



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 07:21 PM UTC

PDB ID : 8PHK / pdb_00008phk
EMDB ID : EMD-17668
Title : fully recruited RfaH bound to E. coli transcription complex paused at ops site
Authors : Zuber, P.K.; Said, N.; Hilal, T.; Loll, B.; Wahl, M.C.; Knauer, S.H.
Deposited on : 2023-06-20
Resolution : 3.10 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:

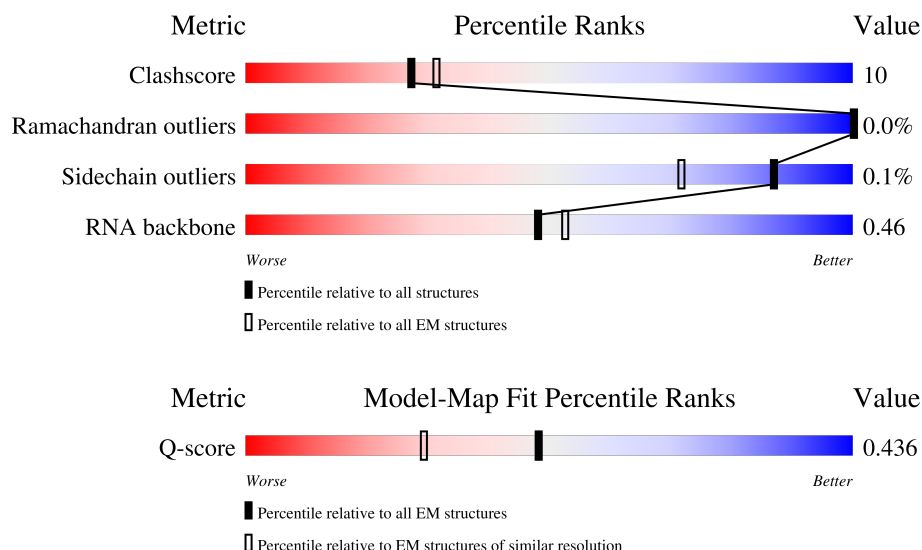
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.10 Å.

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



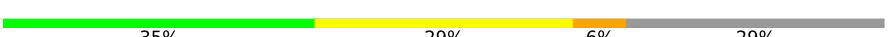
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 (2.60 - 3.60)

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

Mol	Chain	Length	Quality of chain
1	P	164	
2	I	1342	
3	J	1416	

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Mol	Chain	Length	Quality of chain
4	K	91	
5	G	329	
5	H	329	
6	A	40	
7	B	39	
8	R	17	

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 28225 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 Transcription antitermination protein RfaH.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	P	162	Total	C	N	O	S	0	0
			1294	833	223	233	5		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	-1	GLY	-	expression tag	UNP P0AFW0
P	0	HIS	-	expression tag	UNP P0AFW0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	I	1321	Total	C	N	O	S	1	0
			10431	6544	1819	2024	44		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	J	1342	Total	C	N	O	S	0	0
			10440	6560	1861	1969	50		

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	1	VAL	-	expression tag	UNP P0A8T7
J	1408	LEU	-	expression tag	UNP P0A8T7
J	1409	GLU	-	expression tag	UNP P0A8T7
J	1410	VAL	-	expression tag	UNP P0A8T7
J	1411	HIS	-	expression tag	UNP P0A8T7
J	1412	HIS	-	expression tag	UNP P0A8T7
J	1413	HIS	-	expression tag	UNP P0A8T7
J	1414	HIS	-	expression tag	UNP P0A8T7
J	1415	HIS	-	expression tag	UNP P0A8T7

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Chain	Residue	Modelled	Actual	Comment	Reference
J	1416	HIS	-	expression tag	UNP P0A8T7

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	K	83	Total	C	N	O	S	0	0
			655	399	123	132	1		

- Molecule 5 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	G	232	Total	C	N	O	S	1	0
			1807	1125	322	354	6		
5	H	230	Total	C	N	O	S	0	0
			1780	1108	314	352	6		

- Molecule 6 is a DNA chain called non-template DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A	38	Total	C	N	O	P	0	0
			771	367	131	235	38		

- Molecule 7 is a DNA chain called template DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	B	38	Total	C	N	O	P	0	0
			784	370	158	219	37		

- Molecule 8 is a RNA chain called RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	R	12	Total	C	N	O	P	0	0
			260	115	47	86	12		

- Molecule 9 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
9	J	2	Total	Zn	0
			2	2	

- Molecule 10 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

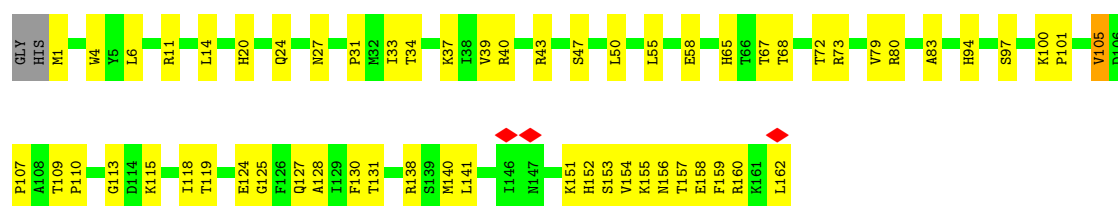
Mol	Chain	Residues	Atoms		AltConf
10	J	1	Total	Mg	0
			1	1	

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.

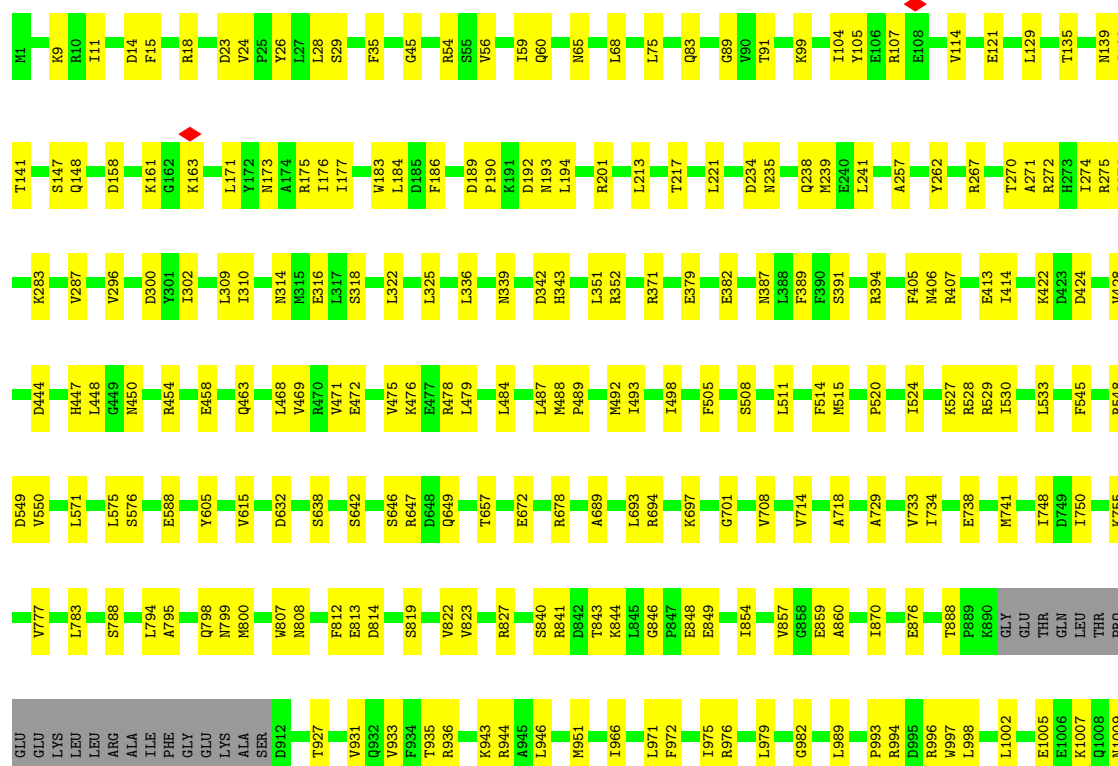
- Molecule 1: Transcription antitermination protein RfaH

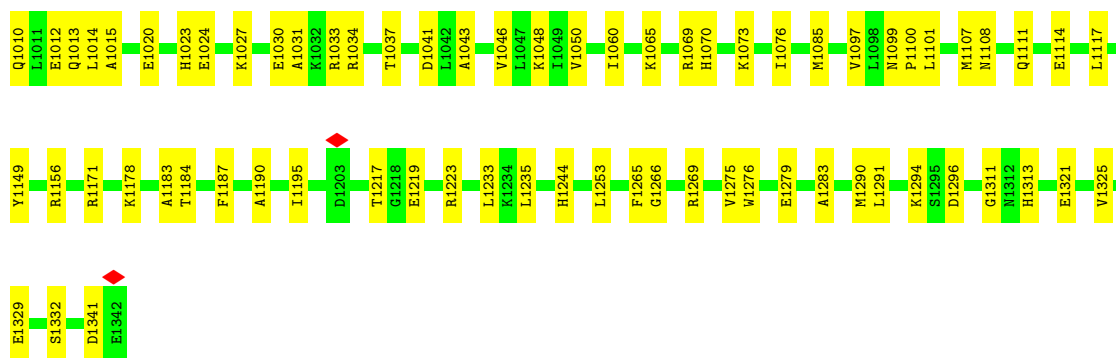
Chain P: 



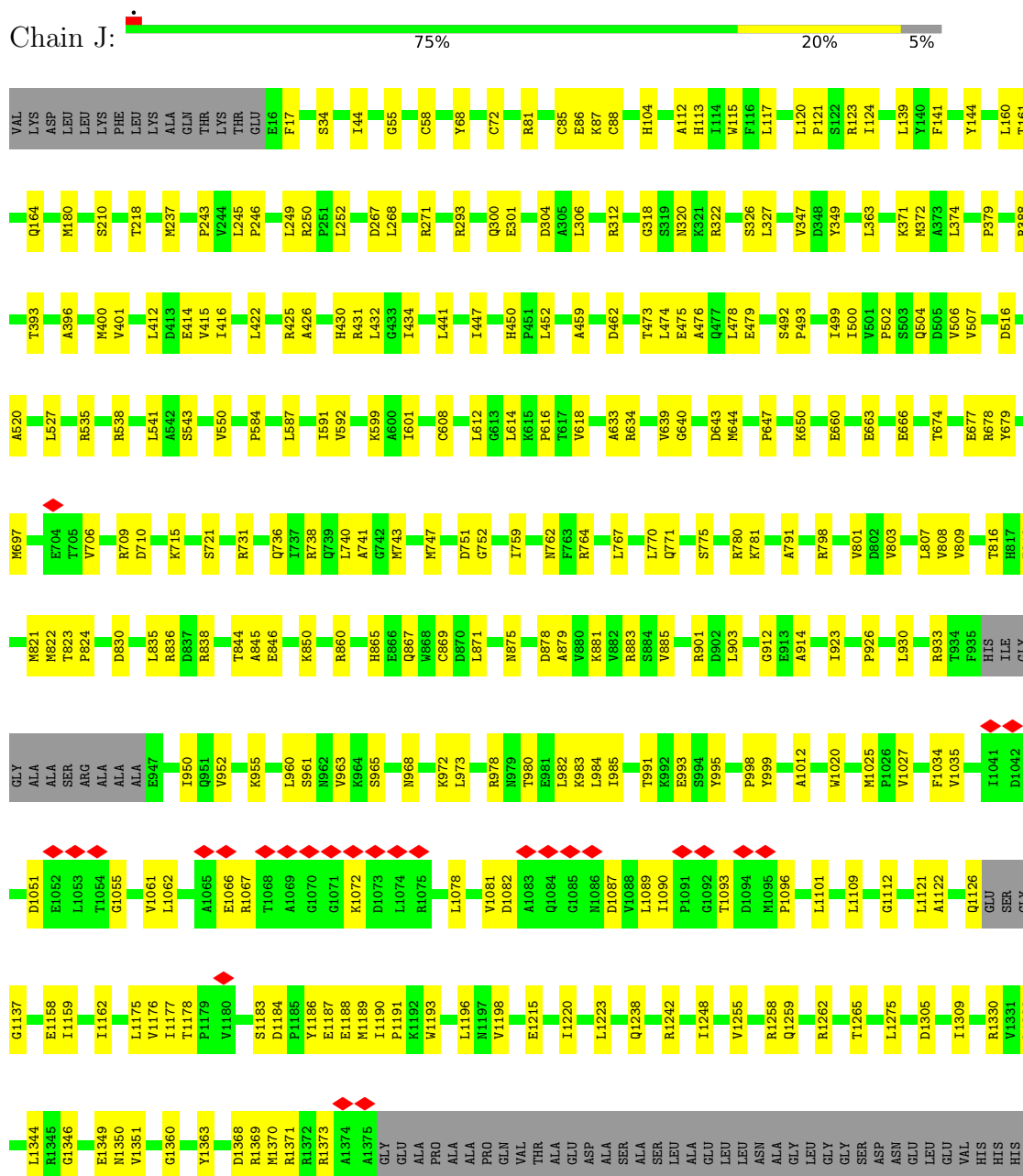
- Molecule 2: DNA-directed RNA polymerase subunit beta

