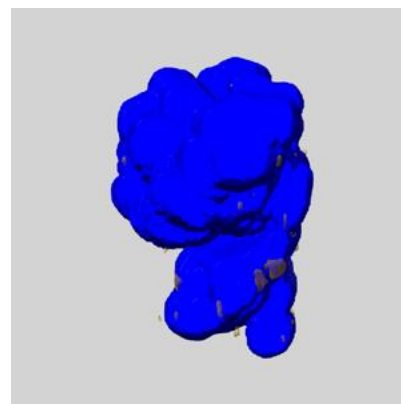
6.6.1 emd_36370_msk_1.map [i](#)



X



Y

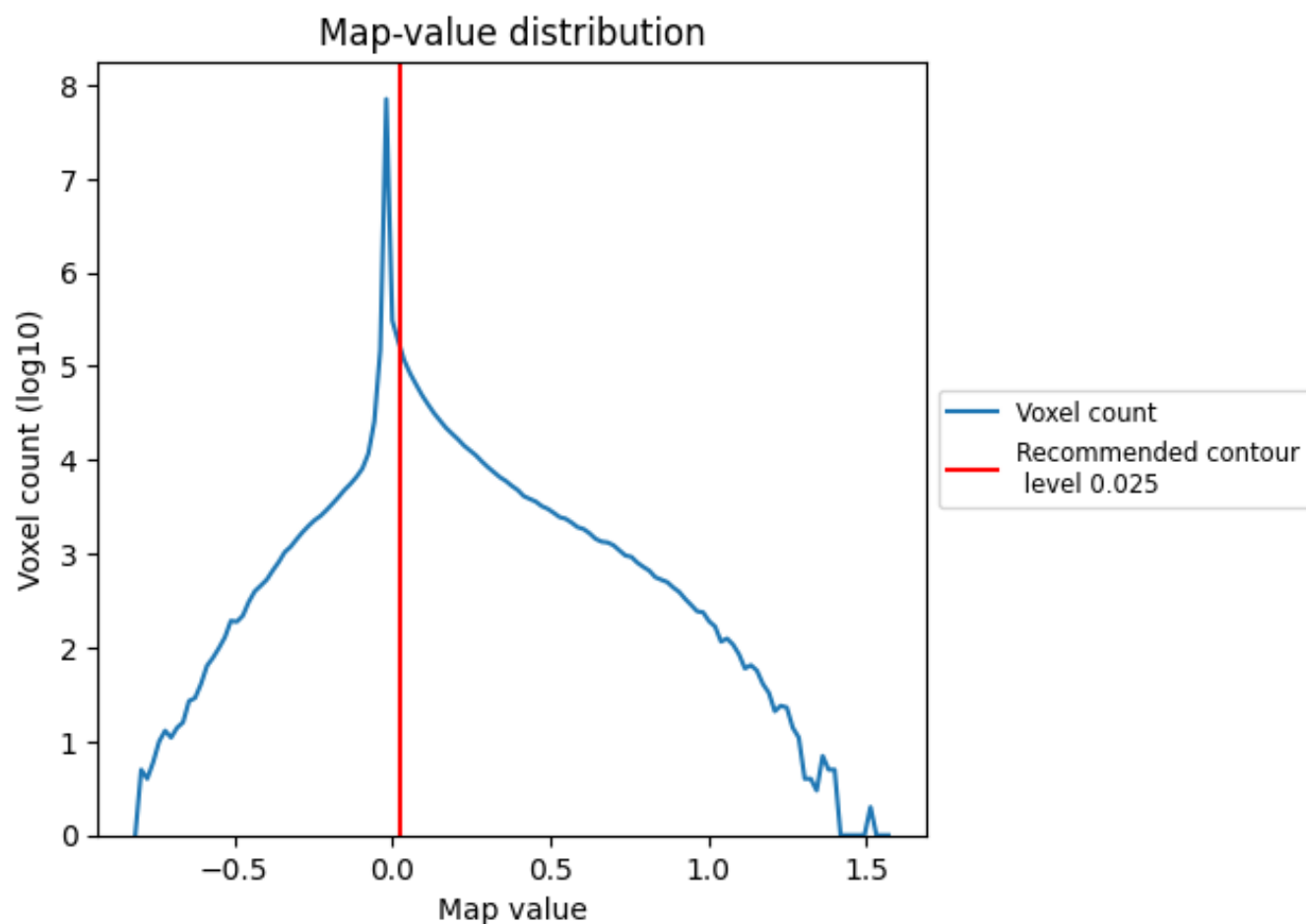


Z

7 Map analysis [i](#)

