



Full wwPDB EM Validation Report ⓘ

Aug 6, 2026 – 09:27 AM JST

PDB ID : 23FJ / pdb_000023fj
EMDB ID : EMD-68925
Title : Cryo-EM structure of SWI/SNF complex from *Chaetomium thermophilum*
Authors : Ma, S.S.; Liu, M.D.; Shen, Q.T.; Chen, Y.
Deposited on : 2026-02-05
Resolution : 2.96 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.dev133
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) : 2.50

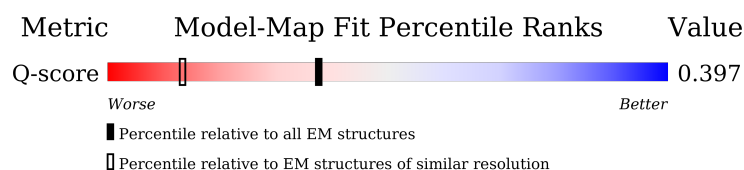
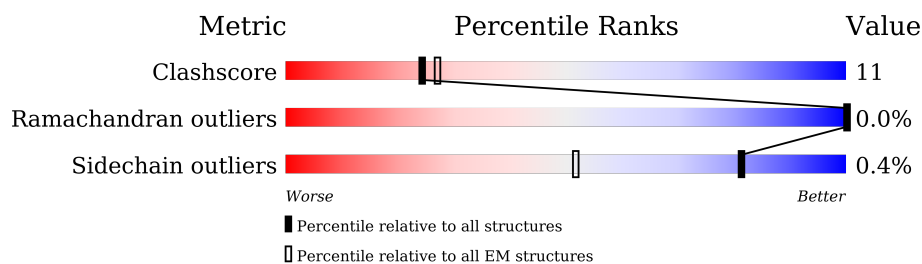
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.96 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.



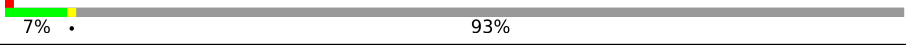
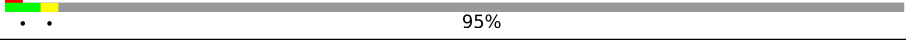
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13155 (2.46 - 3.46)

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	K	1595	
2	N	694	
2	O	694	
3	P	547	

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Mol	Chain	Length	Quality of chain
4	Q	769	
5	R	1301	
6	S	785	
7	T	722	
8	U	627	

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 18703 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 WD40 repeat-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	K	139	Total	C	N	O	S	0	0
			1157	724	226	202	5		

There are 64 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	-58	GLY	-	expression tag	UNP G0SHD8
K	-57	SER	-	expression tag	UNP G0SHD8
K	-56	PRO	-	expression tag	UNP G0SHD8
K	-55	GLN	-	expression tag	UNP G0SHD8
K	-54	GLN	-	expression tag	UNP G0SHD8
K	-53	ASN	-	expression tag	UNP G0SHD8
K	-52	LYS	-	expression tag	UNP G0SHD8
K	-51	THR	-	expression tag	UNP G0SHD8
K	-50	ALA	-	expression tag	UNP G0SHD8
K	-49	ALA	-	expression tag	UNP G0SHD8
K	-48	LEU	-	expression tag	UNP G0SHD8
K	-47	ALA	-	expression tag	UNP G0SHD8
K	-46	GLN	-	expression tag	UNP G0SHD8
K	-45	HIS	-	expression tag	UNP G0SHD8
K	-44	ASP	-	expression tag	UNP G0SHD8
K	-43	GLU	-	expression tag	UNP G0SHD8
K	-42	ALA	-	expression tag	UNP G0SHD8
K	-41	ASP	-	expression tag	UNP G0SHD8
K	-40	TYR	-	expression tag	UNP G0SHD8
K	-39	LYS	-	expression tag	UNP G0SHD8
K	-38	ASP	-	expression tag	UNP G0SHD8
K	-37	HIS	-	expression tag	UNP G0SHD8
K	-36	ASP	-	expression tag	UNP G0SHD8
K	-35	GLY	-	expression tag	UNP G0SHD8
K	-34	ASP	-	expression tag	UNP G0SHD8
K	-33	TYR	-	expression tag	UNP G0SHD8
K	-32	LYS	-	expression tag	UNP G0SHD8
K	-31	ASP	-	expression tag	UNP G0SHD8

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Chain	Residue	Modelled	Actual	Comment	Reference
K	-30	HIS	-	expression tag	UNP G0SHD8
K	-29	ASP	-	expression tag	UNP G0SHD8
K	-28	ILE	-	expression tag	UNP G0SHD8
K	-27	ASP	-	expression tag	UNP G0SHD8
K	-26	TYR	-	expression tag	UNP G0SHD8
K	-25	LYS	-	expression tag	UNP G0SHD8
K	-24	ASP	-	expression tag	UNP G0SHD8
K	-23	ASP	-	expression tag	UNP G0SHD8
K	-22	ASP	-	expression tag	UNP G0SHD8
K	-21	ASP	-	expression tag	UNP G0SHD8
K	-20	LYS	-	expression tag	UNP G0SHD8
K	-19	GLY	-	expression tag	UNP G0SHD8
K	-18	GLY	-	expression tag	UNP G0SHD8
K	-17	SER	-	expression tag	UNP G0SHD8
K	-16	GLY	-	expression tag	UNP G0SHD8
K	-15	GLY	-	expression tag	UNP G0SHD8
K	-14	SER	-	expression tag	UNP G0SHD8
K	-13	LEU	-	expression tag	UNP G0SHD8
K	-12	GLU	-	expression tag	UNP G0SHD8
K	-11	VAL	-	expression tag	UNP G0SHD8
K	-10	LEU	-	expression tag	UNP G0SHD8
K	-9	PHE	-	expression tag	UNP G0SHD8
K	-8	GLN	-	expression tag	UNP G0SHD8
K	-7	GLY	-	expression tag	UNP G0SHD8
K	-6	PRO	-	expression tag	UNP G0SHD8
K	-5	GLY	-	expression tag	UNP G0SHD8
K	-4	GLY	-	expression tag	UNP G0SHD8
K	-3	SER	-	expression tag	UNP G0SHD8
K	-2	GLY	-	expression tag	UNP G0SHD8
K	-1	GLY	-	expression tag	UNP G0SHD8
K	0	SER	-	expression tag	UNP G0SHD8
K	1	GLY	-	expression tag	UNP G0SHD8
K	2	THR	-	expression tag	UNP G0SHD8
K	114	VAL	ILE	conflict	UNP G0SHD8
K	282	ILE	VAL	conflict	UNP G0SHD8
K	1513	THR	ALA	conflict	UNP G0SHD8

- Molecule 2 is a protein called Ssr1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	N	369	Total	C	N	O	S	0	0
			2891	1814	522	541	14		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	O	325	Total	C	N	O	S	0	0
			2611	1643	464	492	12		

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
N	687	ASP	-	expression tag	UNP G0S647
N	688	TYR	-	expression tag	UNP G0S647
N	689	LYS	-	expression tag	UNP G0S647
N	690	ASP	-	expression tag	UNP G0S647
N	691	ASP	-	expression tag	UNP G0S647
N	692	ASP	-	expression tag	UNP G0S647
N	693	ASP	-	expression tag	UNP G0S647
N	694	LYS	-	expression tag	UNP G0S647
O	687	ASP	-	expression tag	UNP G0S647
O	688	TYR	-	expression tag	UNP G0S647
O	689	LYS	-	expression tag	UNP G0S647
O	690	ASP	-	expression tag	UNP G0S647
O	691	ASP	-	expression tag	UNP G0S647
O	692	ASP	-	expression tag	UNP G0S647
O	693	ASP	-	expression tag	UNP G0S647
O	694	LYS	-	expression tag	UNP G0S647

- Molecule 3 is a protein called DM2 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	P	412	Total	C	N	O	S	0	0
			3307	2068	605	626	8		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	191	ASP	ASN	conflict	UNP G0RYN3
P	540	ASP	-	expression tag	UNP G0RYN3
P	541	TYR	-	expression tag	UNP G0RYN3
P	542	LYS	-	expression tag	UNP G0RYN3
P	543	ASP	-	expression tag	UNP G0RYN3
P	544	ASP	-	expression tag	UNP G0RYN3
P	545	ASP	-	expression tag	UNP G0RYN3
P	546	ASP	-	expression tag	UNP G0RYN3
P	547	LYS	-	expression tag	UNP G0RYN3

- Molecule 4 is a protein called DUF1750-domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	Q	178	Total	C	N	O	S	0	0
			1419	890	248	276	5		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	763	ASP	-	expression tag	UNP G0SEZ9
Q	764	TYR	-	expression tag	UNP G0SEZ9
Q	765	LYS	-	expression tag	UNP G0SEZ9
Q	766	ASP	-	expression tag	UNP G0SEZ9
Q	767	ASP	-	expression tag	UNP G0SEZ9
Q	768	ASP	-	expression tag	UNP G0SEZ9
Q	769	ASP	-	expression tag	UNP G0SEZ9
Q	770	LYS	-	expression tag	UNP G0SEZ9

- Molecule 5 is a protein called ARID domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	R	477	Total	C	N	O	S	0	0
			3718	2366	630	700	22		

There are 67 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	-68	GLY	-	expression tag	UNP G0S385
R	-67	SER	-	expression tag	UNP G0S385
R	-66	PRO	-	expression tag	UNP G0S385
R	-65	GLN	-	expression tag	UNP G0S385
R	-64	GLN	-	expression tag	UNP G0S385
R	-63	ASN	-	expression tag	UNP G0S385
R	-62	LYS	-	expression tag	UNP G0S385
R	-61	THR	-	expression tag	UNP G0S385
R	-60	ALA	-	expression tag	UNP G0S385
R	-59	ALA	-	expression tag	UNP G0S385
R	-58	LEU	-	expression tag	UNP G0S385
R	-57	ALA	-	expression tag	UNP G0S385
R	-56	GLN	-	expression tag	UNP G0S385
R	-55	HIS	-	expression tag	UNP G0S385
R	-54	ASP	-	expression tag	UNP G0S385
R	-53	GLU	-	expression tag	UNP G0S385
R	-52	ALA	-	expression tag	UNP G0S385