Chain I: 





• Molecule 3: DNA-directed RNA polymerase subunit beta'



HIS
HIS

- Molecule 4: DNA-directed RNA polymerase subunit omega

Chain K: 

MET A2 R3 Q7 D8 A9 V10 E11 K12 I13 D18 L19 R28 Q31 K35 L38 T47 R52 E53 I54 E55 M60 I63 Q70 E71 Q72 Q73 E74 E75 E76 E79 L80 Q81 A82 V83 T84 ALA ILE ALA GLY ARG ARG

- Molecule 5: DNA-directed RNA polymerase subunit alpha

Chain G: 

MET GLN GLY V5 L13 I16 L31 E32 L39 R45 M51 P52 T57 E58 I61 V64 I78 L82 L83 K86 V90 R91 V92 Q93 V98 K104 V110 T116 V121 E122 I123 Q127 D135 E136 M137 A138 M142

K145 V146 R147 R148 R158 I159 H160 E163 L171 V173 C176 R182 Y185 R191 V192 E193 R194 R195 Q196 D197 L198 L201 E206 D212 E215 R219 T222 L223 L234 R235 ASP VAL ARG GLN PRO GLU VAL LYS GLU ASP VAL LYS SER LEU THR THR VAL ILE LYS ASP VAL LEU PHE ARG

PRO ILE LEU LEU ARG VAL ASP LEU LEU THR VAL ARG SER ALA ALA CYS LEU LEU ALA GLU ILE ALA ILE HIS TYR ILE GLY ASP LEU VAL GLN ARG THR VAL GLU VAL LEU LYS THR ASN LEU GLY LYS LYS SER LEU THR THR VAL ILE LYS ASP VAL LEU PHE ARG

GLY LEU SER LEU GLY MET ARG LEU TRP PRO PRO ALA ASP ASP GLU

- Molecule 5: DNA-directed RNA polymerase subunit alpha

Chain H: 

MET GLN GLY S4 V5 F8 L9 K10 P11 R12 L13 V14 L28 E29 P30 T38 M41 L47 E58 V59 L65 E76 E80 I81 L82 K86 V92 Q93 L100 T101 L102 N103 K104 I107 G108 P109 V110 I115 D118 V121 V124 Q127

L133 I144 R148 G149 R150 P154 H160 E163 D164 E165 R166 P167 I168 L172 V173 D174 A175 C176 V180 E188 V192 D197 K200 T210 V232 D233 LEU ARG ASP VAL ARG LYS VAL GLN PRO GLU VAL VAL GLU LYS VAL ALA PRO PHE ASP PRO ILE LEU

LEU ARG PRO VAL ASP LEU GLU THR VAL ARG SER ALA ASN CYS LEU LYS ALA GLU ALA ILE HIS TYR ILE GLY ASP LEU VAL GLN ARG THR VAL VAL LEU LYS THR PRO ASN LEU GLY LYS SER LEU THR GLU ILE LYS ASP VAL ALA PRO ARG GLY LEU SER

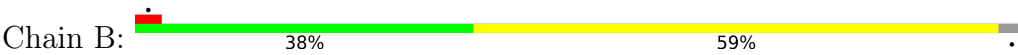
LEU GLY MET ARG LEU LEU ASN TRP PRO PRO ALA ILE ALA ASP GLU

- Molecule 6: non-template DNA

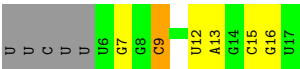
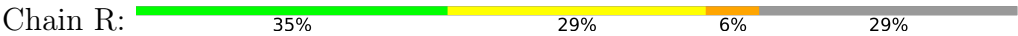
Chain A: 

DC DA C3 C4 A5 A8 C9 G10 C11 G12 G13 G16 G17 T18 A19 G20 C21 G22 T29 T30 G33 A34 T35 C40

- Molecule 7: template DNA



● Molecule 8: RNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	124233	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 ($e^-/\text{\AA}^2$)	42	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	96000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	1.734	Depositor
Minimum map value	-0.000	Depositor
Average map value	0.009	Depositor
Map value standard deviation	0.053	Depositor
Recommended contour level	0.24	Depositor
Map size (Å)	319.488, 319.488, 319.488	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.832, 0.832, 0.832	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 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	P	0.13	0/1325	0.41	0/1796
2	I	0.10	0/10600	0.28	0/14300
3	J	0.09	0/10598	0.24	0/14309
4	K	0.14	0/657	0.41	0/886
5	G	0.10	0/1832	0.28	0/2482
5	H	0.11	0/1802	0.30	0/2443
6	A	0.18	0/860	0.40	0/1324
7	B	0.15	0/883	0.30	0/1362
8	R	0.09	0/290	0.20	0/451
All	All	0.10	0/28847	0.28	0/39353

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 [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	P	1294	0	1315	40	0
2	I	10431	0	10449	205	0
3	J	10440	0	10660	198	0
4	K	655	0	663	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	G	1807	0	1840	39	0
5	H	1780	0	1803	41	0
6	A	771	0	430	15	0
7	B	784	0	424	27	0
8	R	260	0	130	5	0
9	J	2	0	0	0	0
10	J	1	0	0	0	0
All	All	28225	0	27714	546	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