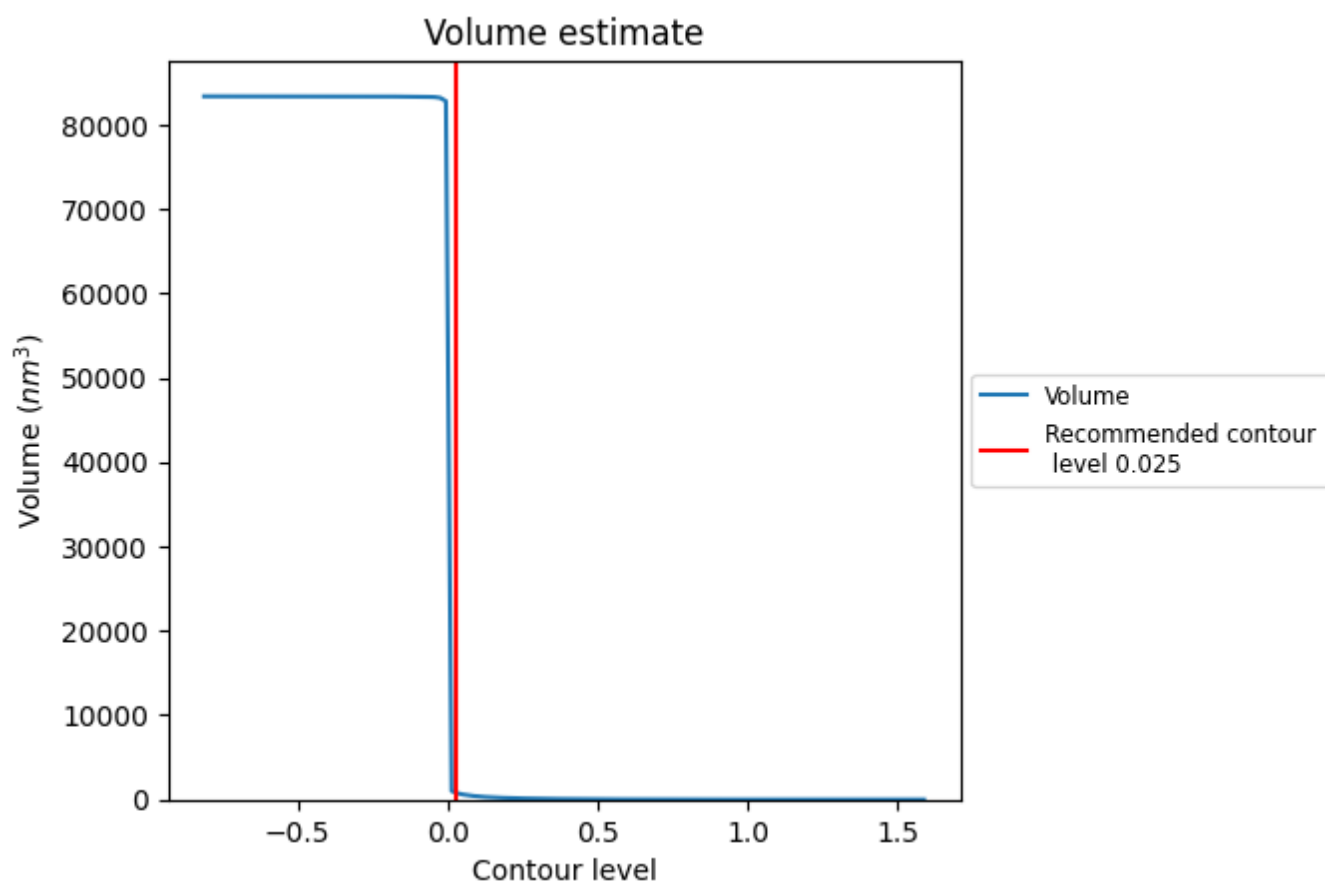
This section contains the results of statistical analysis of the map.

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.