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Chain	Residue	Modelled	Actual	Comment	Reference
R	-51	ASP	-	expression tag	UNP G0S385
R	-50	TYR	-	expression tag	UNP G0S385
R	-49	LYS	-	expression tag	UNP G0S385
R	-48	ASP	-	expression tag	UNP G0S385
R	-47	HIS	-	expression tag	UNP G0S385
R	-46	ASP	-	expression tag	UNP G0S385
R	-45	GLY	-	expression tag	UNP G0S385
R	-44	ASP	-	expression tag	UNP G0S385
R	-43	TYR	-	expression tag	UNP G0S385
R	-42	LYS	-	expression tag	UNP G0S385
R	-41	ASP	-	expression tag	UNP G0S385
R	-40	HIS	-	expression tag	UNP G0S385
R	-39	ASP	-	expression tag	UNP G0S385
R	-38	ILE	-	expression tag	UNP G0S385
R	-37	ASP	-	expression tag	UNP G0S385
R	-36	TYR	-	expression tag	UNP G0S385
R	-35	LYS	-	expression tag	UNP G0S385
R	-34	ASP	-	expression tag	UNP G0S385
R	-33	ASP	-	expression tag	UNP G0S385
R	-32	ASP	-	expression tag	UNP G0S385
R	-31	ASP	-	expression tag	UNP G0S385
R	-30	LYS	-	expression tag	UNP G0S385
R	-29	GLY	-	expression tag	UNP G0S385
R	-28	GLY	-	expression tag	UNP G0S385
R	-27	SER	-	expression tag	UNP G0S385
R	-26	GLY	-	expression tag	UNP G0S385
R	-25	GLY	-	expression tag	UNP G0S385
R	-24	SER	-	expression tag	UNP G0S385
R	-23	LEU	-	expression tag	UNP G0S385
R	-22	GLU	-	expression tag	UNP G0S385
R	-21	VAL	-	expression tag	UNP G0S385
R	-20	LEU	-	expression tag	UNP G0S385
R	-19	PHE	-	expression tag	UNP G0S385
R	-18	GLN	-	expression tag	UNP G0S385
R	-17	GLY	-	expression tag	UNP G0S385
R	-16	PRO	-	expression tag	UNP G0S385
R	-15	GLY	-	expression tag	UNP G0S385
R	-14	GLY	-	expression tag	UNP G0S385
R	-13	SER	-	expression tag	UNP G0S385
R	-12	GLY	-	expression tag	UNP G0S385
R	-11	GLY	-	expression tag	UNP G0S385
R	-10	SER	-	expression tag	UNP G0S385

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Chain	Residue	Modelled	Actual	Comment	Reference
R	-9	GLY	-	expression tag	UNP G0S385
R	-8	THR	-	expression tag	UNP G0S385
R	397	ALA	VAL	conflict	UNP G0S385
R	512	GLY	VAL	conflict	UNP G0S385
R	632	PRO	SER	conflict	UNP G0S385
R	724	ILE	VAL	conflict	UNP G0S385
R	878	SER	GLY	conflict	UNP G0S385
R	1036	SER	ALA	conflict	UNP G0S385

- Molecule 6 is a protein called Snf5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	S	354	Total	C	N	O	S	0	0
			2885	1825	504	545	11		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S	778	ASP	-	expression tag	UNP G0S4S8
S	779	TYR	-	expression tag	UNP G0S4S8
S	780	LYS	-	expression tag	UNP G0S4S8
S	781	ASP	-	expression tag	UNP G0S4S8
S	782	ASP	-	expression tag	UNP G0S4S8
S	783	ASP	-	expression tag	UNP G0S4S8
S	784	ASP	-	expression tag	UNP G0S4S8
S	785	LYS	-	expression tag	UNP G0S4S8

- Molecule 7 is a protein called Nuclear localization protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	T	54	Total	C	N	O	S	0	0
			447	272	89	84	2		

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
T	-7	SER	GLY	conflict	UNP G0SEX4
T	682	SER	PRO	conflict	UNP G0SEX4
T	697	ASP	-	expression tag	UNP G0SEX4
T	698	TYR	-	expression tag	UNP G0SEX4
T	699	LYS	-	expression tag	UNP G0SEX4
T	700	ASP	-	expression tag	UNP G0SEX4

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Chain	Residue	Modelled	Actual	Comment	Reference
T	701	ASP	-	expression tag	UNP G0SEX4
T	702	ASP	-	expression tag	UNP G0SEX4
T	703	ASP	-	expression tag	UNP G0SEX4
T	704	LYS	-	expression tag	UNP G0SEX4

- Molecule 8 is a protein called LYR family protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	U	33	Total	C	N	O	S	0	0
			268	170	54	43	1		

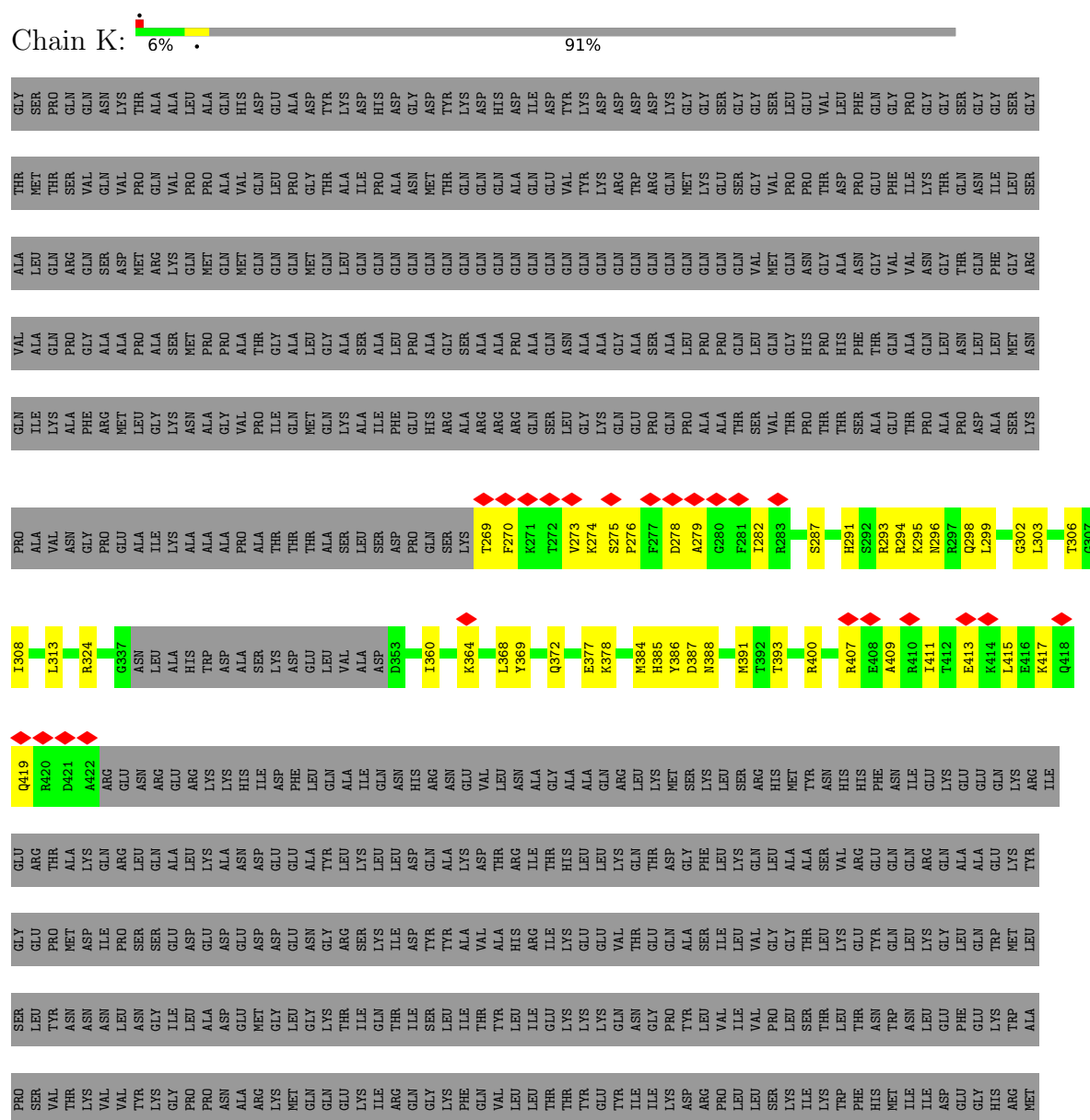
There are 24 discrepancies between the modelled and reference sequences:

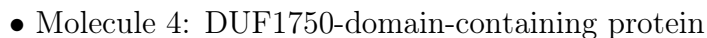
Chain	Residue	Modelled	Actual	Comment	Reference
U	260	ILE	VAL	conflict	UNP G0S145
U	459	PRO	LEU	conflict	UNP G0S145
U	486	VAL	ALA	conflict	UNP G0S145
U	544	ASP	GLY	conflict	UNP G0S145
U	607	GLU	GLY	conflict	UNP G0S145
U	609	ALA	-	expression tag	UNP G0S145
U	610	THR	-	expression tag	UNP G0S145
U	611	GLN	-	expression tag	UNP G0S145
U	612	GLU	-	expression tag	UNP G0S145
U	613	VAL	-	expression tag	UNP G0S145
U	614	LYS	-	expression tag	UNP G0S145
U	615	THR	-	expression tag	UNP G0S145
U	616	GLU	-	expression tag	UNP G0S145
U	617	GLY	-	expression tag	UNP G0S145
U	618	GLU	-	expression tag	UNP G0S145
U	619	LYS	-	expression tag	UNP G0S145
U	620	PRO	-	expression tag	UNP G0S145
U	621	GLU	-	expression tag	UNP G0S145
U	622	HIS	-	expression tag	UNP G0S145
U	623	HIS	-	expression tag	UNP G0S145
U	624	HIS	-	expression tag	UNP G0S145
U	625	HIS	-	expression tag	UNP G0S145
U	626	HIS	-	expression tag	UNP G0S145
U	627	HIS	-	expression tag	UNP G0S145