All (546) 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)
3:J:502:PRO:HB3	3:J:506:VAL:HB	1.64	0.78
5:H:107:ILE:HG13	5:H:109:PRO:HD3	1.67	0.75
2:I:177:ILE:HA	2:I:183:TRP:HB3	1.69	0.74
2:I:488:MET:HE3	2:I:489:PRO:HD2	1.70	0.73
2:I:808:ASN:H	3:J:633:ALA:HB2	1.52	0.73
2:I:1005:GLU:HG2	2:I:1007:LYS:H	1.54	0.73
3:J:1158:GLU:HA	3:J:1223:LEU:HD11	1.71	0.73
2:I:697:LYS:O	2:I:799:ASN:ND2	2.22	0.72
2:I:979:LEU:HD22	2:I:989:LEU:HD22	1.72	0.72
2:I:1108:ASN:ND2	2:I:1111:GLN:OE1	2.22	0.72
2:I:1073:LYS:NZ	8:R:16:G:OP1	2.22	0.71
2:I:993:PRO:HB2	2:I:996:ARG:HH22	1.56	0.71
3:J:72:CYS:HB3	3:J:88:CYS:SG	2.29	0.71
3:J:803:VAL:HG21	3:J:1309:ILE:HB	1.72	0.70
1:P:113:GLY:N	1:P:130:PHE:O	2.24	0.70
3:J:322:ARG:NH2	8:R:9:C:O2'	2.25	0.69
3:J:1089:LEU:HA	3:J:1096:PRO:HA	1.73	0.68
1:P:118:ILE:O	1:P:125:GLY:N	2.27	0.68
3:J:926:PRO:HG2	3:J:1248:ILE:HD11	1.75	0.68
3:J:930:LEU:HD12	3:J:1137:GLY:HA2	1.76	0.68
2:I:1244:HIS:NE2	2:I:1266:GLY:O	2.26	0.68
3:J:245:LEU:O	3:J:250:ARG:NH1	2.28	0.67
2:I:812:PHE:O	2:I:1099:ASN:ND2	2.23	0.67
5:H:108:GLY:HA3	5:H:133:LEU:HB2	1.77	0.67
2:I:1100:PRO:HB3	3:J:639:VAL:HG22	1.77	0.67
5:G:127:GLN:OE1	5:G:127:GLN:N	2.21	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:371:ARG:NH1	6:A:20:DG:OP2	2.23	0.66
2:I:60:GLN:O	2:I:476:LYS:NZ	2.28	0.65
3:J:431:ARG:HD3	3:J:493:PRO:HG3	1.76	0.65
3:J:120:LEU:O	3:J:1330:ARG:NH1	2.29	0.65
3:J:747:MET:HE2	3:J:775:SER:HA	1.78	0.65
5:H:127:GLN:OE1	5:H:127:GLN:N	2.24	0.65
1:P:113:GLY:H	1:P:131:THR:HA	1.62	0.65
5:H:65:LEU:HD13	5:H:168:ILE:HD12	1.79	0.65
3:J:1360:GLY:O	3:J:1363:TYR:HB3	1.96	0.64
2:I:1219:GLU:N	2:I:1219:GLU:OE1	2.30	0.64
4:K:8:ASP:OD2	4:K:9:ALA:N	2.31	0.64
2:I:498:ILE:HD12	2:I:498:ILE:H	1.62	0.63
2:I:748:ILE:HD12	2:I:966:ILE:HG13	1.81	0.63
1:P:157:THR:HA	1:P:160:ARG:HH22	1.63	0.63
5:G:182:ARG:HB3	5:G:206:GLU:HB3	1.82	0.62
2:I:1269:ARG:NH1	7:B:20:DG:OP1	2.32	0.62
3:J:584:PRO:HG2	3:J:587:LEU:HD23	1.81	0.62
3:J:1346:GLY:O	3:J:1350:ASN:ND2	2.32	0.62
3:J:751:ASP:OD1	3:J:752:GLY:N	2.33	0.62
2:I:91:THR:HG22	2:I:139:ASN:H	1.64	0.62
2:I:549:ASP:OD1	2:I:550:VAL:N	2.32	0.62
3:J:968:ASN:OD1	3:J:972:LYS:N	2.33	0.62
1:P:115:LYS:HD2	1:P:127:GLN:HB2	1.82	0.62
2:I:478:ARG:O	2:I:478:ARG:NH1	2.29	0.62
3:J:985:ILE:HG12	3:J:991:THR:HA	1.80	0.61
3:J:850:LYS:NZ	3:J:875:ASN:OD1	2.34	0.61
3:J:492:SER:HB2	3:J:499:ILE:HD11	1.83	0.61
5:G:137:ASN:O	5:G:137:ASN:ND2	2.27	0.61
3:J:415:VAL:HG23	3:J:416:ILE:HG23	1.82	0.61
1:P:131:THR:HB	1:P:140:MET:HE1	1.82	0.61
3:J:614:LEU:HD23	4:K:7:GLN:HB2	1.83	0.61
3:J:535:ARG:NH1	5:H:176:CYS:SG	2.73	0.61
2:I:533:LEU:HD21	2:I:571:LEU:HD13	1.83	0.60
1:P:27:ASN:HB3	1:P:58:GLU:HB3	1.84	0.60
2:I:843:THR:OG1	2:I:846:GLY:O	2.19	0.60
2:I:471:VAL:HG21	2:I:498:ILE:HD11	1.83	0.60
2:I:189:ASP:HB3	2:I:193:ASN:HB2	1.82	0.60
2:I:976:ARG:HB2	2:I:997:TRP:HZ3	1.67	0.60
2:I:1041:ASP:OD1	2:I:1041:ASP:N	2.35	0.60
2:I:1117:LEU:HD13	2:I:1195:ILE:HG12	1.83	0.60
5:H:188:GLU:OE1	5:H:200:LYS:NZ	2.35	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:28:LEU:HD22	2:I:527:LYS:HD2	1.83	0.60
2:I:234:ASP:OD1	2:I:238:GLN:NE2	2.35	0.60
2:I:642:SER:HB2	3:J:770:LEU:HD21	1.83	0.60
7:B:26:DG:H2'	7:B:27:DC:C6	2.36	0.60
1:P:119:THR:HA	1:P:125:GLY:H	1.66	0.59
3:J:1090:ILE:HB	3:J:1093:THR:HB	1.84	0.59
2:I:267:ARG:HH12	2:I:270:THR:HG23	1.68	0.59
2:I:646:SER:HB3	2:I:649:GLN:HG3	1.83	0.59
5:H:93:GLN:HA	5:H:148:ARG:HH22	1.67	0.59
1:P:155:LYS:HB3	1:P:158:GLU:HG2	1.85	0.59
2:I:23:ASP:OD1	2:I:24:VAL:N	2.35	0.59
2:I:158:ASP:OD1	2:I:173:ASN:ND2	2.35	0.59
3:J:846:GLU:HG2	3:J:881:LYS:HE3	1.85	0.59
2:I:1073:LYS:HD2	3:J:462:ASP:HB2	1.84	0.58
3:J:1051:ASP:HB2	3:J:1055:GLY:H	1.67	0.58
3:J:1078:LEU:HG	3:J:1101:LEU:HD21	1.86	0.58
2:I:302:ILE:HA	2:I:309:LEU:HA	1.85	0.58
2:I:615:VAL:HG22	2:I:638:SER:HB2	1.84	0.58
3:J:1176:VAL:HG22	3:J:1187:GLU:HG3	1.86	0.58
2:I:444:ASP:HB3	2:I:447:HIS:HB2	1.83	0.58
3:J:1087:ASP:OD1	3:J:1087:ASP:N	2.35	0.58
2:I:1020:GLU:HA	2:I:1023:HIS:NE2	2.18	0.58
3:J:599:LYS:HE3	3:J:599:LYS:HA	1.85	0.58
3:J:697:MET:HE2	3:J:741:ALA:HB3	1.86	0.58
3:J:807:LEU:HD22	3:J:1259:GLN:HE21	1.68	0.58
5:G:104:LYS:HG2	5:G:110:VAL:HG22	1.84	0.58
2:I:819:SER:HB2	2:I:1085:MET:HG3	1.86	0.58
3:J:527:LEU:HB2	3:J:550:VAL:HG12	1.86	0.58
3:J:141:PHE:HB3	3:J:293:ARG:HE	1.69	0.58
3:J:1259:GLN:OE1	3:J:1262:ARG:NH1	2.36	0.58
5:G:13:LEU:HD11	5:G:16:ILE:HD11	1.85	0.57
5:G:61:ILE:HG12	5:G:142:MET:HG3	1.85	0.57
2:I:982:GLY:HA3	2:I:1002:LEU:HD21	1.86	0.57
3:J:591:ILE:HG13	3:J:592:VAL:HG13	1.87	0.57
1:P:33:ILE:HD11	1:P:101:PRO:HD2	1.87	0.57
5:G:98:VAL:HG11	5:G:121:VAL:HG21	1.86	0.57
2:I:271:ALA:HA	2:I:274:ILE:HD12	1.86	0.57
5:G:86:LYS:NZ	5:G:176:CYS:SG	2.77	0.57
3:J:901:ARG:HG2	3:J:903:LEU:H	1.70	0.56
5:G:45:ARG:HE	5:H:38:THR:HG22	1.68	0.56
7:B:27:DC:H2'	7:B:28:DC:C6	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:1069:ARG:NH2	2:I:1114:GLU:OE2	2.33	0.56
3:J:1035:VAL:O	3:J:1112:GLY:N	2.38	0.56
2:I:104:ILE:HG12	2:I:484:LEU:HD22	1.86	0.56
5:H:107:ILE:HD12	5:H:108:GLY:H	1.70	0.56
5:G:93:GLN:OE1	5:G:93:GLN:N	2.34	0.56
2:I:26:TYR:HB3	2:I:29:SER:HB3	1.87	0.56
5:G:5:VAL:O	5:H:150:ARG:NH2	2.32	0.56
3:J:978:ARG:HA	3:J:999:TYR:HB2	1.86	0.56
3:J:1188:GLU:C	3:J:1189:MET:HE2	2.31	0.56
3:J:1370:MET:HE2	3:J:1370:MET:HA	1.88	0.56
5:G:158:ARG:NH2	5:G:173:VAL:O	2.38	0.56
3:J:821:MET:HE2	3:J:879:ALA:HB1	1.87	0.55
5:H:14:VAL:HG13	5:H:28:LEU:HD11	1.88	0.55
3:J:268:LEU:HD13	3:J:306:LEU:HA	1.86	0.55
5:H:10:LYS:HB3	5:H:12:ARG:HH11	1.72	0.55
8:R:15:C:H2'	8:R:16:G:C8	2.42	0.55
1:P:154:VAL:HG23	1:P:159:PHE:HE2	1.71	0.55
5:G:191:ARG:HH12	5:G:196:THR:HG22	1.71	0.55
2:I:35:PHE:HE2	2:I:129:LEU:HD12	1.72	0.55
3:J:822:MET:HE1	3:J:838:ARG:HE	1.72	0.55
2:I:241:LEU:N	2:I:283:LYS:O	2.34	0.55
3:J:121:PRO:HD2	3:J:123:ARG:HH12	1.71	0.55
3:J:393:THR:HG23	3:J:396:ALA:H	1.71	0.55
3:J:1175:LEU:HB2	3:J:1190:ILE:HD11	1.89	0.55
3:J:502:PRO:HB2	3:J:507:VAL:HG13	1.89	0.55
5:G:185:TYR:HB2	5:G:201:LEU:HD11	1.88	0.55
2:I:936:ARG:NH2	2:I:1046:VAL:O	2.40	0.55
3:J:318:GLY:N	3:J:322:ARG:O	2.39	0.55
2:I:217:THR:HG23	2:I:351:LEU:HD21	1.89	0.54
2:I:406:ASN:ND2	2:I:413:GLU:O	2.40	0.54
2:I:993:PRO:O	2:I:996:ARG:NH1	2.40	0.54
3:J:1061:VAL:HG21	3:J:1101:LEU:HB3	1.88	0.54
4:K:72:GLN:NE2	4:K:76:GLU:OE2	2.39	0.54
3:J:1034:PHE:HB2	3:J:1081:VAL:HG23	1.89	0.54
2:I:841:ARG:HA	2:I:1046:VAL:HA	1.88	0.54
5:G:92:VAL:O	5:G:148:ARG:NH2	2.32	0.54
5:H:76:GLU:HG2	5:H:80:GLU:HG2	1.89	0.54
5:H:100:LEU:HD21	5:H:121:VAL:HG11	1.89	0.54
3:J:644:MET:O	3:J:764:ARG:NH1	2.38	0.54
3:J:808:VAL:HG12	3:J:914:ALA:HA	1.89	0.54
2:I:876:GLU:HG3	2:I:927:THR:HG22	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:1109:LEU:HD21	3:J:1121:LEU:HD23	1.88	0.54
2:I:1070:HIS:NE2	2:I:1114:GLU:OE1	2.40	0.54
3:J:836:ARG:NH1	3:J:869:CYS:SG	2.81	0.54
5:H:164:ASP:OD1	5:H:165:GLU:N	2.40	0.54
2:I:1290:MET:HG3	3:J:347:VAL:HG11	1.90	0.54
3:J:950:ILE:HG21	3:J:982:LEU:HD11	1.89	0.54
5:G:51:MET:HE3	5:G:52:PRO:HD2	1.90	0.54
7:B:27:DC:H2'	7:B:28:DC:H6	1.73	0.54
2:I:1020:GLU:HA	2:I:1023:HIS:CE1	2.42	0.53
2:I:59:ILE:HB	2:I:68:LEU:HB3	1.90	0.53
3:J:697:MET:HE1	3:J:738:ARG:HA	1.90	0.53
3:J:885:VAL:HG11	3:J:1255:VAL:HG22	1.91	0.53
6:A:22:DG:H5'	6:A:22:DG:C8	2.43	0.53
5:G:32:GLU:OE1	5:H:150:ARG:NH1	2.42	0.53
3:J:709:ARG:NH2	3:J:710:ASP:O	2.41	0.53
3:J:965:SER:HB2	3:J:973:LEU:HG	1.91	0.53
2:I:876:GLU:N	2:I:876:GLU:OE2	2.42	0.53
2:I:1275:VAL:O	2:I:1279:GLU:HG3	2.09	0.53
1:P:37:LYS:O	1:P:43:ARG:HA	2.08	0.53
3:J:1025:MET:HG3	3:J:1126:GLN:HE22	1.74	0.53
4:K:38:LEU:N	4:K:53:GLU:OE2	2.41	0.53
2:I:548:ARG:O	3:J:780:ARG:NH1	2.41	0.53
2:I:733:VAL:HG22	2:I:750:ILE:HG12	1.90	0.53
2:I:1217:THR:HG23	5:H:41:ASN:HD21	1.74	0.53
3:J:1162:ILE:HG22	3:J:1178:THR:HB	1.91	0.52
2:I:694:ARG:HH21	5:G:83:LEU:HD23	1.74	0.52
3:J:363:LEU:HD23	3:J:618:VAL:HG12	1.92	0.52
3:J:374:LEU:HD11	3:J:401:VAL:HG13	1.91	0.52
2:I:296:VAL:HG12	2:I:316:GLU:HA	1.90	0.52
2:I:1031:ALA:N	2:I:1034:ARG:HH21	2.06	0.52
2:I:104:ILE:HG23	2:I:484:LEU:HD13	1.90	0.52
2:I:943:LYS:HA	2:I:946:LEU:HD12	1.92	0.52
2:I:1311:GLY:O	4:K:31:GLN:NE2	2.43	0.52
4:K:18:ASP:OD1	4:K:18:ASP:N	2.36	0.52