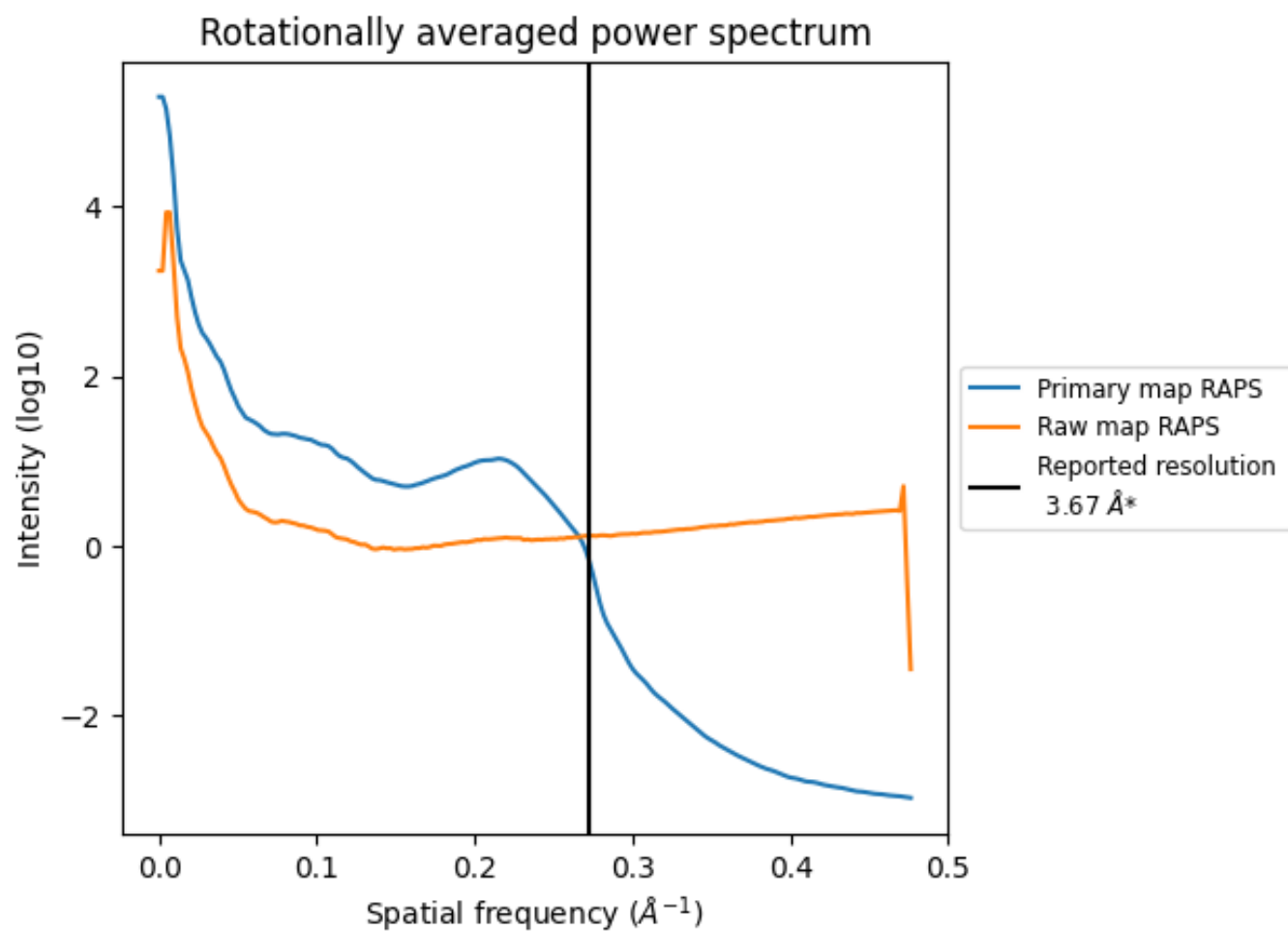
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 847 nm^3 ; this corresponds to an approximate mass of 765 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