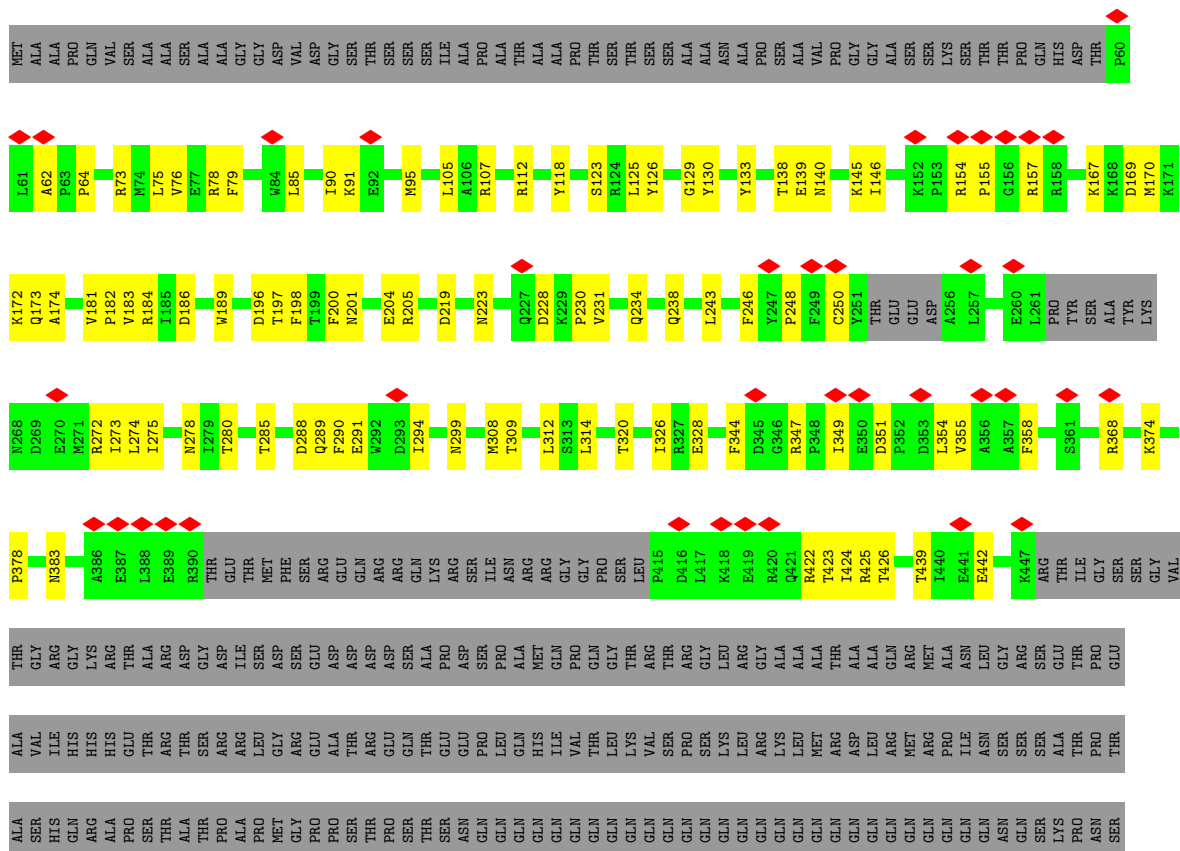
3 Residue-property plots

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: WD40 repeat-containing protein

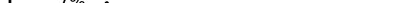






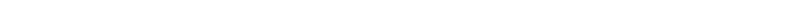
GLY	HIS	ARG	GLU	LYS	VAL	ALA	ALA	ARG	LEU	ALA	LYS	GLN	GLN	GLY	PRO	ASP	GLN	ALA	ASP	TYR	LYS	ASP	ASP	LYS
ASP	THR	GLU	THR	ASN	THR	ALA	GLN	LEU	PRO	LEU	LYS	GLY	PRO	ASP	PRO	ILE	ASN	GLN	PHE	TYR	ARG	LEU	PRO	TYR
SER	SER	ASN	LEU	GLN	ASN	GLN	ILE	ARG	VAL	PRO	ALA	PRO	PRO	SER	GLY	ASN	GLN	ASN	PRO	PRO	PRO	GLU	TRP	ILE

- Molecule 7: Nuclear localization protein

Chain T:  7% 93%

[illegible]

- Molecule 8: LYR family protein

Chain U:  95%

MET
 ALA
 PRO
 PRO
 GLN
 PHE
 ARG
 THR
 ALA
 THR
 GLN
 THR
 ARG
 ARG
 GLY
 ALA
 ARG
 SER
 GLY
 PHE
 VAL
 GLU
 GLN
 ASP
 PHE
 PHE
 GLU
 GLY
 LEU
 PRO
 VAL
 VAL
 GLN
 TRP
 ARG
 GLN
 ARG
 GLN
 GLU
 TRP
 VAL
 THR
 THR
 THR
 PRO
 PRO
 VAL
 VAL
 GLN
 VAL
 THR
 THR
 GLN
 GLN
 SER
 ASP
 R55
 W56
 A57
 L60
 M64

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

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	158634	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.885	Depositor
Minimum map value	-0.008	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.019	Depositor
Recommended contour level	0.201	Depositor
Map size (Å)	476.99997, 476.99997, 476.99997	wwPDB
Map dimensions	450, 450, 450	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	K	0.28	0/1173	0.48	0/1560
2	N	0.33	1/2946 (0.0%)	0.50	3/3990 (0.1%)
2	O	0.25	0/2662	0.46	2/3602 (0.1%)
3	P	0.27	0/3367	0.46	0/4541
4	Q	0.23	0/1442	0.39	0/1934
5	R	0.29	0/3801	0.47	1/5179 (0.0%)
6	S	0.25	0/2954	0.42	0/3997
7	T	0.33	0/458	0.52	0/621
8	U	0.13	0/276	0.33	0/373
All	All	0.28	1/19079 (0.0%)	0.46	6/25797 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	N	482	ALA	CA-CB	-5.44	1.45	1.53

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	O	205	TYR	N-CA-C	-7.95	103.53	113.55
5	R	1069	ARG	N-CA-C	-6.89	101.96	110.65
2	N	482	ALA	N-CA-C	-5.72	106.19	112.72
2	N	668	ALA	CB-CA-C	-5.72	109.96	116.54
2	N	144	ASN	N-CA-C	-5.28	106.42	112.86
2	O	437	LEU	CB-CA-C	-5.27	110.06	117.23

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	K	1157	0	1200	44	0
2	N	2891	0	2851	71	0
2	O	2611	0	2565	65	0
3	P	3307	0	3283	96	0
4	Q	1419	0	1398	47	0
5	R	3718	0	3727	82	0
6	S	2885	0	2798	73	0
7	T	447	0	418	3	0
8	U	268	0	271	9	0
All	All	18703	0	18511	397	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 11.