6:A:16:DG:H1'	6:A:19:DA:H61	1.75	0.52
2:I:339:ASN:HB2	2:I:343:HIS:H	1.74	0.52
2:I:689:ALA:HB2	2:I:1233:LEU:HD23	1.91	0.52
2:I:813:GLU:HG2	2:I:814:ASP:OD1	2.09	0.52
3:J:426:ALA:HB1	7:B:20:DG:H1'	1.92	0.52
3:J:781:LYS:HD2	3:J:933:ARG:HD3	1.92	0.52
3:J:1067:ARG:O	3:J:1072:LYS:NZ	2.41	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:H:118:ASP:HB2	5:H:121:VAL:HG22	1.91	0.52
3:J:587:LEU:HD21	3:J:608:CYS:HA	1.91	0.52
4:K:73:GLN:HA	4:K:76:GLU:HG2	1.92	0.52
7:B:26:DG:H2'	7:B:27:DC:H6	1.72	0.52
1:P:1:MET:HA	1:P:1:MET:HE2	1.90	0.51
2:I:141:THR:HB	2:I:514:PHE:HE1	1.76	0.51
2:I:1031:ALA:HA	2:I:1034:ARG:HE	1.75	0.51
3:J:300:GLN:NE2	3:J:304:ASP:OD1	2.43	0.51
2:I:147:SER:HB2	2:I:530:ILE:HG22	1.92	0.51
2:I:545:PHE:HD2	3:J:933:ARG:HH11	1.57	0.51
3:J:541:LEU:HD21	5:H:154:PRO:HD3	1.93	0.51
5:G:137:ASN:HD22	5:G:137:ASN:C	2.17	0.51
2:I:272:ARG:HA	2:I:275:ARG:HD2	1.92	0.51
2:I:524:ILE:HD12	2:I:708:VAL:HG13	1.93	0.51
3:J:422:LEU:HD23	3:J:434:ILE:HD11	1.92	0.51
3:J:507:VAL:HG12	3:J:601:ILE:HD12	1.92	0.51
3:J:674:THR:OG1	3:J:677:GLU:OE1	2.27	0.51
7:B:23:DA:H2'	7:B:24:DC:C6	2.46	0.51
2:I:1219:GLU:OE2	3:J:634:ARG:NH1	2.43	0.51
2:I:407:ARG:HH21	2:I:414:ILE:HD12	1.76	0.51
2:I:488:MET:HE3	2:I:489:PRO:CD	2.40	0.51
2:I:1065:LYS:HE2	2:I:1235:LEU:HD12	1.92	0.51
2:I:1325:VAL:O	2:I:1329:GLU:HG3	2.10	0.51
3:J:473:THR:HG23	3:J:476:ALA:H	1.76	0.51
2:I:176:ILE:HD11	2:I:428:VAL:HG11	1.92	0.50
3:J:502:PRO:HG2	3:J:601:ILE:HG21	1.93	0.50
3:J:816:THR:HG22	3:J:818:GLU:H	1.77	0.50
1:P:4:TRP:CE2	1:P:58:GLU:HB2	2.46	0.50
2:I:18:ARG:O	2:I:1156:ARG:NH1	2.41	0.50
2:I:394:ARG:HG3	2:I:394:ARG:HH11	1.77	0.50
3:J:830:ASP:OD1	3:J:830:ASP:N	2.43	0.50
5:G:192:VAL:HB	5:G:198:LEU:HD12	1.92	0.50
2:I:99:LYS:HG2	2:I:121:GLU:HG2	1.92	0.50
3:J:372:MET:HE1	3:J:447:ILE:HD11	1.92	0.50
1:P:68:THR:O	1:P:72:THR:OG1	2.28	0.50
1:P:124:GLU:O	3:J:87:LYS:NZ	2.43	0.50
2:I:469:VAL:O	2:I:472:GLU:HG3	2.11	0.50
2:I:1341:ASP:HA	3:J:17:PHE:HA	1.94	0.50
7:B:24:DC:H2'	7:B:25:DC:C6	2.47	0.50
2:I:444:ASP:O	2:I:450:ASN:ND2	2.45	0.50
5:H:102:LEU:HD13	5:H:115:ILE:HG13	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:729:ALA:HB1	2:I:755:LYS:HE3	1.93	0.50
2:I:807:TRP:HB2	2:I:1097:VAL:HG11	1.93	0.50
1:P:128:ALA:HB3	1:P:141:LEU:HD23	1.94	0.49
2:I:1291:LEU:HD11	3:J:1351:VAL:HG13	1.94	0.49
5:G:90:VAL:HG23	5:G:123:ILE:HD13	1.94	0.49
3:J:650:LYS:HE3	3:J:762:ASN:HD21	1.76	0.49
7:B:25:DC:H2'	7:B:26:DG:C8	2.46	0.49
2:I:1107:MET:HE3	2:I:1107:MET:HA	1.94	0.49
2:I:1223:ARG:NH2	3:J:721:SER:OG	2.45	0.49
5:H:86:LYS:HD3	5:H:174:ASP:HB2	1.95	0.49
2:I:28:LEU:HD21	2:I:524:ILE:HG12	1.94	0.49
3:J:218:THR:HG23	3:J:1275:LEU:HD23	1.95	0.49
3:J:326:SER:OG	3:J:327:LEU:N	2.44	0.49
7:B:19:DC:H2'	7:B:20:DG:C8	2.48	0.49
3:J:450:HIS:HE1	3:J:452:LEU:HD12	1.78	0.49
3:J:141:PHE:O	3:J:293:ARG:NH2	2.46	0.49
3:J:141:PHE:HA	3:J:180:MET:HE3	1.94	0.49
5:H:92:VAL:O	5:H:148:ARG:NH2	2.45	0.49
2:I:1283:ALA:HA	3:J:479:GLU:OE2	2.12	0.49
3:J:349:TYR:HE1	3:J:379:PRO:HG2	1.77	0.49
3:J:1177:ILE:HG13	3:J:1186:TYR:HD2	1.78	0.49
2:I:1009:ASN:O	2:I:1012:GLU:HG3	2.12	0.49
7:B:23:DA:H2'	7:B:24:DC:H6	1.78	0.49
1:P:20:HIS:O	1:P:24:GLN:HG2	2.13	0.48
7:B:9:DG:H2''	7:B:10:DA:H8	1.78	0.48
7:B:25:DC:H2'	7:B:26:DG:H8	1.78	0.48
2:I:933:VAL:HG22	2:I:1050:VAL:HG22	1.94	0.48
2:I:234:ASP:OD1	2:I:235:ASN:N	2.46	0.48
2:I:1276:TRP:CD2	3:J:801:VAL:HG11	2.48	0.48
2:I:1060:ILE:HD11	2:I:1076:ILE:HG13	1.96	0.48
5:G:193:GLU:CD	5:G:194:GLN:H	2.21	0.48
2:I:148:GLN:HB2	2:I:511:LEU:HD11	1.95	0.48
2:I:672:GLU:HB2	3:J:767:LEU:H	1.77	0.48
3:J:267:ASP:O	3:J:271:ARG:HG2	2.13	0.48
7:B:36:DT:H2''	7:B:37:DG:C8	2.48	0.48
2:I:1290:MET:HA	2:I:1294:LYS:HD3	1.96	0.48
3:J:885:VAL:HG12	3:J:1258:ARG:HD3	1.96	0.48
3:J:952:VAL:HG22	3:J:984:LEU:HD21	1.95	0.48
3:J:960:LEU:HB3	3:J:963:VAL:HG11	1.95	0.48
5:G:82:LEU:HD21	5:G:171:LEU:HD12	1.95	0.48
3:J:759:ILE:HG12	3:J:771:GLN:HG2	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:K:3:ARG:NH2	4:K:55:GLU:OE2	2.46	0.48
3:J:871:LEU:O	3:J:875:ASN:ND2	2.47	0.47
2:I:1290:MET:HE2	2:I:1290:MET:HB2	1.84	0.47
2:I:972:PHE:HA	2:I:975:ILE:HG12	1.96	0.47
6:A:8:DA:H2''	6:A:9:DC:H5'	1.96	0.47
7:B:3:DA:H2''	7:B:4:DA:C8	2.50	0.47
2:I:1031:ALA:HA	2:I:1034:ARG:NE	2.29	0.47
3:J:845:ALA:HA	3:J:883:ARG:HG3	1.96	0.47
5:H:104:LYS:HG2	5:H:110:VAL:HG22	1.95	0.47
2:I:213:LEU:HD13	2:I:422:LYS:HG2	1.95	0.47
2:I:520:PRO:HG3	2:I:714:VAL:HG21	1.96	0.47
1:P:31:PRO:HB2	1:P:50:LEU:HB3	1.95	0.47
2:I:171:LEU:HD21	2:I:190:PRO:HG3	1.97	0.47
2:I:678:ARG:HG3	2:I:1108:ASN:HB3	1.96	0.47
2:I:823:VAL:HG22	2:I:1060:ILE:HG23	1.95	0.47
2:I:1030:GLU:C	2:I:1034:ARG:HH21	2.23	0.47
2:I:1313:HIS:HB2	3:J:474:LEU:HG	1.97	0.47
3:J:478:LEU:HG	4:K:47:THR:HB	1.96	0.47
3:J:998:PRO:HG2	3:J:1020:TRP:CE2	2.49	0.47
3:J:1215:GLU:HB2	3:J:1220:ILE:HD11	1.96	0.47
5:H:47:LEU:HD22	5:H:180:VAL:HG21	1.97	0.47
3:J:1190:ILE:HG21	3:J:1196:LEU:HD11	1.96	0.47
5:G:31:LEU:HA	5:G:31:LEU:HD23	1.72	0.47
2:I:201:ARG:HH21	6:A:22:DG:H1	1.62	0.47
5:G:212:ASP:HB3	5:G:215:GLU:HB2	1.95	0.47
2:I:1253:LEU:HD23	2:I:1253:LEU:H	1.80	0.47
2:I:173:ASN:HA	2:I:186:PHE:O	2.15	0.46
2:I:339:ASN:HD22	2:I:342:ASP:HB3	1.79	0.46
2:I:492:MET:SD	2:I:492:MET:N	2.75	0.46
2:I:788:SER:OG	2:I:795:ALA:O	2.28	0.46
5:G:31:LEU:HD11	5:G:39:LEU:HD12	1.96	0.46
4:K:70:GLN:HA	4:K:73:GLN:HG3	1.96	0.46
2:I:56:VAL:HG21	2:I:468:LEU:HG	1.96	0.46
3:J:121:PRO:O	3:J:123:ARG:NH1	2.48	0.46
5:G:13:LEU:HD21	5:G:16:ILE:HG12	1.97	0.46
5:G:222:THR:OG1	5:H:232:VAL:O	2.32	0.46
5:H:127:GLN:H	5:H:127:GLN:CD	2.21	0.46
6:A:16:DG:H1'	6:A:19:DA:N6	2.30	0.46
2:I:718:ALA:HB2	2:I:783:LEU:HD21	1.97	0.46
3:J:961:SER:OG	3:J:983:LYS:NZ	2.49	0.46
5:G:234:LEU:HD23	5:G:234:LEU:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B:24:DC:H2'	7:B:25:DC:H6	1.80	0.46
2:I:998:LEU:HD11	2:I:1015:ALA:HB2	1.97	0.46
3:J:85:CYS:SG	3:J:86:GLU:N	2.88	0.46
3:J:747:MET:HB3	3:J:747:MET:HE3	1.81	0.46
3:J:1062:LEU:HD23	3:J:1066:GLU:HB3	1.97	0.46
2:I:528:ARG:NH2	2:I:576:SER:O	2.41	0.46
5:H:10:LYS:HB3	5:H:12:ARG:NH1	2.29	0.46
5:H:58:GLU:HB3	5:H:172:LEU:HD23	1.98	0.46
1:P:34:THR:HA	1:P:47:SER:HA	1.97	0.46
2:I:314:ASN:OD1	2:I:352:ARG:NH2	2.38	0.46
3:J:246:PRO:HD2	3:J:249:LEU:HD22	1.98	0.46
3:J:807:LEU:HD23	3:J:1255:VAL:HG13	1.98	0.46
5:G:57:THR:HG22	5:G:58:GLU:HG3	1.97	0.46
2:I:239:MET:HG2	2:I:287:VAL:CG2	2.46	0.46
3:J:430:HIS:CD2	3:J:432:LEU:HB2	2.50	0.46
3:J:978:ARG:NH2	3:J:1198:VAL:HA	2.30	0.46
7:B:9:DG:H2''	7:B:10:DA:C8	2.51	0.46
3:J:452:LEU:HB3	3:J:500:ILE:HG23	1.97	0.46
3:J:824:PRO:HD3	3:J:835:LEU:HB2	1.98	0.46
3:J:844:THR:OG1	3:J:860:ARG:O	2.34	0.46
5:H:124:VAL:HG11	5:H:210:THR:HA	1.98	0.46
2:I:849:GLU:OE1	2:I:849:GLU:N	2.48	0.45
3:J:1265:THR:OG1	3:J:1305:ASP:OD2	2.32	0.45
1:P:11:ARG:HE	1:P:11:ARG:HB3	1.60	0.45
2:I:971:LEU:O	2:I:975:ILE:HG23	2.15	0.45
4:K:52:ARG:O	4:K:55:GLU:HB2	2.17	0.45
2:I:487:LEU:HD13	2:I:492:MET:HE1	1.99	0.45
2:I:1101:LEU:HD12	3:J:504:GLN:HB3	1.98	0.45
2:I:1332:SER:HA	3:J:243:PRO:HB2	1.97	0.45
5:G:90:VAL:HG11	5:G:146:VAL:HG21	1.98	0.45
2:I:1023:HIS:O	2:I:1027:LYS:HG3	2.17	0.45
3:J:984:LEU:HB2	3:J:993:GLU:HB2	1.98	0.45
5:G:135:ASP:HB3	5:G:138:ALA:HB2	1.97	0.45
6:A:34:DA:H2'	6:A:35:DT:H71	1.97	0.45
1:P:97:SER:O	1:P:100:LYS:NZ	2.48	0.45
1:P:138:ARG:O	1:P:153:SER:OG	2.34	0.45
3:J:1159:ILE:HG13	3:J:1177:ILE:HG21	1.98	0.45
3:J:644:MET:HG2	3:J:740:LEU:HD12	1.98	0.45
3:J:1035:VAL:O	3:J:1112:GLY:CA	2.65	0.45
6:A:33:DG:H2''	6:A:34:DA:H8	1.82	0.45
2:I:844:LYS:HA	2:I:844:LYS:HD3	1.89	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:612:LEU:HD12	3:J:616:PRO:HG2	1.99	0.44
4:K:8:ASP:O	4:K:11:GLU:HG2	2.18	0.44
2:I:951:MET:HE2	2:I:951:MET:N	2.31	0.44
3:J:210:SER:OG	7:B:6:DA:OP2	2.31	0.44
5:G:61:ILE:HB	5:G:64:VAL:HB	1.99	0.44
2:I:454:ARG:HG3	2:I:458:GLU:HB3	1.98	0.44
2:I:936:ARG:NH2	2:I:1043:ALA:O	2.47	0.44
3:J:824:PRO:HD3	3:J:835:LEU:HD13	1.99	0.44
1:P:115:LYS:HG2	1:P:162:LEU:HD22	1.99	0.44
2:I:161:LYS:HB2	2:I:163:LYS:HE3	1.99	0.44
2:I:800:MET:HE1	2:I:822:VAL:HG13	1.99	0.44
3:J:731:ARG:HD2	3:J:731:ARG:HA	1.72	0.44
2:I:1217:THR:HA	5:H:41:ASN:ND2	2.32	0.44
3:J:400:MET:HE3	3:J:400:MET:HB2	1.79	0.44