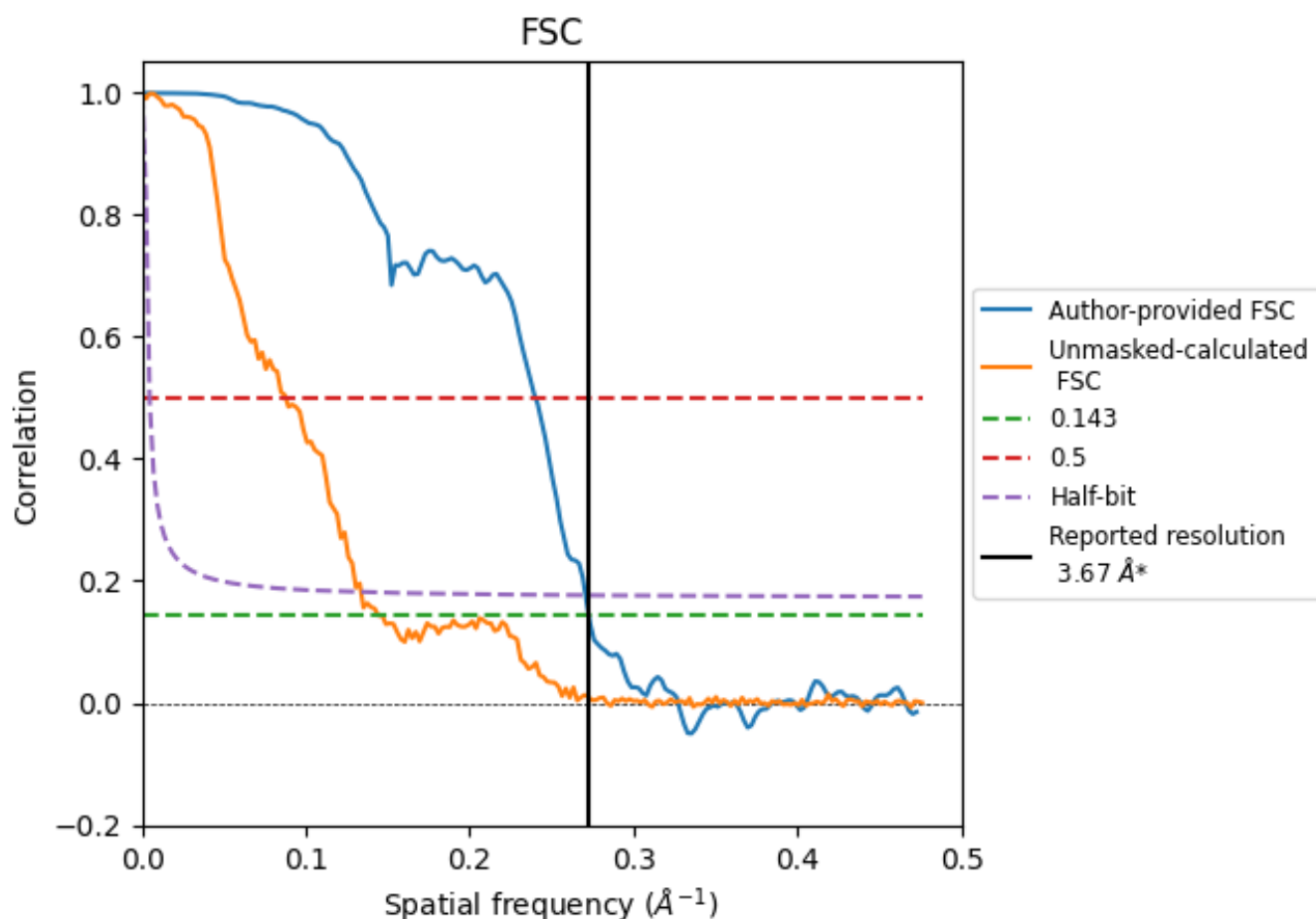


*Reported resolution corresponds to spatial frequency of 0.272 $\text{\AA}^{-1}$

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 0.272 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

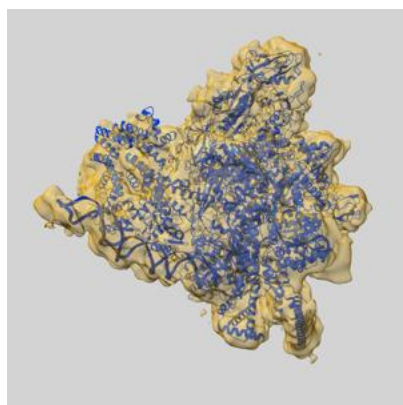
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.67	-	-
Author-provided FSC curve	3.67	4.16	3.69
Unmasked-calculated*	6.82	11.42	7.49

*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 6.82 differs from the reported value 3.67 by more than 10 %

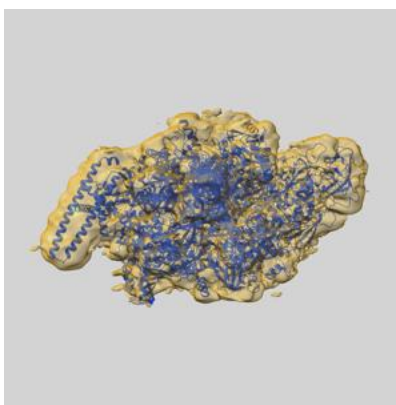
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-36370 and PDB model 8JKE. Per-residue inclusion information can be found in section [3](#) on page [8](#).