All (397) 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:P:335:GLU:HB3	3:P:338:ASN:HB3	1.55	0.87
2:O:445:MET:HE2	2:O:448:SER:HB3	1.62	0.82
5:R:1044:ASP:HB2	5:R:1045:PRO:HD3	1.62	0.80
5:R:964:PRO:HD3	5:R:1019:LYS:HD3	1.68	0.75
1:K:299:LEU:HD13	4:Q:319:LEU:HD13	1.70	0.74
3:P:303:LEU:HD23	3:P:348:ILE:HG21	1.69	0.73
2:O:607:ARG:HG3	5:R:1230:VAL:HG13	1.69	0.72
2:O:604:GLU:HG3	4:Q:412:LYS:HE2	1.70	0.72
5:R:986:PRO:HB2	5:R:1000:PRO:HB2	1.71	0.72
3:P:342:ASP:H	3:P:345:LEU:HB2	1.53	0.72
5:R:807:LEU:HD21	6:S:146:ILE:HD11	1.72	0.71
8:U:68:SER:HA	8:U:71:LEU:HD23	1.72	0.71
5:R:1023:ARG:HG2	5:R:1026:PRO:HD2	1.73	0.70
2:N:174:THR:HG22	6:S:157:ARG:HH12	1.57	0.70
2:N:583:LYS:NZ	3:P:433:ASP:OD1	2.23	0.70
3:P:223:PHE:HA	3:P:292:GLU:HB2	1.72	0.69
6:S:288:ASP:HB3	6:S:378:PRO:HA	1.74	0.69
5:R:1157:MET:HE1	5:R:1209:GLU:HG2	1.73	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:Q:455:ILE:HD13	4:Q:458:ARG:HH21	1.57	0.68
2:O:118:ILE:O	2:O:206:GLN:NE2	2.27	0.67
6:S:157:ARG:NH1	6:S:219:ASP:OD1	2.28	0.67
1:K:384:MET:HE3	5:R:885:LEU:HD22	1.76	0.66
3:P:332:GLU:HB2	3:P:335:GLU:HB2	1.76	0.65
2:N:186:VAL:HG11	6:S:198:PHE:HB2	1.76	0.65
4:Q:347:ILE:HG12	4:Q:372:LEU:HB2	1.78	0.65
2:O:419:VAL:HG11	3:P:524:ARG:HD2	1.77	0.64
5:R:1157:MET:HE3	5:R:1157:MET:HA	1.78	0.64
6:S:62:ALA:O	6:S:64:PRO:HD3	1.97	0.64
5:R:756:ALA:HA	5:R:759:LYS:HE2	1.81	0.63
5:R:1126:LEU:HD22	5:R:1159:LEU:HD11	1.79	0.63
4:Q:347:ILE:HD13	4:Q:376:PHE:HB2	1.79	0.63
1:K:378:LYS:HG2	3:P:493:GLY:HA2	1.82	0.62
2:N:661:MET:HE2	4:Q:469:VAL:HG22	1.80	0.62
4:Q:347:ILE:HA	4:Q:372:LEU:HD12	1.82	0.62
5:R:767:SER:HB2	6:S:112:ARG:HG3	1.82	0.62
2:O:161:PHE:CD1	2:O:183:LEU:HD11	2.35	0.62
5:R:964:PRO:O	5:R:1023:ARG:NH2	2.31	0.61
2:N:223:PHE:HB3	2:N:226:ILE:HG22	1.81	0.61
2:N:150:THR:H	2:N:153:VAL:HB	1.65	0.61
3:P:219:ARG:HB3	3:P:222:HIS:HB2	1.83	0.61
1:K:279:ALA:HB1	1:K:303:LEU:HD21	1.80	0.61
2:N:186:VAL:CG1	6:S:198:PHE:HB2	2.30	0.60
2:O:419:VAL:CG1	3:P:524:ARG:HD2	2.31	0.60
1:K:393:THR:OG1	3:P:488:ASP:OD1	2.20	0.60
1:K:324:ARG:NH1	2:O:434:SER:OG	2.34	0.60
2:O:147:ASN:HD22	2:O:150:LYS:HG2	1.66	0.60
5:R:842:ALA:HB2	5:R:902:ILE:HG21	1.84	0.60
2:N:633:ALA:HB1	2:N:648:VAL:HG22	1.83	0.59
4:Q:372:LEU:HD23	4:Q:372:LEU:H	1.66	0.59
5:R:1025:GLU:CG	5:R:1026:PRO:HD3	2.33	0.59
2:N:214:HIS:O	2:N:216:GLY:N	2.33	0.58
8:U:64:MET:HE1	8:U:80:ARG:HA	1.85	0.58
1:K:413:GLU:O	1:K:417:LYS:N	2.34	0.58
2:N:580:MET:HE2	2:N:583:LYS:HD3	1.85	0.58
2:N:140:GLU:OE1	2:N:191:ARG:NH2	2.37	0.58
1:K:386:TYR:OH	2:O:235:GLN:OE1	2.21	0.58
2:N:632:GLN:N	2:N:632:GLN:OE1	2.37	0.58
4:Q:375:GLU:OE2	4:Q:379:ARG:NH2	2.37	0.58
4:Q:307:TYR:HD2	5:R:754:LEU:HD11	1.69	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:P:497:GLY:HA3	6:S:107:ARG:HD3	1.85	0.58
2:N:626:VAL:HG21	2:O:619:PHE:HZ	1.69	0.57
3:P:293:ASP:HB2	3:P:296:ARG:HD3	1.86	0.57
3:P:407:ARG:NH1	3:P:410:SER:OG	2.37	0.57
3:P:132:VAL:N	3:P:394:TYR:O	2.36	0.57
1:K:302:GLY:O	6:S:78:ARG:NH2	2.38	0.57
2:O:159:ARG:HG2	2:O:197:LEU:HD11	1.86	0.57
3:P:297:PHE:HB3	3:P:367:LEU:HD21	1.85	0.57
6:S:248:PRO:HB2	8:U:82:ALA:HB1	1.87	0.57
2:N:186:VAL:HG22	6:S:200:PHE:HA	1.87	0.56
2:O:148:ARG:HH22	6:S:347:ARG:HH22	1.52	0.56
4:Q:472:ASP:OD1	4:Q:472:ASP:N	2.38	0.56
5:R:850:VAL:O	5:R:938:ARG:NH1	2.38	0.56
2:O:125:TRP:HE1	2:O:134:ILE:HD11	1.71	0.56
2:O:142:PHE:HA	2:O:150:LYS:HB3	1.88	0.56
2:O:208:ASP:N	2:O:208:ASP:OD1	2.39	0.56
1:K:294:ARG:NH1	4:Q:312:GLU:OE1	2.39	0.56
6:S:184:ARG:NH1	6:S:328:GLU:OE1	2.38	0.56
1:K:308:ILE:HG12	2:O:465:VAL:HG22	1.88	0.55
1:K:400:ARG:O	5:R:907:ARG:NH2	2.31	0.55
5:R:950:ASP:O	5:R:954:ASP:HB2	2.05	0.55
6:S:320:THR:HG1	6:S:425:ARG:HH12	1.54	0.55
6:S:273:ILE:HD13	6:S:294:ILE:HD11	1.88	0.55
4:Q:282:PHE:HB3	5:R:1072:MET:HE2	1.89	0.55
6:S:172:LYS:HD2	6:S:205:ARG:HH22	1.72	0.55
5:R:779:ASN:HB2	6:S:138:THR:HA	1.87	0.55
2:O:458:SER:HB2	6:S:90:ILE:HG12	1.89	0.55
6:S:197:THR:O	6:S:425:ARG:NH2	2.38	0.55
3:P:336:LYS:HE2	3:P:337:ARG:HE	1.72	0.54
3:P:413:TYR:HA	3:P:419:ASN:ND2	2.23	0.54
5:R:1227:GLU:HA	5:R:1230:VAL:HB	1.87	0.54
2:O:172:GLU:HG3	7:T:378:ARG:HG2	1.89	0.54
4:Q:343:LEU:HD21	4:Q:380:VAL:HG23	1.89	0.54
5:R:853:SER:O	5:R:938:ARG:NH1	2.40	0.54
4:Q:339:GLU:OE2	4:Q:339:GLU:N	2.29	0.54
2:N:466:VAL:HG22	2:N:550:PRO:HD3	1.90	0.54
3:P:77:LEU:HD22	3:P:81:VAL:HG21	1.88	0.54
2:O:441:ILE:HG13	2:O:443:LEU:H	1.72	0.53
5:R:760:ILE:HD12	6:S:105:LEU:HD21	1.91	0.53
3:P:520:SER:OG	3:P:524:ARG:NH2	2.41	0.53
2:N:665:PRO:HG3	4:Q:468:THR:HG21	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:127:ASP:OD1	2:O:127:ASP:N	2.40	0.53
6:S:290:PHE:CZ	6:S:308:MET:HE1	2.44	0.53
3:P:425:THR:HA	3:P:428:GLU:HG2	1.90	0.52
2:O:614:LEU:HD22	3:P:327:LEU:HD13	1.91	0.52
5:R:884:MET:HE3	5:R:885:LEU:H	1.73	0.52
2:N:117:ILE:HD13	6:S:133:TYR:CZ	2.44	0.52
2:N:423:LEU:HD21	2:N:482:ALA:HB3	1.91	0.52
2:O:186:ASP:OD2	6:S:299:ASN:ND2	2.41	0.52
1:K:369:TYR:HA	1:K:372:GLN:HB3	1.90	0.52
2:N:616:ARG:HD2	2:O:612:LEU:HD13	1.92	0.52
4:Q:339:GLU:H	4:Q:339:GLU:CD	2.16	0.52
6:S:274:LEU:HD11	6:S:289:GLN:HB2	1.91	0.52
1:K:282:ILE:HD11	4:Q:321:PRO:HB2	1.91	0.52
2:O:121:SER:O	2:O:122:TYR:HB3	2.09	0.51
2:O:441:ILE:HD13	3:P:504:THR:OG1	2.10	0.51
3:P:456:MET:HE3	3:P:463:PHE:CD2	2.45	0.51
3:P:296:ARG:HB2	3:P:370:LEU:HD13	1.91	0.51
4:Q:411:ILE:HG13	4:Q:459:VAL:HG22	1.92	0.51
6:S:184:ARG:HH21	6:S:423:THR:HB	1.75	0.51
6:S:312:LEU:O	7:T:387:ARG:HD2	2.10	0.51
8:U:82:ALA:HA	8:U:86:ARG:HE	1.74	0.51
1:K:377:GLU:HG2	3:P:494:LEU:HD23	1.92	0.51
2:O:207:VAL:HG23	2:O:212:ARG:HH11	1.76	0.51
2:N:609:ARG:NH2	4:Q:411:ILE:O	2.43	0.51
3:P:397:ARG:HG2	4:Q:472:ASP:HB3	1.92	0.51
2:N:143:ASN:OD1	6:S:174:ALA:HB1	2.10	0.51
2:O:197:LEU:HD23	2:O:200:TRP:CD1	2.46	0.51
3:P:279:ASP:OD1	3:P:279:ASP:N	2.41	0.51
6:S:234:GLN:O	6:S:238:GLN:HG3	2.11	0.51
1:K:384:MET:HE2	1:K:384:MET:HA	1.93	0.51
3:P:355:PHE:HD1	3:P:357:PRO:HD2	1.75	0.51
5:R:1043:THR:O	5:R:1044:ASP:C	2.54	0.51
5:R:1163:ILE:O	5:R:1167:ILE:HG12	2.11	0.51
2:N:551:LEU:HD22	3:P:461:VAL:HG22	1.94	0.50
4:Q:308:GLN:HG2	5:R:754:LEU:HD12	1.91	0.50
2:N:191:ARG:HD2	6:S:170:MET:HE1	1.91	0.50
4:Q:308:GLN:O	4:Q:312:GLU:HG2	2.12	0.50
5:R:1025:GLU:HG2	5:R:1026:PRO:HD3	1.94	0.50
1:K:306:THR:HG21	6:S:85:LEU:HD13	1.94	0.50
3:P:229:VAL:HG23	3:P:286:ILE:HG22	1.94	0.50
3:P:287:ASN:HD21	3:P:372:PRO:HG2	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:269:THR:OG1	1:K:270:PHE:N	2.38	0.49
2:N:486:ALA:HB1	2:N:490:LYS:HE3	1.94	0.49
2:O:463:MET:HE2	4:Q:318:LEU:HD11	1.93	0.49
1:K:308:ILE:O	2:O:464:SER:OG	2.28	0.49
1:K:287:SER:HA	4:Q:328:GLU:HG2	1.94	0.49
3:P:227:LEU:HD23	3:P:227:LEU:H	1.76	0.49
3:P:235:ARG:NH2	3:P:280:GLU:OE1	2.46	0.49
8:U:73:PRO:HA	8:U:76:GLN:HB2	1.95	0.49
6:S:140:ASN:HD21	6:S:145:LYS:HB2	1.76	0.49
6:S:272:ARG:NE	6:S:291:GLU:OE2	2.44	0.49
1:K:388:ASN:O	5:R:798:ARG:HD2	2.12	0.49
2:N:380:ARG:HD3	6:S:73:ARG:HH12	1.77	0.49
5:R:1171:ARG:O	5:R:1175:GLU:HG2	2.13	0.49
6:S:201:ASN:HB3	6:S:204:GLU:HB2	1.94	0.49
3:P:63:HIS:HA	3:P:66:LYS:HE2	1.94	0.49
4:Q:418:LEU:HB2	4:Q:455:ILE:HG21	1.95	0.49
2:O:127:ASP:O	2:O:159:ARG:NH2	2.46	0.49
3:P:130:MET:N	3:P:396:ILE:O	2.44	0.49
3:P:167:ILE:HB	3:P:272:ILE:HB	1.95	0.49
5:R:777:LEU:HD13	5:R:803:THR:HG23	1.95	0.49
3:P:48:ALA:HA	5:R:820:PRO:HG2	1.95	0.48
2:N:420:LEU:HD12	2:N:458:SER:HB2	1.94	0.48
2:N:119:PRO:HG3	2:N:204:TYR:CE1	2.48	0.48
2:O:414:THR:HG23	2:O:417:GLU:H	1.79	0.48
2:O:594:MET:HE1	4:Q:401:MET:SD	2.54	0.48
3:P:274:PHE:HD1	3:P:276:ARG:HG2	1.78	0.48
3:P:524:ARG:HA	3:P:527:VAL:HG12	1.96	0.48
3:P:419:ASN:ND2	3:P:421:SER:OG	2.40	0.48
2:N:389:ILE:HG23	2:N:493:LEU:HD23	1.95	0.48
4:Q:331:ASP:OD2	4:Q:332:LEU:N	2.47	0.48
2:N:654:ALA:HB3	2:N:655:PRO:HD3	1.95	0.47
5:R:798:ARG:O	5:R:802:ASP:N	2.39	0.47
2:O:594:MET:HA	2:O:597:MET:HG2	1.95	0.47
2:O:184:ALA:HB2	6:S:368:ARG:HD2	1.97	0.47
1:K:308:ILE:HD12	1:K:313:LEU:HD22	1.95	0.47
5:R:758:TRP:NE1	5:R:762:GLU:OE1	2.48	0.47
2:N:590:TYR:HE2	3:P:425:THR:HG21	1.80	0.47
3:P:402:ASP:OD1	3:P:402:ASP:N	2.47	0.47
5:R:1061:ILE:HA	5:R:1083:LEU:HD21	1.97	0.47
6:S:285:THR:HG22	6:S:383:ASN:HB2	1.97	0.47
8:U:64:MET:HG3	8:U:65:PRO:HD2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:406:ILE:O	2:O:410:VAL:HG23	2.15	0.47
3:P:322:TRP:HA	3:P:325:ILE:HG12	1.97	0.47
2:N:185:ASP:O	2:N:189:ILE:HG13	2.15	0.47
3:P:489:GLY:HA3	5:R:768:LYS:HD3	1.97	0.47
5:R:1191:ASN:OD1	5:R:1192:VAL:N	2.48	0.47
6:S:91:LYS:O	6:S:95:MET:HG3	2.15	0.47
1:K:294:ARG:NH1	4:Q:315:GLU:OE1	2.49	0.46
2:N:399:TYR:CD2	2:N:405:GLN:HB3	2.51	0.46
3:P:419:ASN:ND2	3:P:422:TYR:H	2.13	0.46
2:O:204:ASN:HA	2:O:207:VAL:HG13	1.98	0.46
3:P:348:ILE:HA	3:P:366:HIS:CD2	2.51	0.46
6:S:354:LEU:O	6:S:358:PHE:N	2.37	0.46
3:P:299:LEU:HD21	3:P:312:ALA:HB3	1.97	0.46
3:P:337:ARG:O	3:P:355:PHE:HA	2.16	0.46
4:Q:407:ARG:HG3	4:Q:407:ARG:HH11	1.79	0.46
5:R:962:ILE:O	5:R:966:ILE:HG13	2.15	0.46
5:R:1109:LEU:HB3	5:R:1192:VAL:HG21	1.97	0.46
1:K:293:ARG:HG3	1:K:295:LYS:HB3	1.97	0.46
2:N:180:ARG:NH1	6:S:426:THR:O	2.49	0.46
2:N:483:ASN:HD22	2:N:483:ASN:HA	1.43	0.46
5:R:996:ARG:HD3	5:R:1112:GLY:HA2	1.98	0.46
5:R:1014:VAL:HG22	5:R:1056:LEU:HG	1.97	0.46