3:J:678:ARG:HG3	3:J:679:TYR:N	2.33	0.44
2:I:107:ARG:HA	2:I:107:ARG:CZ	2.48	0.44
7:B:12:DA:H2''	7:B:13:DA:H8	1.83	0.44
2:I:840:SER:OG	2:I:848:GLU:O	2.34	0.44
7:B:4:DA:H2''	7:B:5:DG:C8	2.53	0.44
2:I:83:GLN:H	2:I:83:GLN:CD	2.24	0.44
2:I:318:SER:O	2:I:322:LEU:HG	2.18	0.44
3:J:44:ILE:HD12	3:J:252:LEU:HD12	1.99	0.44
3:J:301:GLU:OE2	3:J:312:ARG:NH1	2.51	0.44
2:I:342:ASP:OD1	2:I:343:HIS:ND1	2.51	0.44
5:H:30:PRO:HG3	5:H:192:VAL:HG21	2.00	0.44
2:I:693:LEU:HD12	2:I:694:ARG:HG2	2.00	0.43
2:I:1296:ASP:HB3	2:I:1321:GLU:H	1.83	0.43
5:G:64:VAL:HG11	5:G:78:ILE:HG21	2.00	0.43
2:I:738:GLU:HA	2:I:741:MET:SD	2.59	0.43
2:I:976:ARG:HB2	2:I:997:TRP:CZ3	2.48	0.43
3:J:743:MET:HE2	3:J:743:MET:HB3	1.87	0.43
3:J:822:MET:HE2	3:J:838:ARG:HB3	2.00	0.43
4:K:13:ILE:HG13	4:K:19:LEU:HB2	2.00	0.43
1:P:109:THR:N	1:P:110:PRO:HD3	2.33	0.43
3:J:736:GLN:O	3:J:740:LEU:HD23	2.18	0.43
3:J:751:ASP:OD1	3:J:751:ASP:C	2.61	0.43
3:J:1183:SER:OG	3:J:1184:ASP:N	2.52	0.43
2:I:859:GLU:OE1	2:I:860:ALA:N	2.52	0.43
2:I:65:ASN:HB3	2:I:107:ARG:HD3	2.01	0.43
2:I:300:ASP:N	2:I:300:ASP:OD1	2.51	0.43
4:K:72:GLN:HA	4:K:75:GLN:HG3	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:9:LYS:HG2	2:I:1171:ARG:HH11	1.84	0.43
2:I:89:GLY:HA2	2:I:140:GLY:HA3	2.00	0.43
2:I:1010:GLN:O	2:I:1013:GLN:HG2	2.18	0.43
3:J:124:ILE:HG12	3:J:237:MET:HE3	2.01	0.43
3:J:1189:MET:HE2	3:J:1189:MET:N	2.34	0.43
3:J:1368:ASP:O	3:J:1371:ARG:HG2	2.18	0.43
5:H:11:PRO:O	5:H:12:ARG:NH1	2.51	0.43
3:J:55:GLY:H	3:J:58:CYS:HB2	1.83	0.43
2:I:854:ILE:HB	2:I:857:VAL:HG21	2.01	0.43
1:P:80:ARG:NH1	1:P:83:ALA:O	2.52	0.43
2:I:175:ARG:HA	2:I:184:LEU:O	2.19	0.43
3:J:823:THR:HG22	3:J:879:ALA:HA	2.00	0.43
1:P:151:LYS:HD2	1:P:152:HIS:N	2.34	0.43
1:P:154:VAL:HG23	1:P:159:PHE:CE2	2.53	0.43
3:J:1177:ILE:HB	3:J:1186:TYR:HB3	2.01	0.43
3:J:1349:GLU:OE1	3:J:1349:GLU:N	2.38	0.43
1:P:20:HIS:HB3	1:P:72:THR:HG22	2.00	0.42
2:I:387:ASN:HA	2:I:391:SER:HB3	2.00	0.42
3:J:68:TYR:HE1	3:J:81:ARG:HD3	1.84	0.42
3:J:144:TYR:HA	3:J:180:MET:SD	2.58	0.42
3:J:538:ARG:HH12	3:J:634:ARG:HD2	1.83	0.42
3:J:640:GLY:N	3:J:643:ASP:OD2	2.41	0.42
3:J:709:ARG:HG2	3:J:710:ASP:H	1.84	0.42
3:J:791:ALA:HA	7:B:18:DA:C8	2.54	0.42
3:J:933:ARG:HA	3:J:933:ARG:HD2	1.76	0.42
2:I:75:LEU:HD23	2:I:75:LEU:HA	1.86	0.42
2:I:234:ASP:H	2:I:238:GLN:HE22	1.66	0.42
2:I:935:THR:HG23	2:I:1048:LYS:HG2	2.01	0.42
3:J:320:ASN:OD1	3:J:320:ASN:N	2.52	0.42
3:J:520:ALA:HB1	3:J:543:SER:HB3	2.01	0.42
8:R:12:U:H2'	8:R:13:A:C8	2.54	0.42
1:P:6:LEU:HD23	1:P:79:VAL:HG11	2.00	0.42
1:P:14:LEU:HG	1:P:55:LEU:HD11	2.01	0.42
2:I:14:ASP:HA	2:I:1183:ALA:HB3	2.01	0.42
2:I:99:LYS:HB3	2:I:99:LYS:HE3	1.64	0.42
2:I:257:ALA:HB3	2:I:262:TYR:HE2	1.84	0.42
5:H:115:ILE:HD12	5:H:115:ILE:H	1.84	0.42
6:A:4:DC:H2''	6:A:5:DA:C8	2.55	0.42
1:P:65:HIS:HD2	1:P:67:THR:HG22	1.85	0.42
2:I:1276:TRP:HH2	3:J:798:ARG:HG3	1.85	0.42
5:G:137:ASN:ND2	5:G:137:ASN:C	2.75	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:223:ILE:HG12	5:H:8:PHE:HE2	1.84	0.42
6:A:29:DT:H2'	6:A:30:DT:H71	2.01	0.42
1:P:73:ARG:HA	6:A:17:DG:C6	2.55	0.42
2:I:189:ASP:O	2:I:192:ASP:N	2.52	0.42
2:I:468:LEU:HD12	2:I:468:LEU:HA	1.85	0.42
2:I:463:GLN:HG3	2:I:505:PHE:HB2	2.02	0.42
2:I:701:GLY:O	2:I:1184:THR:N	2.37	0.42
6:A:12:DG:H2''	6:A:13:DG:C8	2.55	0.42
2:I:734:ILE:HD13	2:I:777:VAL:HG21	2.02	0.42
3:J:371:LYS:H	3:J:371:LYS:HG2	1.62	0.42
3:J:865:HIS:CE1	3:J:867:GLN:HB2	2.55	0.42
5:G:45:ARG:NE	5:H:38:THR:HG22	2.35	0.42
2:I:194:LEU:HD12	2:I:194:LEU:HA	1.81	0.42
2:I:379:GLU:O	2:I:382:GLU:HG3	2.19	0.42
2:I:1244:HIS:HE1	2:I:1265:PHE:HA	1.84	0.42
5:H:82:LEU:HD13	5:H:173:VAL:HG12	2.01	0.42
2:I:23:ASP:OD1	2:I:23:ASP:C	2.62	0.42
2:I:310:ILE:HD12	2:I:325:LEU:HD12	2.02	0.42
2:I:944:ARG:HA	2:I:944:ARG:HD2	1.83	0.42
3:J:475:GLU:OE1	4:K:28:ARG:NH2	2.53	0.42
3:J:706:VAL:HG22	3:J:715:LYS:HD2	2.02	0.42
3:J:963:VAL:HB	3:J:980:THR:HG23	2.01	0.42
3:J:1238:GLN:HB3	3:J:1242:ARG:HH12	1.85	0.42
3:J:1332:LEU:HD23	3:J:1332:LEU:HA	1.90	0.42
3:J:1369:ARG:O	3:J:1373:ARG:HG2	2.20	0.42
4:K:76:GLU:O	4:K:79:GLU:HG2	2.19	0.42
2:I:11:ILE:O	2:I:1149:TYR:OH	2.32	0.41
2:I:15:PHE:CG	2:I:1190:ALA:HB2	2.55	0.41
2:I:184:LEU:HD11	2:I:389:PHE:CZ	2.54	0.41
2:I:657:THR:HB	2:I:1187:PHE:HB2	2.02	0.41
3:J:144:TYR:N	3:J:160:LEU:O	2.53	0.41
3:J:982:LEU:HD21	3:J:995:TYR:HB2	2.02	0.41
6:A:11:DC:H2''	6:A:12:DG:C8	2.55	0.41
6:A:33:DG:H2''	6:A:34:DA:C8	2.55	0.41
1:P:65:HIS:CD2	1:P:67:THR:HG22	2.55	0.41
2:I:135:THR:HG22	2:I:515:MET:HE1	2.02	0.41
2:I:448:LEU:HD12	2:I:448:LEU:HA	1.89	0.41
2:I:588:GLU:HG3	2:I:605:TYR:HD2	1.86	0.41
3:J:113:HIS:CE1	3:J:115:TRP:HB2	2.55	0.41
3:J:663:GLU:O	3:J:666:GLU:HG3	2.19	0.41
4:K:60:ASN:HB3	4:K:63:ILE:HG22	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:221:LEU:HB3	2:I:336:LEU:HD21	2.02	0.41
5:H:4:SER:OG	5:H:5:VAL:N	2.52	0.41
2:I:405:PHE:CE2	2:I:424:ASP:HB3	2.56	0.41
2:I:475:VAL:CG2	2:I:493:ILE:HG22	2.51	0.41
2:I:508:SER:O	2:I:508:SER:OG	2.36	0.41
2:I:870:ILE:HG21	2:I:931:VAL:HG11	2.02	0.41
3:J:327:LEU:HD23	3:J:327:LEU:HA	1.90	0.41
3:J:660:GLU:O	3:J:663:GLU:HG3	2.19	0.41
5:G:58:GLU:HB2	5:G:145:LYS:HD3	2.01	0.41
7:B:11:DA:H2''	7:B:12:DA:H8	1.86	0.41
8:R:12:U:H2'	8:R:13:A:H8	1.85	0.41
3:J:1051:ASP:HB2	3:J:1055:GLY:N	2.33	0.41
7:B:31:DC:H2''	7:B:32:DG:N7	2.35	0.41
1:P:94:HIS:O	1:P:97:SER:OG	2.37	0.41
1:P:130:PHE:HA	1:P:141:LEU:HG	2.01	0.41
2:I:272:ARG:NH1	2:I:276:GLN:HB2	2.35	0.41
2:I:972:PHE:HB3	2:I:994:ARG:NH2	2.36	0.41
3:J:117:LEU:HD12	3:J:124:ILE:HD12	2.03	0.41
3:J:412:LEU:O	3:J:416:ILE:HG12	2.20	0.41
3:J:1027:VAL:HB	3:J:1122:ALA:H	1.85	0.41
3:J:1067:ARG:HG2	3:J:1072:LYS:HD3	2.03	0.41
1:P:105:VAL:HG13	1:P:107:PRO:HD2	2.02	0.41
2:I:479:LEU:HD12	2:I:479:LEU:HA	1.88	0.41
2:I:708:VAL:HG11	2:I:794:LEU:HD22	2.03	0.41
3:J:416:ILE:HD11	3:J:441:LEU:HG	2.02	0.41
3:J:1344:LEU:HD22	3:J:1344:LEU:H	1.86	0.41
7:B:18:DA:H2'	7:B:19:DC:H6	1.85	0.41
2:I:107:ARG:HA	2:I:107:ARG:NE	2.36	0.41
4:K:35:LYS:HA	4:K:35:LYS:HD3	1.77	0.41
1:P:39:VAL:O	1:P:40:ARG:HG2	2.21	0.41
1:P:156:ASN:HA	1:P:159:PHE:CE1	2.56	0.41
2:I:45:GLY:HA3	2:I:54:ARG:NE	2.35	0.41
2:I:105:TYR:HE1	2:I:114:VAL:HG12	1.86	0.41
2:I:993:PRO:N	2:I:996:ARG:HH12	2.19	0.41
2:I:1034:ARG:HA	2:I:1037:THR:OG1	2.21	0.41
2:I:1178:LYS:HE2	2:I:1178:LYS:HB2	1.93	0.41
3:J:112:ALA:HB3	3:J:139:LEU:HD21	2.03	0.41
3:J:388:ARG:NH2	3:J:414:GLU:OE1	2.52	0.41
3:J:425:ARG:HD2	3:J:459:ALA:HB2	2.02	0.41
3:J:1082:ASP:OD1	3:J:1082:ASP:N	2.46	0.41
5:H:166:ARG:HD3	5:H:166:ARG:HA	1.77	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:9:DC:H2''	6:A:10:DG:C8	2.56	0.41
3:J:161:THR:HG23	3:J:164:GLN:H	1.86	0.41
2:I:575:LEU:HD23	2:I:575:LEU:HA	1.82	0.40
3:J:1191:PRO:HB3	3:J:1193:TRP:CH2	2.56	0.40
5:H:59:VAL:HG23	5:H:144:ILE:HD13	2.01	0.40
1:P:115:LYS:HE2	1:P:115:LYS:HB2	1.88	0.40
2:I:975:ILE:HG22	2:I:1014:LEU:HD13	2.03	0.40
2:I:1033:ARG:O	2:I:1037:THR:OG1	2.34	0.40
3:J:923:ILE:O	3:J:926:PRO:HD2	2.21	0.40
5:G:116:THR:O	5:G:116:THR:OG1	2.33	0.40
2:I:632:ASP:HA	2:I:647:ARG:HE	1.87	0.40
2:I:798:GLN:NE2	2:I:827:ARG:O	2.53	0.40
2:I:848:GLU:OE1	2:I:888:THR:OG1	2.34	0.40
3:J:516:ASP:OD1	3:J:516:ASP:N	2.54	0.40
4:K:8:ASP:OD2	4:K:8:ASP:C	2.65	0.40
7:B:2:DG:H2''	7:B:3:DA:C8	2.56	0.40
2:I:1024:GLU:HA	2:I:1027:LYS:NZ	2.36	0.40
3:J:647:PRO:HG3	3:J:697:MET:HB2	2.04	0.40
3:J:809:VAL:HG23	3:J:912:GLY:H	1.85	0.40
3:J:903:LEU:HD12	3:J:903:LEU:HA	1.87	0.40
5:H:188:GLU:HB2	5:H:200:LYS:HZ2	1.87	0.40
7:B:31:DC:H2''	7:B:32:DG:C8	2.57	0.40
3:J:34:SER:HB2	3:J:104:HIS:HB3	2.04	0.40
3:J:878:ASP:OD1	3:J:878:ASP:N	2.54	0.40
3:J:955:LYS:HG2	3:J:1012:ALA:HA	2.03	0.40
3:J:1238:GLN:HB3	3:J:1242:ARG:NH1	2.36	0.40
5:H:118:ASP:OD1	5:H:118:ASP:N	2.53	0.40
7:B:5:DG:H1'	7:B:6:DA:H5'	2.03	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	P	160/164 (98%)	149 (93%)	10 (6%)	1 (1%)	21	52
2	I	1318/1342 (98%)	1300 (99%)	18 (1%)	0	100	100
3	J	1321/1416 (93%)	1283 (97%)	38 (3%)	0	100	100
4	K	81/91 (89%)	80 (99%)	1 (1%)	0	100	100
5	G	231/329 (70%)	224 (97%)	7 (3%)	0	100	100
5	H	228/329 (69%)	218 (96%)	10 (4%)	0	100	100
All	All	3339/3671 (91%)	3254 (98%)	84 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	P	105	VAL