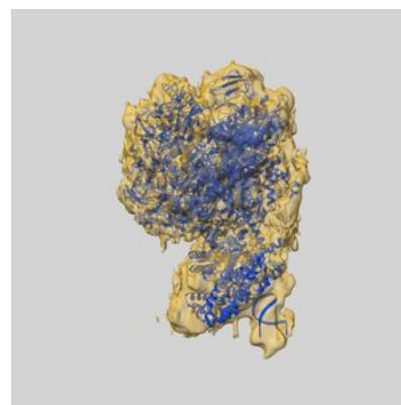
9.1 Map-model overlay [i](#)



X



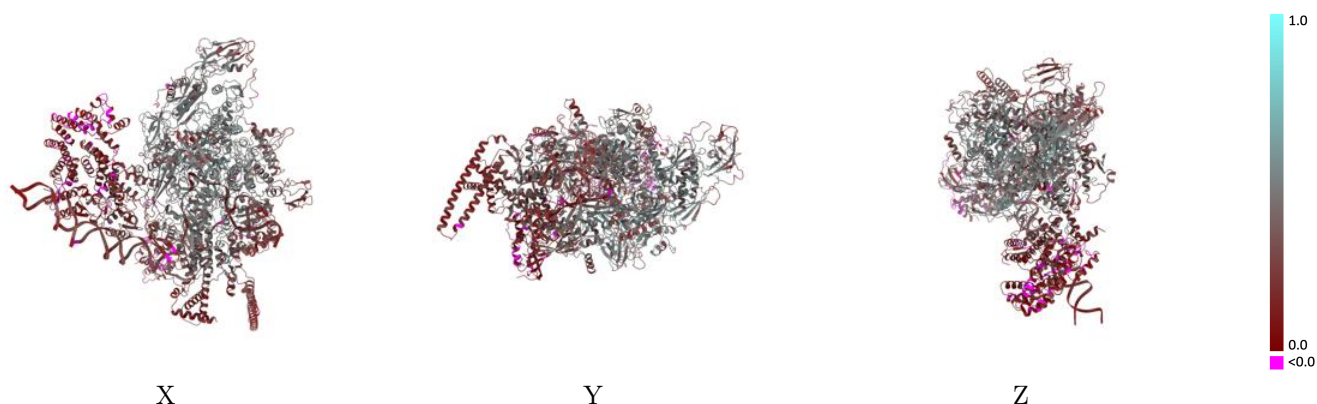
Y



Z

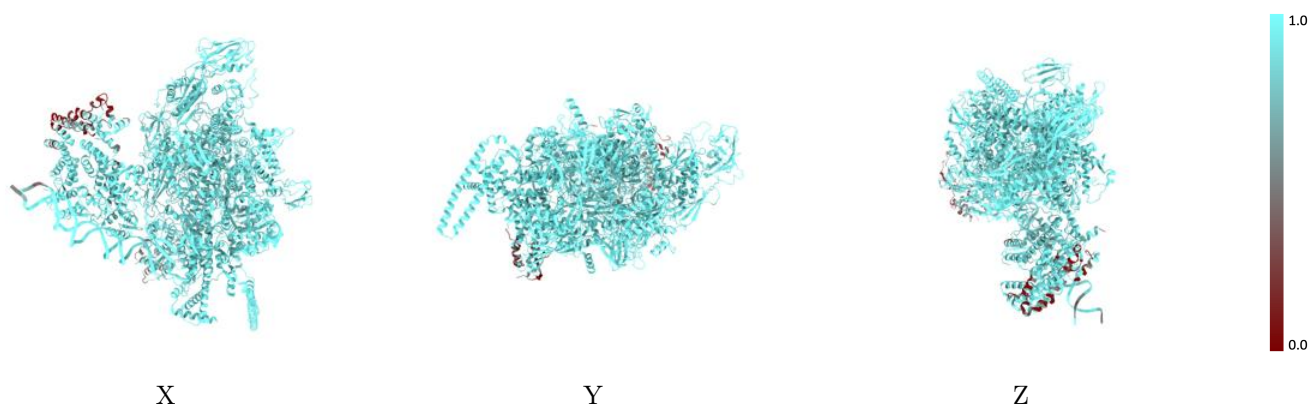
The images above show the 3D surface view of the map at the recommended contour level 0.025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