5:R:1070:HIS:HB2	5:R:1071:PRO:HD3	1.98	0.46
1:K:278:ASP:HB3	1:K:282:ILE:H	1.81	0.46
5:R:866:GLU:OE2	5:R:1007:HIS:NE2	2.48	0.46
6:S:186:ASP:O	6:S:238:GLN:NE2	2.32	0.46
3:P:336:LYS:HD3	3:P:336:LYS:H	1.80	0.46
6:S:278:ASN:ND2	6:S:422:ARG:HD3	2.31	0.46
1:K:291:HIS:NE2	4:Q:320:SER:OG	2.41	0.46
2:O:166:TYR:CE2	2:O:203:ILE:HA	2.51	0.46
2:N:403:TRP:HE1	2:N:478:THR:HG21	1.81	0.45
3:P:407:ARG:HH22	3:P:411:SER:HB2	1.80	0.45
3:P:380:ARG:NH2	3:P:392:THR:OG1	2.38	0.45
5:R:777:LEU:HD12	5:R:807:LEU:HD13	1.98	0.45
2:N:223:PHE:CG	2:N:226:ILE:CG2	2.99	0.45
2:N:398:ARG:HD3	2:N:399:TYR:CE1	2.51	0.45
4:Q:407:ARG:HH12	4:Q:408:SER:HB2	1.81	0.45
5:R:968:ILE:O	5:R:968:ILE:HG13	2.14	0.45
5:R:1043:THR:HG22	5:R:1045:PRO:HD2	1.98	0.45
3:P:274:PHE:CD1	3:P:276:ARG:HG2	2.52	0.45
5:R:752:HIS:CD2	5:R:752:HIS:N	2.83	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:R:848:LEU:HD23	5:R:895:ALA:HB2	1.98	0.45
6:S:189:TRP:HE1	6:S:230:PRO:HG2	1.82	0.45
5:R:1221:ALA:O	5:R:1225:MET:HG2	2.16	0.45
6:S:181:VAL:HG23	6:S:183:VAL:HG23	1.98	0.45
2:N:141:PHE:CG	2:N:154:TYR:HB2	2.52	0.45
3:P:334:GLU:HG3	3:P:335:GLU:OE2	2.16	0.45
1:K:274:LYS:HE3	6:S:76:VAL:HG12	1.99	0.45
2:N:465:VAL:HG21	2:O:465:VAL:HB	1.97	0.45
2:O:135:GLU:HG2	2:O:196:PHE:HZ	1.81	0.45
6:S:275:ILE:HD12	6:S:326:ILE:HG12	1.99	0.45
1:K:360:ILE:O	1:K:364:LYS:HG2	2.16	0.45
2:N:179:ARG:NH2	6:S:196:ASP:OD1	2.43	0.45
2:N:617:LEU:O	2:N:621:ARG:HG2	2.16	0.45
3:P:481:GLU:HA	5:R:768:LYS:NZ	2.32	0.45
8:U:80:ARG:O	8:U:80:ARG:NE	2.50	0.45
2:N:126:ASP:OD2	2:N:129:THR:OG1	2.35	0.45
2:N:469:LEU:HD21	2:O:462:VAL:HG11	1.99	0.45
3:P:228:THR:OG1	3:P:287:ASN:HB3	2.16	0.45
2:O:603:ARG:HD3	2:O:603:ARG:HA	1.71	0.44
4:Q:398:HIS:O	4:Q:402:MET:HB2	2.16	0.44
6:S:280:THR:HB	6:S:424:ILE:HG12	1.99	0.44
2:N:187:CYS:SG	6:S:204:GLU:HG2	2.58	0.44
2:N:616:ARG:HH12	2:O:615:ASP:CB	2.31	0.44
2:O:431:TYR:CD1	2:O:431:TYR:N	2.84	0.44
5:R:1119:LEU:O	5:R:1123:THR:HG23	2.17	0.44
2:O:438:ASP:N	2:O:438:ASP:OD1	2.51	0.44
3:P:289:TYR:CZ	3:P:372:PRO:HG3	2.52	0.44
3:P:481:GLU:HA	5:R:768:LYS:HZ1	1.83	0.44
1:K:368:LEU:HD22	2:O:393:LEU:HD13	1.98	0.44
2:O:180:ARG:HG3	2:O:187:VAL:HG12	2.00	0.44
3:P:288:LEU:HD23	3:P:375:LEU:HD12	2.00	0.44
5:R:1226:ALA:O	5:R:1230:VAL:HG23	2.16	0.44
2:O:573:VAL:HG21	4:Q:334:LEU:HG	1.99	0.44
4:Q:301:GLU:HG3	5:R:758:TRP:CH2	2.53	0.44
5:R:788:SER:HB3	5:R:796:GLU:HB3	1.99	0.44
6:S:75:LEU:HD23	6:S:75:LEU:HA	1.88	0.44
6:S:118:TYR:HB2	6:S:125:LEU:HD21	1.99	0.44
6:S:181:VAL:HG21	6:S:243:LEU:HD23	1.98	0.44
6:S:351:ASP:HB2	6:S:355:VAL:HG13	2.00	0.44
3:P:300:SER:O	3:P:304:ALA:N	2.35	0.44
2:N:131:HIS:ND1	2:N:133:ILE:HG22	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:614:LEU:HD13	2:N:661:MET:HG3	2.00	0.44
2:N:119:PRO:HG2	2:N:200:GLY:HA3	2.00	0.43
3:P:336:LYS:HG2	3:P:337:ARG:HG3	1.99	0.43
5:R:869:VAL:HG12	5:R:873:LYS:HE3	2.00	0.43
1:K:296:ASN:O	1:K:298:GLN:HG3	2.18	0.43
1:K:385:HIS:O	5:R:798:ARG:NH1	2.51	0.43
3:P:295:GLU:HB3	3:P:313:THR:HG23	2.00	0.43
3:P:503:VAL:C	3:P:505:ALA:H	2.27	0.43
4:Q:307:TYR:CD2	5:R:754:LEU:HD11	2.52	0.43
4:Q:418:LEU:HD12	4:Q:451:SER:HA	2.00	0.43
6:S:184:ARG:HA	6:S:197:THR:HG22	2.00	0.43
2:N:578:ASN:ND2	4:Q:351:GLN:O	2.34	0.43
2:O:121:SER:C	2:O:123:SER:H	2.26	0.43
4:Q:460:GLU:O	4:Q:464:GLY:N	2.52	0.43
5:R:1003:GLU:H	5:R:1007:HIS:CE1	2.36	0.43
2:N:126:ASP:OD1	2:N:126:ASP:N	2.52	0.43
2:N:625:GLU:O	2:N:628:GLU:HB2	2.19	0.43
3:P:219:ARG:NE	3:P:221:SER:HB3	2.33	0.43
5:R:894:ARG:NH2	5:R:897:ASP:OD1	2.48	0.43
3:P:313:THR:N	3:P:316:GLU:OE2	2.49	0.43
3:P:514:LYS:HE3	5:R:884:MET:HE1	2.00	0.43
2:N:661:MET:HA	4:Q:469:VAL:HA	1.99	0.43
2:O:135:GLU:OE1	2:O:155:TYR:OH	2.30	0.43
2:O:494:ARG:NH1	2:O:562:ALA:O	2.51	0.43
2:N:423:LEU:CD2	2:N:482:ALA:CB	2.96	0.43
3:P:300:SER:HA	3:P:368:ARG:NH2	2.33	0.43
5:R:867:ASP:OD1	5:R:870:ARG:NH2	2.52	0.43
1:K:409:ALA:HA	5:R:1085:GLN:NE2	2.34	0.43
2:N:157:TYR:O	2:N:161:MET:HG3	2.19	0.43
5:R:944:THR:OG1	5:R:947:ASP:OD2	2.37	0.43
5:R:1105:THR:HG23	5:R:1173:LEU:HD22	1.99	0.43
5:R:1113:ASP:OD1	5:R:1113:ASP:N	2.52	0.43
2:N:393:LEU:HD21	2:N:493:LEU:HB2	2.01	0.43
2:N:569:MET:O	2:N:573:VAL:HG23	2.19	0.43
2:O:437:LEU:HB3	2:O:438:ASP:H	1.62	0.43
3:P:163:TYR:H	3:P:277:PRO:HA	1.83	0.43
5:R:1069:ARG:O	5:R:1072:MET:N	2.44	0.43
1:K:387:ASP:O	5:R:894:ARG:NH1	2.48	0.42
2:N:642:PHE:O	2:N:646:GLN:HG3	2.18	0.42
3:P:365:PRO:HG2	3:P:366:HIS:CE1	2.54	0.42
6:S:250:CYS:H	6:S:344:PHE:HZ	1.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:561:LEU:HD12	4:Q:317:ILE:HG12	2.00	0.42
4:Q:401:MET:HE2	4:Q:401:MET:HB3	1.73	0.42
4:Q:466:HIS:CD2	4:Q:468:THR:HG23	2.55	0.42
5:R:756:ALA:O	5:R:760:ILE:HG12	2.19	0.42
5:R:809:HIS:CD2	5:R:810:LYS:HG3	2.54	0.42
5:R:1069:ARG:O	5:R:1070:HIS:C	2.62	0.42
5:R:1210:TRP:HB3	5:R:1216:LEU:HD11	2.01	0.42
3:P:449:LYS:HZ3	3:P:453:LEU:HD11	1.84	0.42
6:S:374:LYS:HB3	6:S:374:LYS:HE3	1.80	0.42
2:O:202:LEU:HD23	2:O:202:LEU:H	1.85	0.42
3:P:297:PHE:HA	3:P:370:LEU:HB2	2.01	0.42
3:P:335:GLU:OE2	3:P:335:GLU:N	2.42	0.42
6:S:223:ASN:O	6:S:228:ASP:HB2	2.20	0.42
6:S:439:THR:OG1	6:S:442:GLU:OE1	2.37	0.42
2:N:453:LEU:HD13	2:N:457:GLN:HE21	1.85	0.42
2:O:431:TYR:N	2:O:431:TYR:HD1	2.17	0.42
3:P:134:ILE:HG13	3:P:392:THR:HB	2.01	0.42
6:S:173:GLN:HE22	6:S:204:GLU:HA	1.84	0.42
1:K:415:LEU:O	1:K:419:GLN:HB2	2.20	0.42
2:O:441:ILE:HG21	3:P:504:THR:OG1	2.20	0.42
6:S:351:ASP:HB3	6:S:354:LEU:HB2	2.02	0.42
1:K:368:LEU:HD23	2:O:422:PHE:CE1	2.54	0.42
1:K:384:MET:HG3	3:P:501:GLU:OE2	2.20	0.42
3:P:281:ASN:HA	3:P:379:ILE:O	2.20	0.42
3:P:321:VAL:O	3:P:325:ILE:HG23	2.19	0.42
2:N:391:ARG:NH1	2:N:410:VAL:O	2.52	0.42
2:N:463:MET:HE2	2:N:463:MET:HB2	1.87	0.42
2:O:139:LEU:HD11	2:O:155:TYR:CE1	2.55	0.42
2:O:232:ARG:HG3	6:S:126:TYR:O	2.20	0.42
2:O:147:ASN:OD1	2:O:148:ARG:N	2.53	0.42
3:P:135:SER:HB3	3:P:391:PRO:HB3	2.02	0.42
3:P:282:VAL:H	3:P:379:ILE:HB	1.84	0.42
3:P:325:ILE:O	3:P:331:GLN:N	2.51	0.42
5:R:1195:PRO:O	5:R:1198:SER:OG	2.38	0.42
6:S:205:ARG:HH11	8:U:56:TRP:HB2	1.85	0.42
4:Q:343:LEU:HD11	4:Q:380:VAL:HA	2.02	0.41
2:N:414:THR:OG1	2:N:417:GLU:HG2	2.20	0.41
1:K:273:VAL:HG22	1:K:275:SER:H	1.85	0.41
2:O:568:GLU:O	2:O:571:ARG:HG2	2.20	0.41
3:P:355:PHE:CD1	3:P:357:PRO:HD2	2.54	0.41
5:R:1025:GLU:HG3	5:R:1026:PRO:HD3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:S:129:GLY:HA3	6:S:138:THR:OG1	2.20	0.41
2:N:570:THR:HG21	3:P:86:ILE:HD11	2.03	0.41
2:O:141:GLU:CD	2:O:142:PHE:H	2.27	0.41
3:P:79:ASP:N	3:P:79:ASP:OD1	2.53	0.41
8:U:78:LEU:HD23	8:U:78:LEU:HA	1.91	0.41
1:K:391:MET:CE	5:R:904:THR:HG21	2.51	0.41
3:P:435:GLN:HB2	4:Q:353:PHE:CD1	2.55	0.41
5:R:896:VAL:HG13	5:R:942:MET:HE3	2.01	0.41
6:S:228:ASP:HB3	6:S:231:VAL:HG12	2.03	0.41
2:N:384:TRP:HA	2:N:413:ARG:HH21	1.85	0.41
2:N:662:THR:HG22	2:N:664:GLN:H	1.85	0.41
3:P:77:LEU:HD23	3:P:440:MET:HE1	2.02	0.41
3:P:224:PHE:HZ	3:P:288:LEU:HD12	1.86	0.41
3:P:517:VAL:O	3:P:521:GLN:HG3	2.21	0.41
1:K:407:ARG:HE	1:K:407:ARG:HB3	1.69	0.41
2:N:453:LEU:HD23	2:N:453:LEU:HA	1.90	0.41
6:S:182:PRO:HD2	6:S:246:PHE:CE1	2.56	0.41
1:K:274:LYS:HZ1	6:S:79:PHE:HB2	1.86	0.41
1:K:276:PRO:HB2	1:K:279:ALA:H	1.85	0.41
2:N:632:GLN:H	2:N:632:GLN:CD	2.28	0.41
2:N:647:GLU:HA	2:N:650:ALA:HB3	2.02	0.41
2:O:125:TRP:HE1	2:O:134:ILE:CD1	2.33	0.41
2:O:161:PHE:CD1	2:O:183:LEU:CD1	3.04	0.41
3:P:134:ILE:HA	3:P:166:LYS:O	2.21	0.41
3:P:134:ILE:HD11	3:P:394:TYR:CE1	2.56	0.41
3:P:299:LEU:HD22	3:P:303:LEU:HD12	2.03	0.41
3:P:336:LYS:HD3	3:P:336:LYS:N	2.36	0.41
3:P:517:VAL:HG23	3:P:520:SER:H	1.85	0.41
6:S:130:TYR:HB2	6:S:138:THR:HG23	2.03	0.41
6:S:169:ASP:HA	6:S:205:ARG:HH21	1.86	0.41
3:P:283:ASN:HA	3:P:378:THR:HG23	2.02	0.41
7:T:386:MET:O	7:T:390:TYR:N	2.51	0.40
2:N:469:LEU:HD22	2:N:557:ARG:NH2	2.35	0.40
2:N:634:ALA:HB2	2:N:648:VAL:HG21	2.02	0.40
2:O:441:ILE:HG22	2:O:446:LEU:HD12	2.04	0.40
3:P:324:TYR:CE2	3:P:345:LEU:HD21	2.56	0.40
3:P:449:LYS:NZ	3:P:453:LEU:HD11	2.36	0.40
4:Q:372:LEU:HA	4:Q:375:GLU:HB3	2.03	0.40
1:K:407:ARG:HD2	1:K:411:ILE:HG12	2.03	0.40
2:N:160:PHE:HE2	2:N:178:CYS:HA	1.86	0.40
2:O:184:ALA:HB2	6:S:368:ARG:CD	2.50	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:Q:407:ARG:HG3	4:Q:407:ARG:NH1	2.37	0.40
5:R:875:GLU:O	5:R:875:GLU:HG2	2.22	0.40
6:S:154:ARG:NE	6:S:155:PRO:HD2	2.36	0.40
3:P:227:LEU:CD1	3:P:272:ILE:HG21	2.51	0.40
5:R:884:MET:HE3	5:R:885:LEU:N	2.36	0.40
1:K:387:ASP:C	5:R:894:ARG:HH12	2.29	0.40
1:K:391:MET:HE1	5:R:904:THR:HG21	2.02	0.40
5:R:824:PRO:HB2	6:S:146:ILE:HD13	2.03	0.40
6:S:123:SER:HB3	6:S:139:GLU:OE1	2.21	0.40
6:S:309:THR:HG23	6:S:314:LEU:HB2	2.03	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	K	135/1595 (8%)	123 (91%)	12 (9%)	0	100	100
2	N	361/694 (52%)	326 (90%)	35 (10%)	0	100	100
2	O	319/694 (46%)	295 (92%)	24 (8%)	0	100	100
3	P	402/547 (74%)	364 (90%)	38 (10%)	0	100	100
4	Q	174/769 (23%)	162 (93%)	12 (7%)	0	100	100
5	R	473/1301 (36%)	459 (97%)	13 (3%)	1 (0%)	43	66
6	S	346/785 (44%)	331 (96%)	15 (4%)	0	100	100
7	T	52/722 (7%)	43 (83%)	9 (17%)	0	100	100
8	U	31/627 (5%)	28 (90%)	3 (10%)	0	100	100
All	All	2293/7734 (30%)	2131 (93%)	161 (7%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	R	1070	HIS