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	P	142/143 (99%)	142 (100%)	0	100	100
2	I	1141/1157 (99%)	1139 (100%)	2 (0%)	87	89
3	J	1125/1177 (96%)	1125 (100%)	0	100	100
4	K	70/75 (93%)	70 (100%)	0	100	100
5	G	201/286 (70%)	198 (98%)	3 (2%)	57	75
5	H	198/286 (69%)	198 (100%)	0	100	100
All	All	2877/3124 (92%)	2872 (100%)	5 (0%)	87	89

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	I	529[A]	ARG
2	I	529[B]	ARG
5	G	137	ASN
5	G	219[A]	ARG

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Mol	Chain	Res	Type
5	G	219[B]	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	P	18	GLN
1	P	24	GLN
2	I	339	ASN
2	I	357	ASN
2	I	554	HIS
2	I	752	ASN
2	I	767	GLN
2	I	1108	ASN
2	I	1111	GLN
2	I	1237	HIS
3	J	158	GLN
3	J	164	GLN
3	J	200	GLN
3	J	206	ASN
3	J	266	ASN
3	J	365	GLN
3	J	465	GLN
3	J	469	HIS
3	J	488	ASN
3	J	708	ASN
3	J	910	ASN
3	J	1279	GLN
4	K	7	GLN
5	H	41	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
8	R	11/17 (64%)	2 (18%)	0

All (2) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	R	7	G
8	R	9	C

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

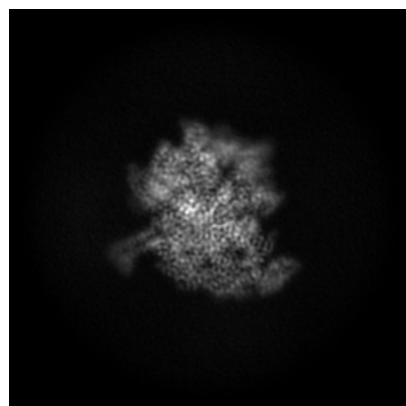
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-17668. These allow visual inspection of the internal detail of the map and identification of artifacts.

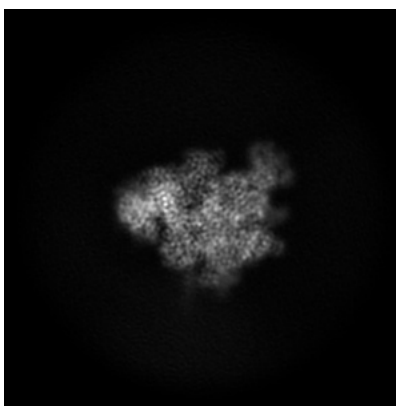
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

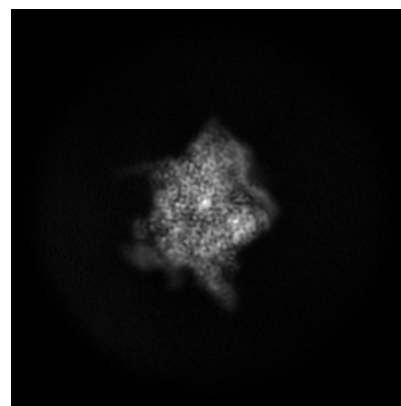
6.1.1 Primary map



X

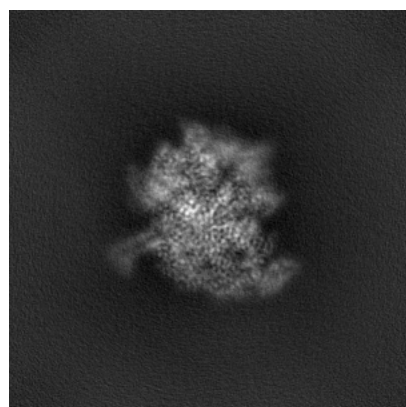


Y

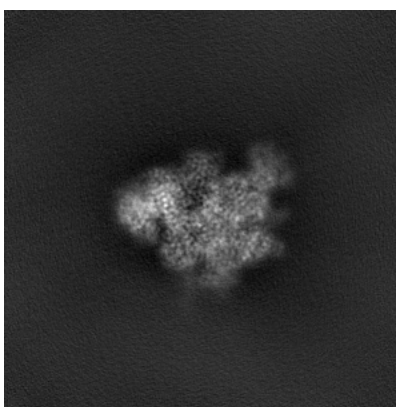


Z

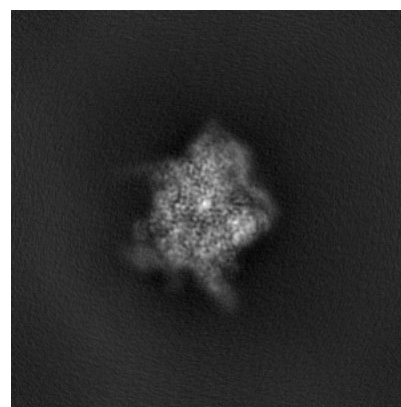
6.1.2 Raw map



X



Y

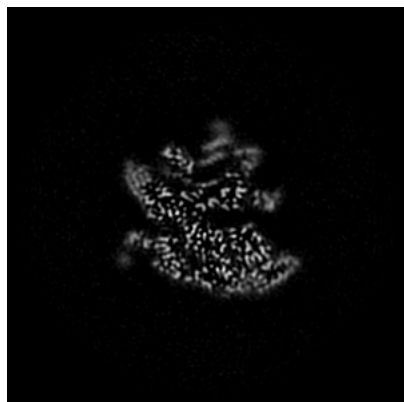


Z

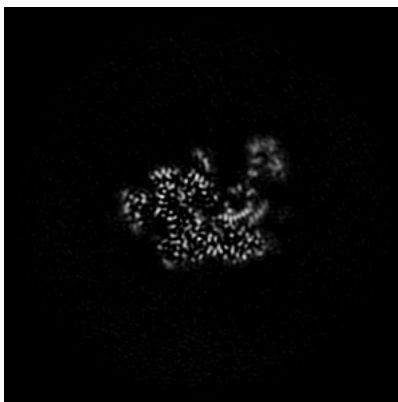
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

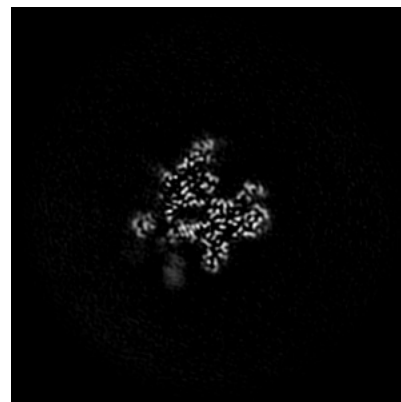
6.2.1 Primary map



X Index: 192

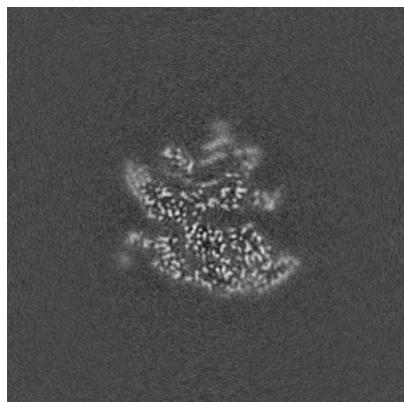


Y Index: 192

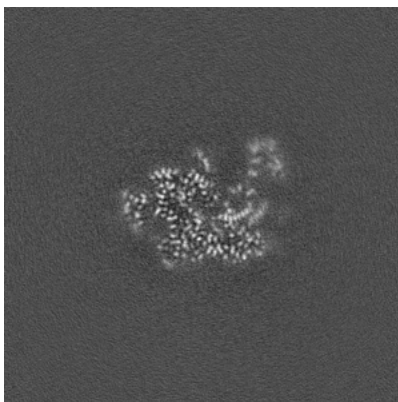


Z Index: 192

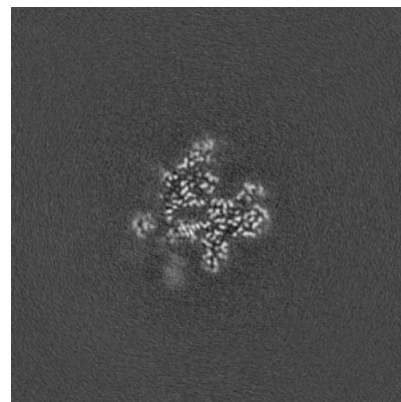
6.2.2 Raw map



X Index: 192



Y Index: 192

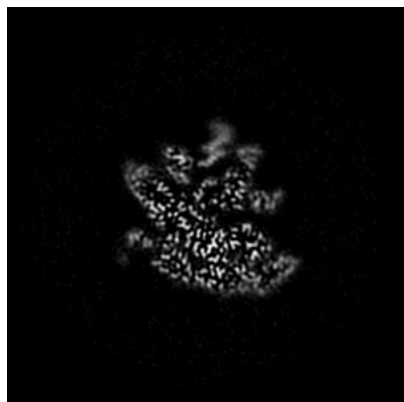


Z Index: 192

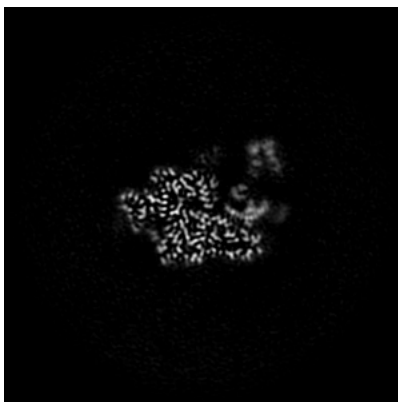
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