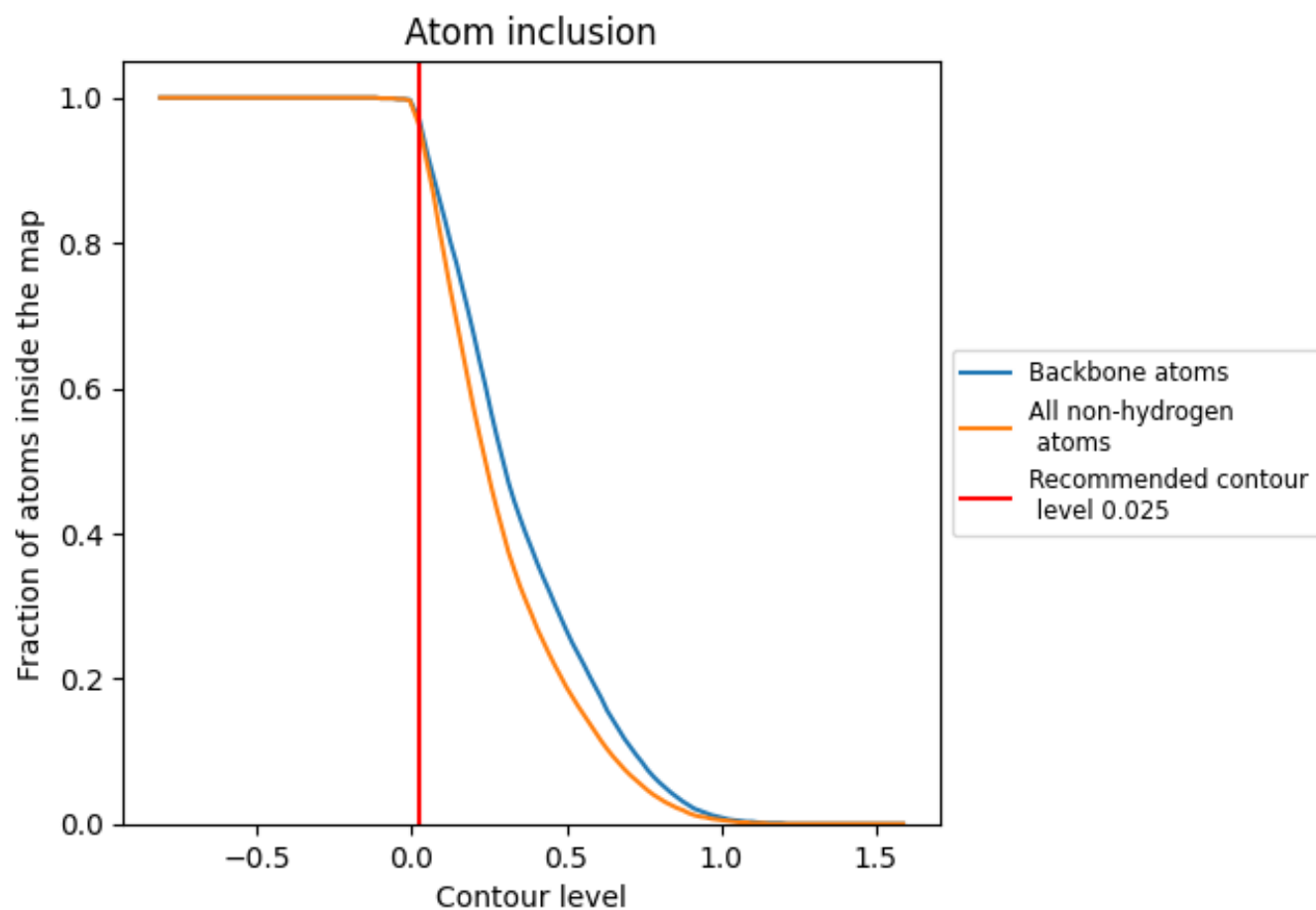
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.025).

9.4 Atom inclusion ⓘ



At the recommended contour level, 97% of all backbone atoms, 96% 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 (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9610	 0.3410
A	 0.9900	 0.4520
B	 0.9930	 0.3970
C	 0.9910	 0.4280
D	 0.9930	 0.4070
E	 0.9760	 0.3580
F	 0.9950	 0.2780
G	 0.9640	 0.1650
H	 0.6440	 0.1050
I	 0.9660	 0.1840
J	 0.8520	 0.1150
K	 0.5320	 0.0890
O	 0.9810	 0.2380
P	 0.9660	 0.2260