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	K	122/1356 (9%)	122 (100%)	0	100	100
2	N	300/562 (53%)	299 (100%)	1 (0%)	86	92
2	O	277/562 (49%)	277 (100%)	0	100	100
3	P	353/462 (76%)	350 (99%)	3 (1%)	73	85
4	Q	148/598 (25%)	148 (100%)	0	100	100
5	R	413/1070 (39%)	411 (100%)	2 (0%)	81	90
6	S	313/675 (46%)	311 (99%)	2 (1%)	78	89
7	T	47/562 (8%)	47 (100%)	0	100	100
8	U	28/508 (6%)	28 (100%)	0	100	100
All	All	2001/6355 (32%)	1993 (100%)	8 (0%)	81	92

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

Mol	Chain	Res	Type
2	N	483	ASN
3	P	223	PHE
3	P	293	ASP
3	P	392	THR
5	R	752	HIS
5	R	1072	MET
6	S	167	LYS
6	S	349	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
2	N	214	HIS

Continued on next page...

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Mol	Chain	Res	Type
2	N	404	ASN
2	N	483	ASN
2	N	492	ASN
2	N	592	ASN
2	N	627	GLN
2	O	211	GLN
2	O	405	GLN
3	P	315	GLN
3	P	331	GLN
3	P	471	GLN
4	Q	309	GLN
4	Q	323	GLN
4	Q	357	GLN
4	Q	466	HIS
4	Q	482	GLN
5	R	744	GLN
5	R	752	HIS
5	R	794	HIS
5	R	961	ASN
5	R	1070	HIS
5	R	1204	GLN
6	S	173	GLN
7	T	392	ASN
8	U	69	HIS

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](#)

There are no ligands in this entry.

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.