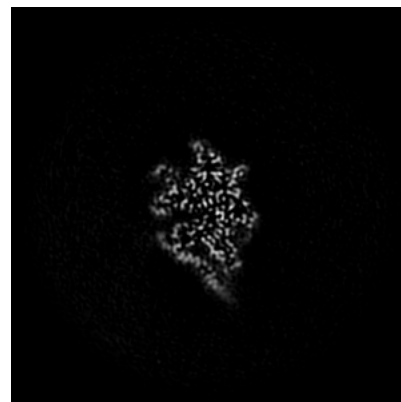
6.3.1 Primary map



X Index: 190

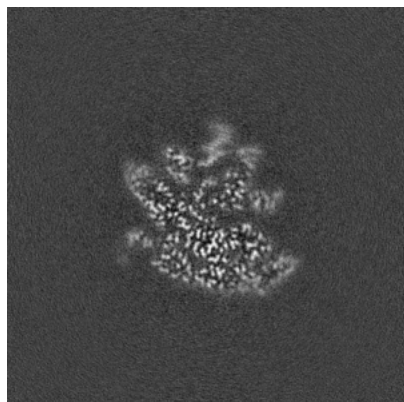


Y Index: 195

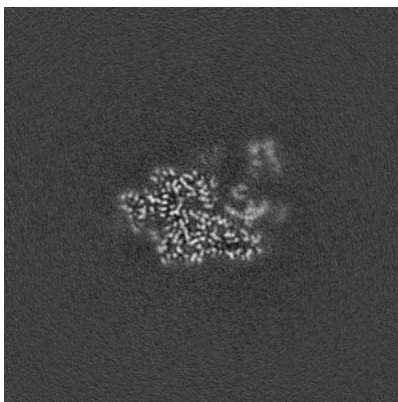


Z Index: 161

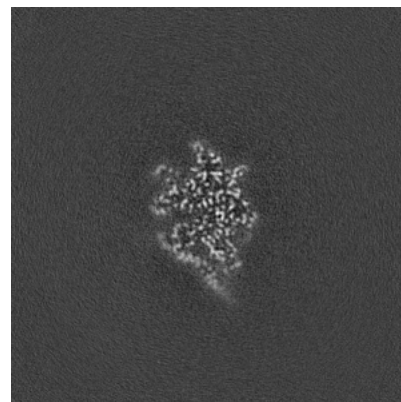
6.3.2 Raw map



X Index: 190



Y Index: 195

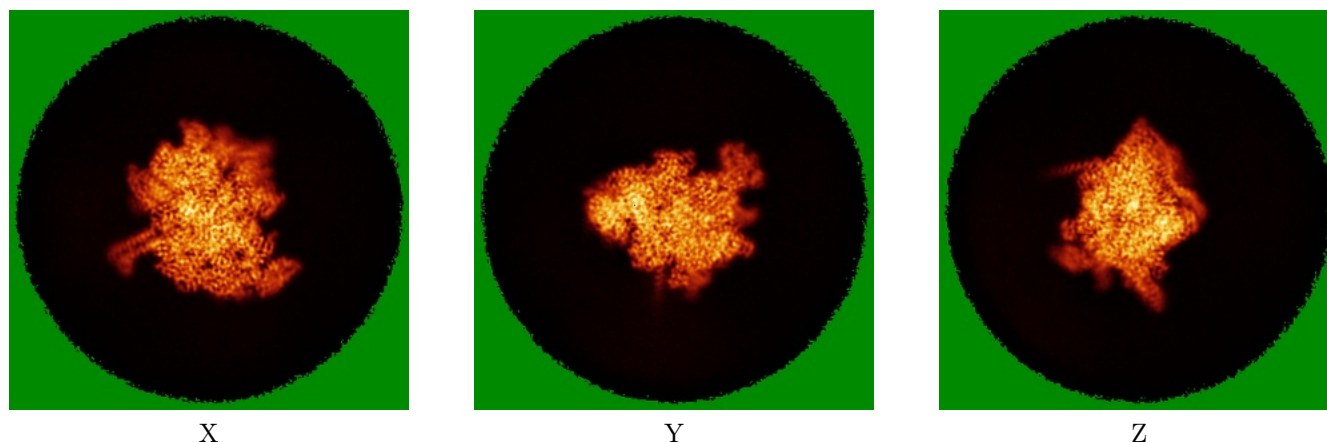


Z Index: 161

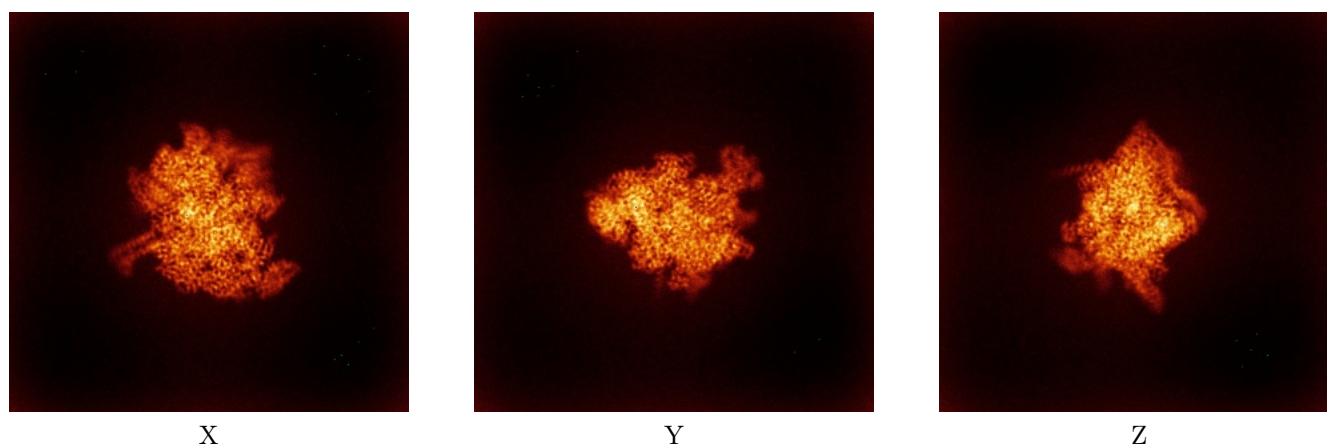
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

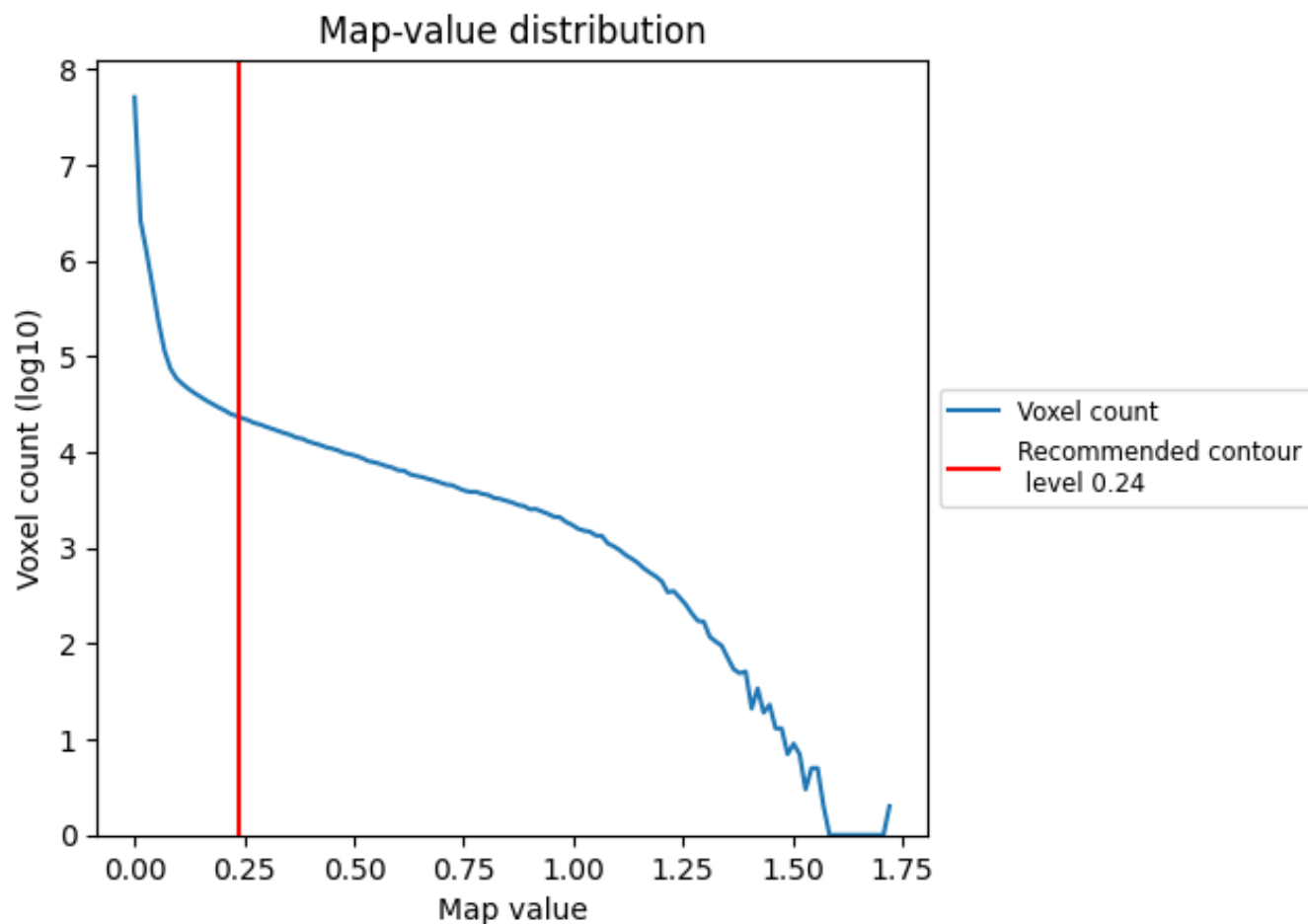
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

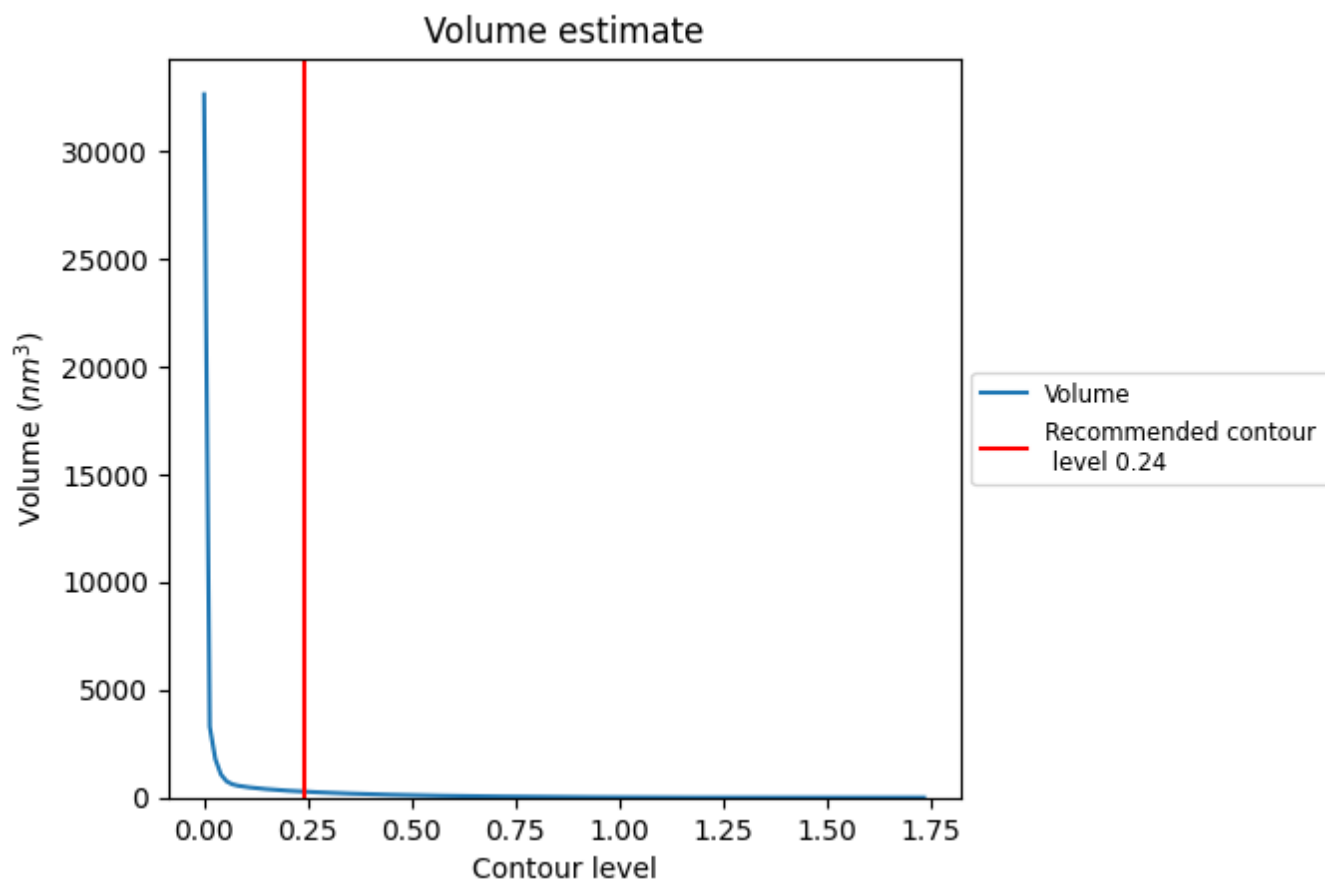
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

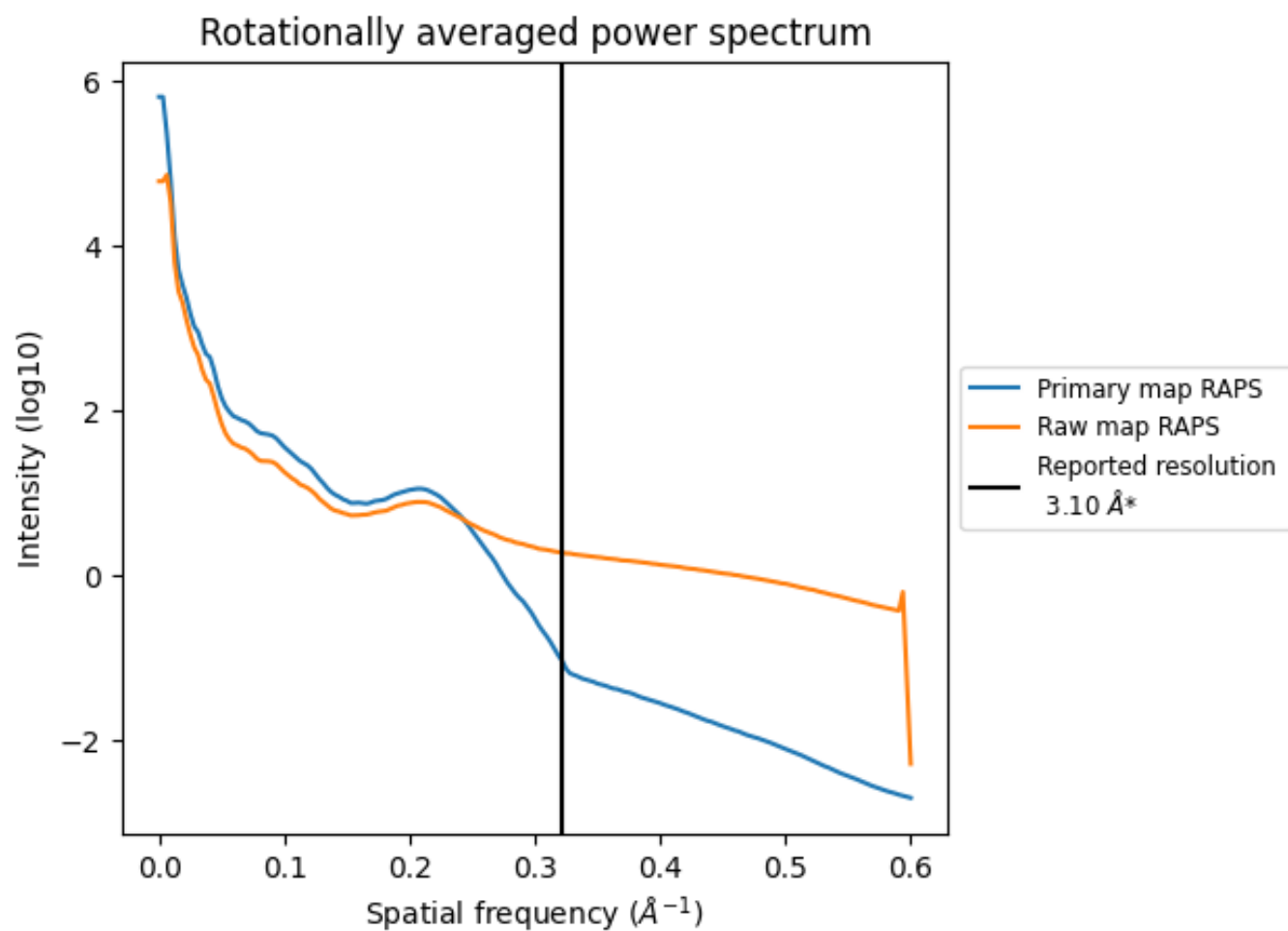
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 276 nm^3 ; this corresponds to an approximate mass of 250 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 ⓘ