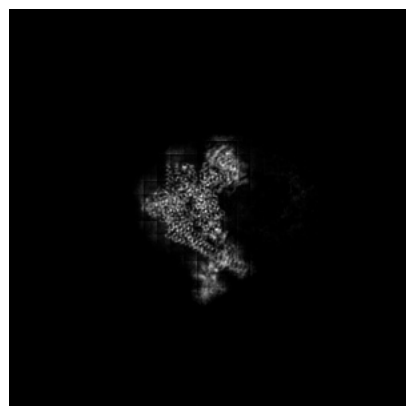
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-68925. 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](#)

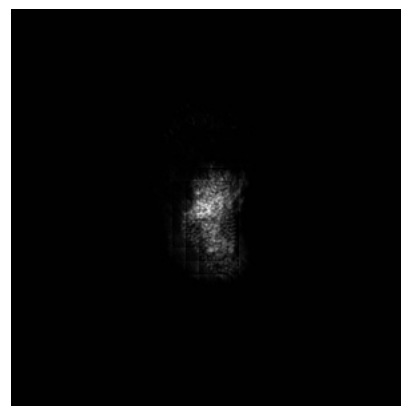
6.1.1 Primary map



X

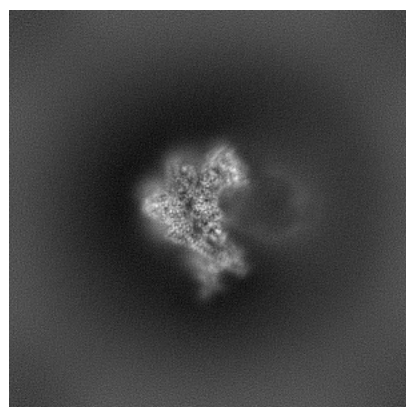


Y

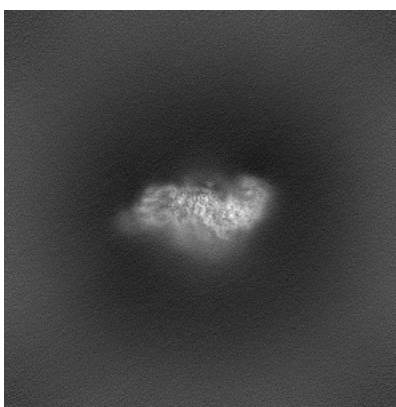


Z

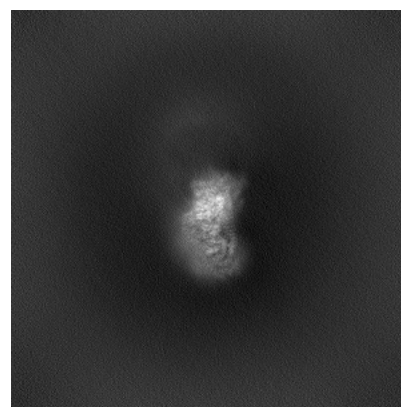
6.1.2 Raw map



X



Y

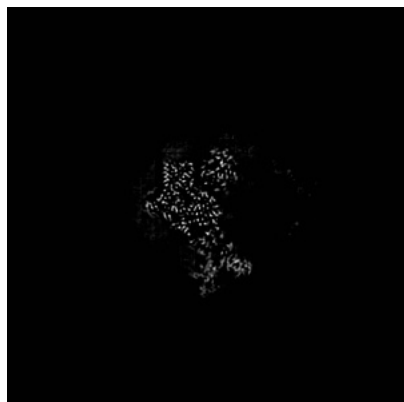


Z

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

6.2 Central slices [i](#)

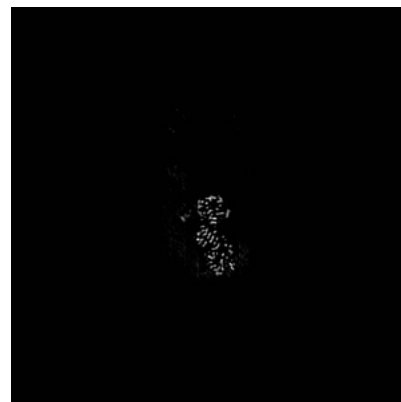
6.2.1 Primary map



X Index: 225

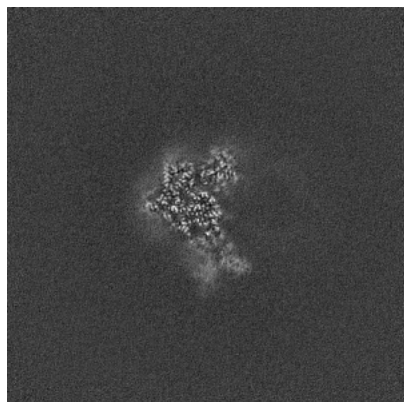


Y Index: 225

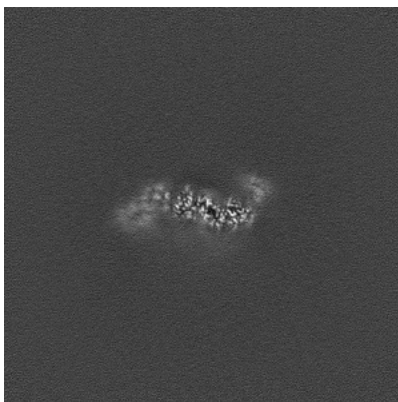


Z Index: 225

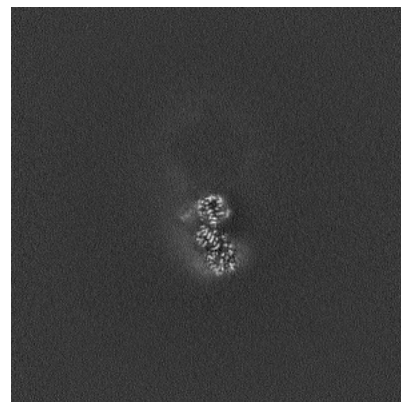
6.2.2 Raw map



X Index: 225



Y Index: 225

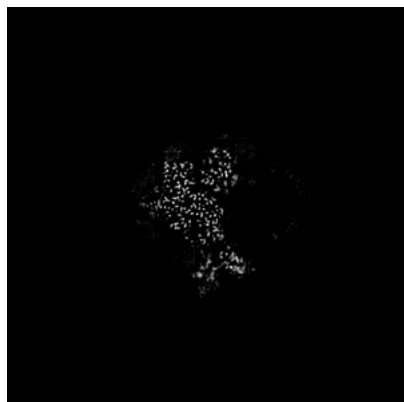


Z Index: 225

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

6.3 Largest variance slices [i](#)

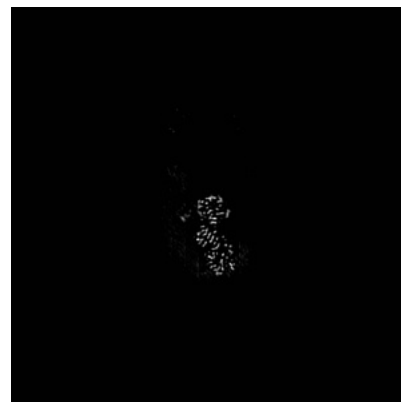
6.3.1 Primary map



X Index: 227

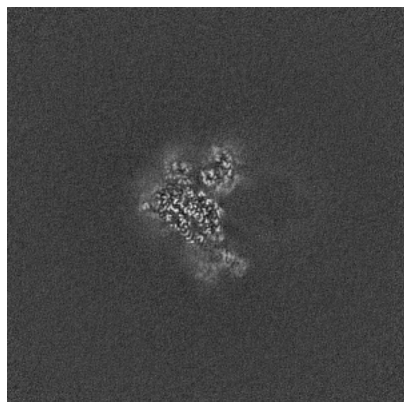


Y Index: 219

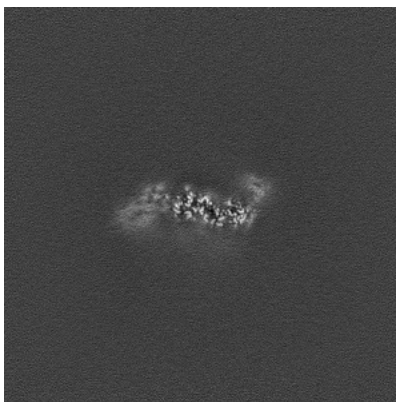


Z Index: 225

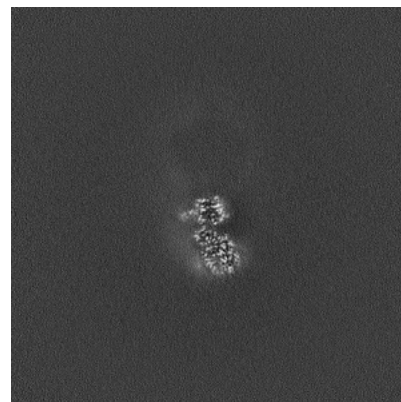
6.3.2 Raw map



X Index: 229



Y Index: 226

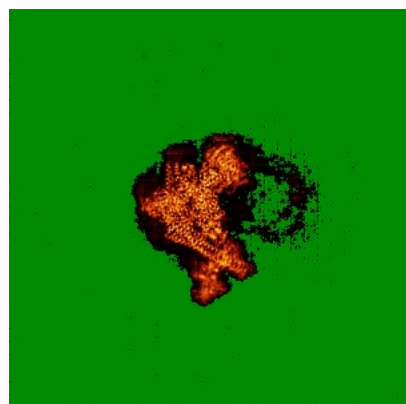


Z Index: 228

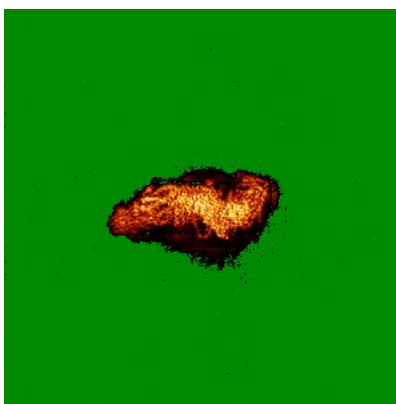
The images above show the largest variance slices of the map in three orthogonal directions.