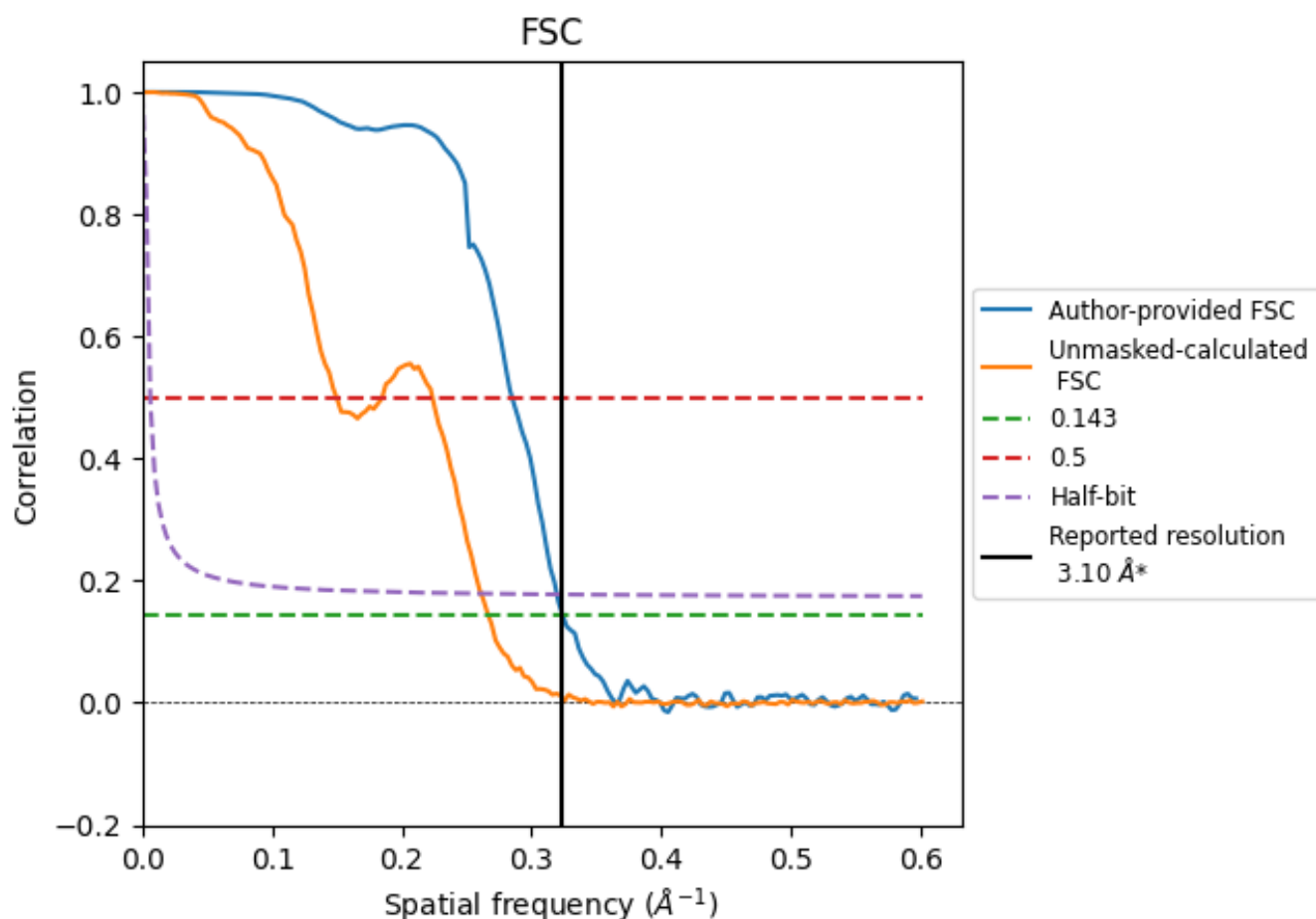


*Reported resolution corresponds to spatial frequency of $0.323 \text{ \AA}^{-1}$

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 0.323 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.09	3.51	3.13
Unmasked-calculated*	3.75	6.68	3.83

*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 3.75 differs from the reported value 3.1 by more than 10 %

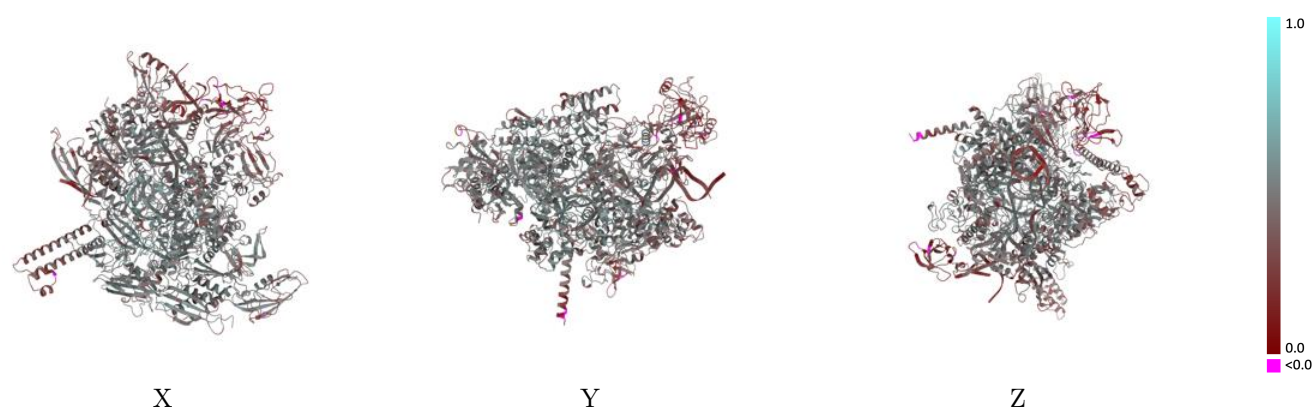
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-17668 and PDB model 8PHK. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)

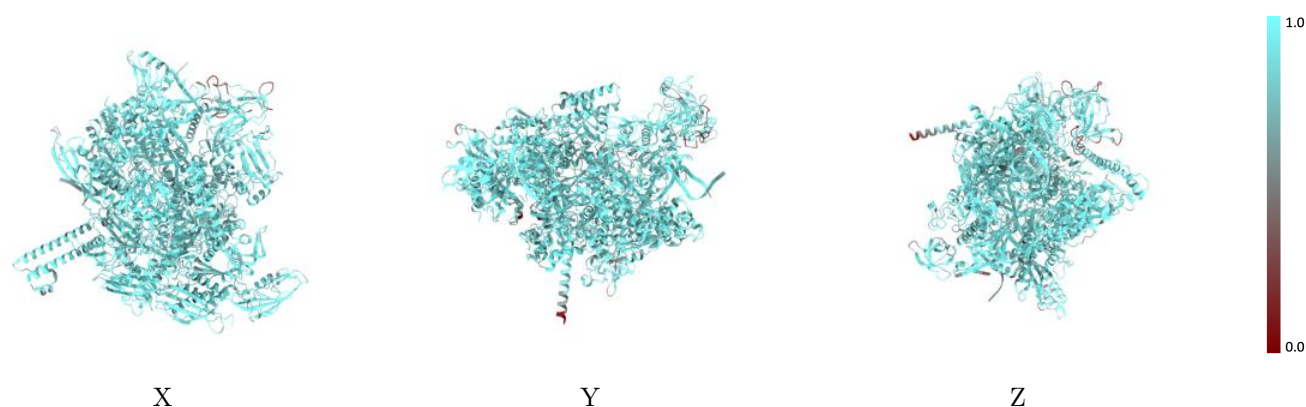
This section was not generated.

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



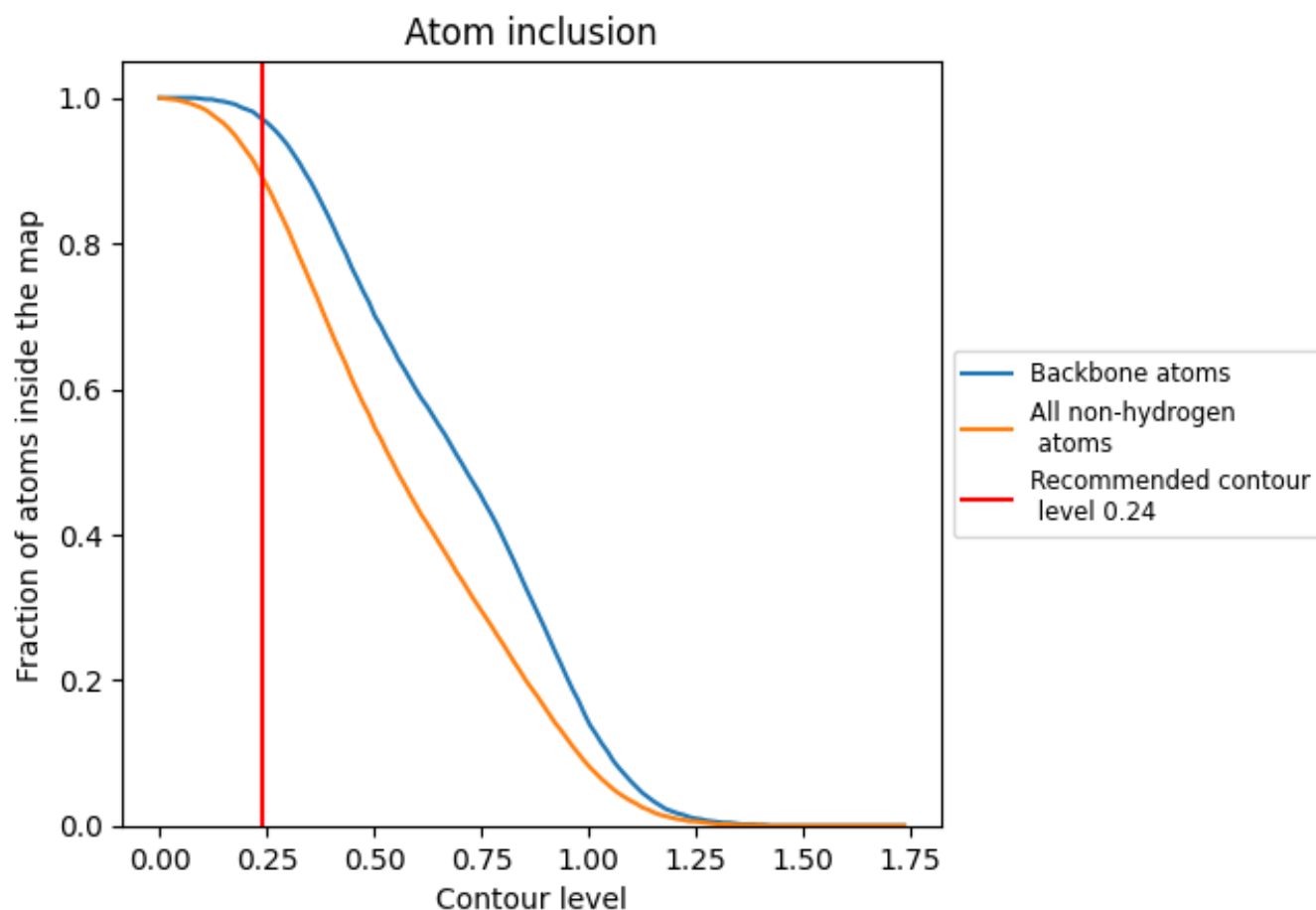
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.24).

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 89% 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 (0.24) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8900	0.4360
A	0.8950	0.3570
B	0.9230	0.3780
G	0.9020	0.4700
H	0.8890	0.4260
I	0.9000	0.4550
J	0.8800	0.4350
K	0.8000	0.4110
P	0.8910	0.3450
R	0.9460	0.4740

1.0

0.0

<0.0