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

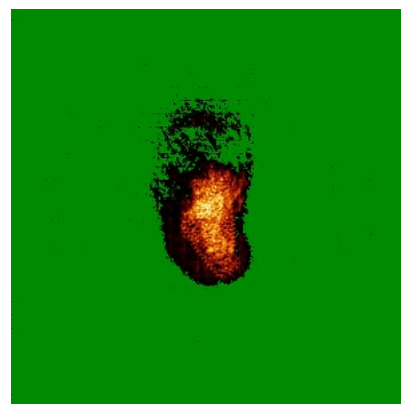
6.4.1 Primary map



X

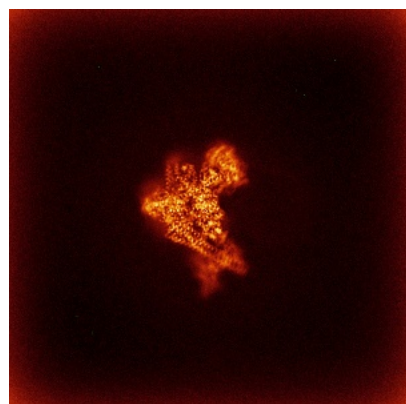


Y

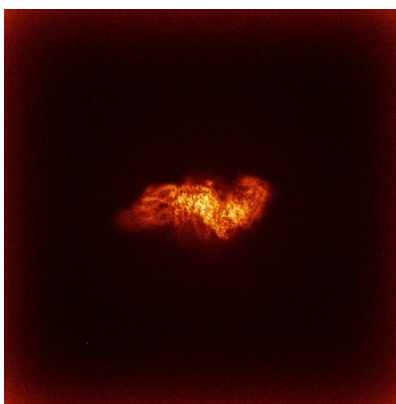


Z

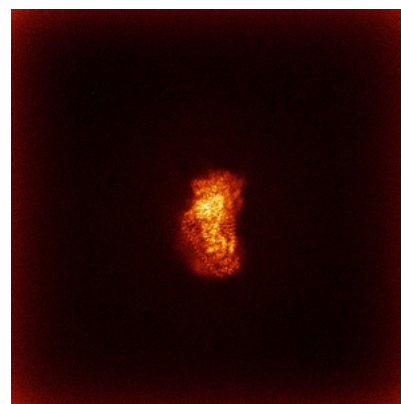
6.4.2 Raw map



X



Y

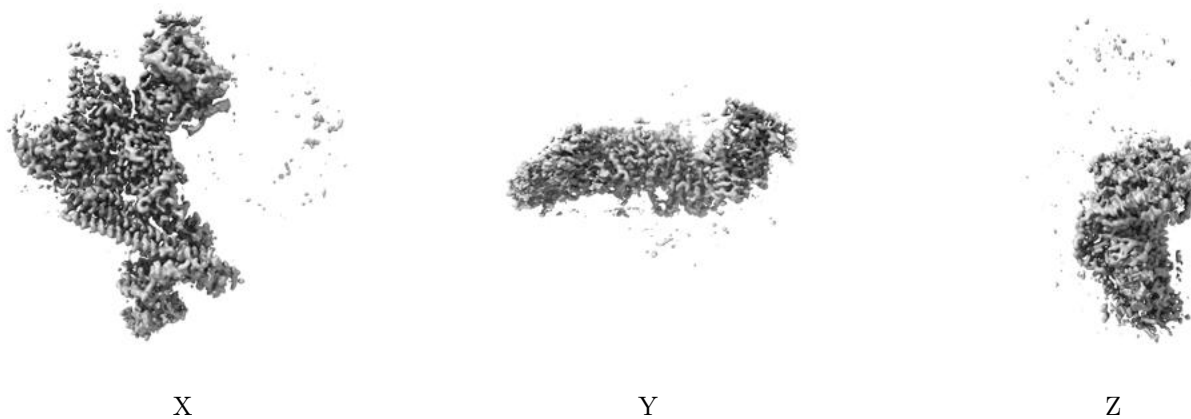


Z

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.

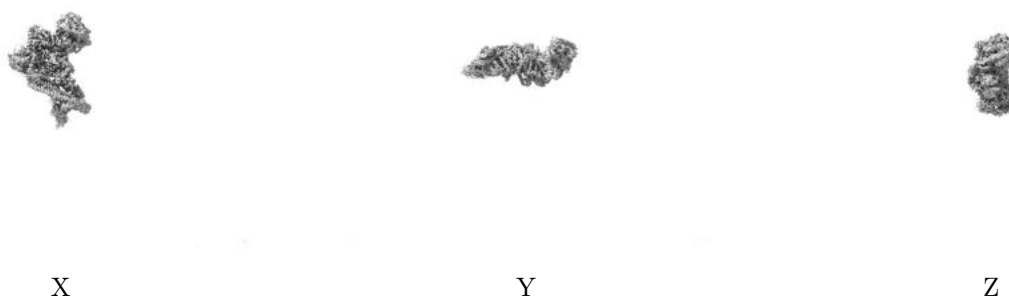
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.201. 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



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

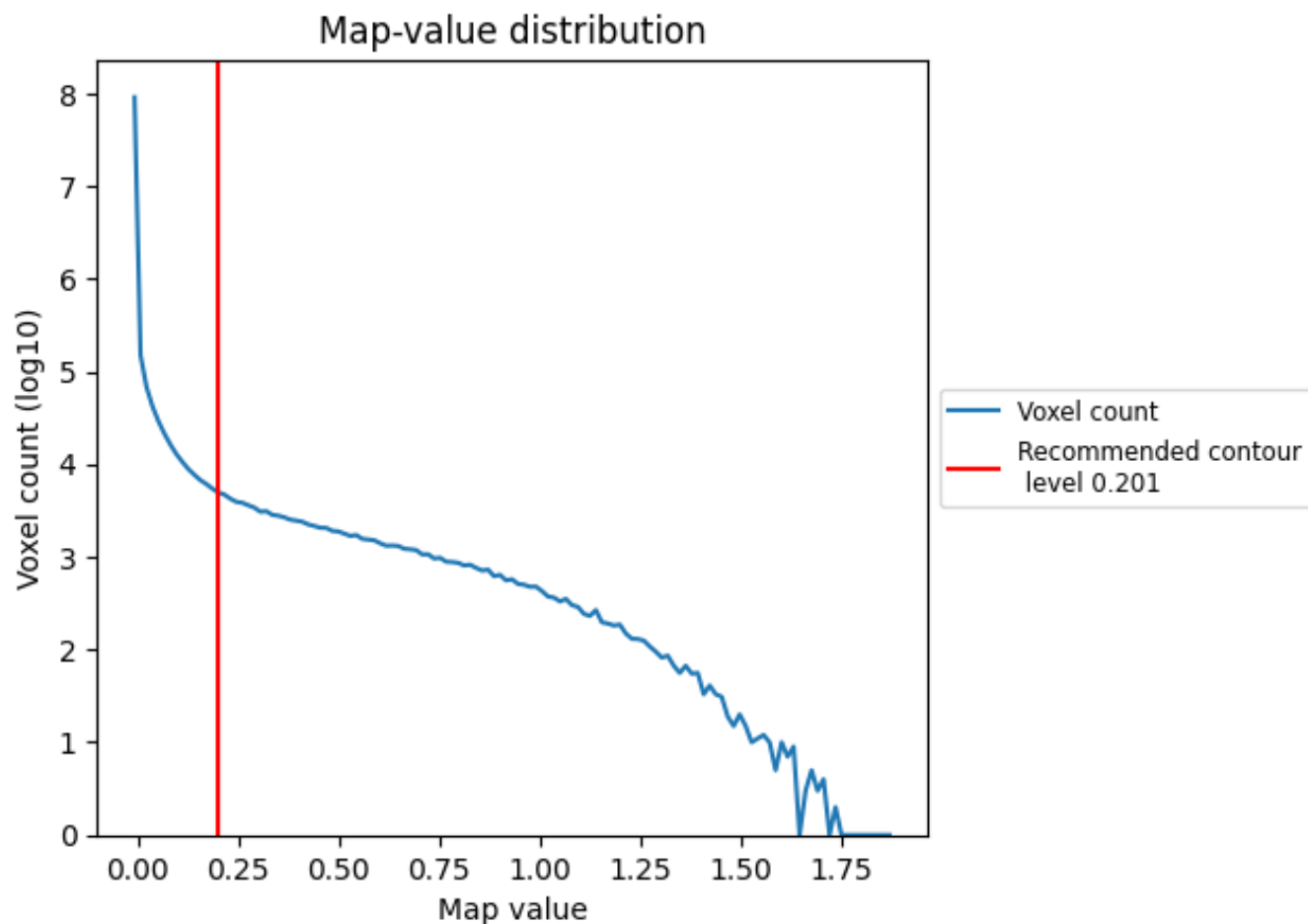
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

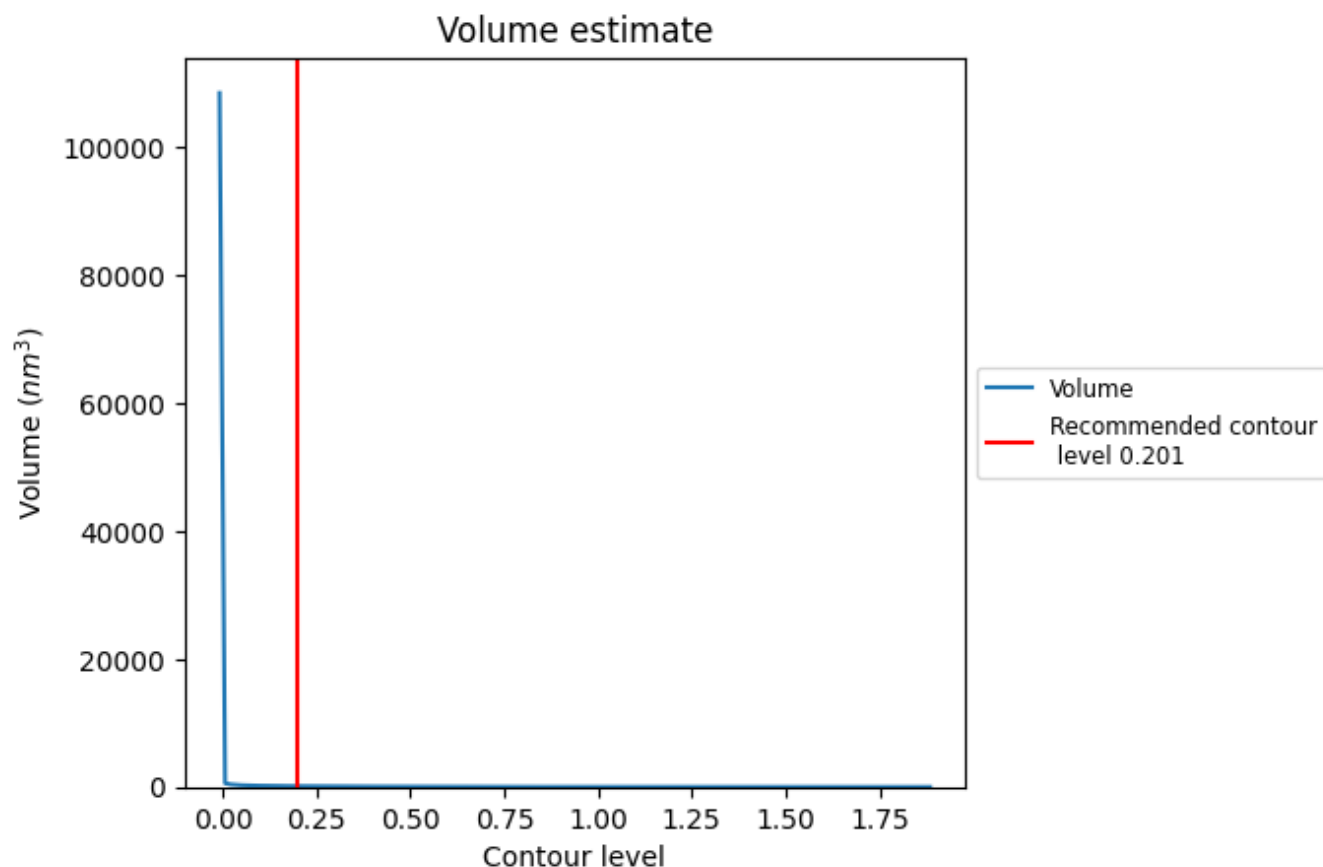
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

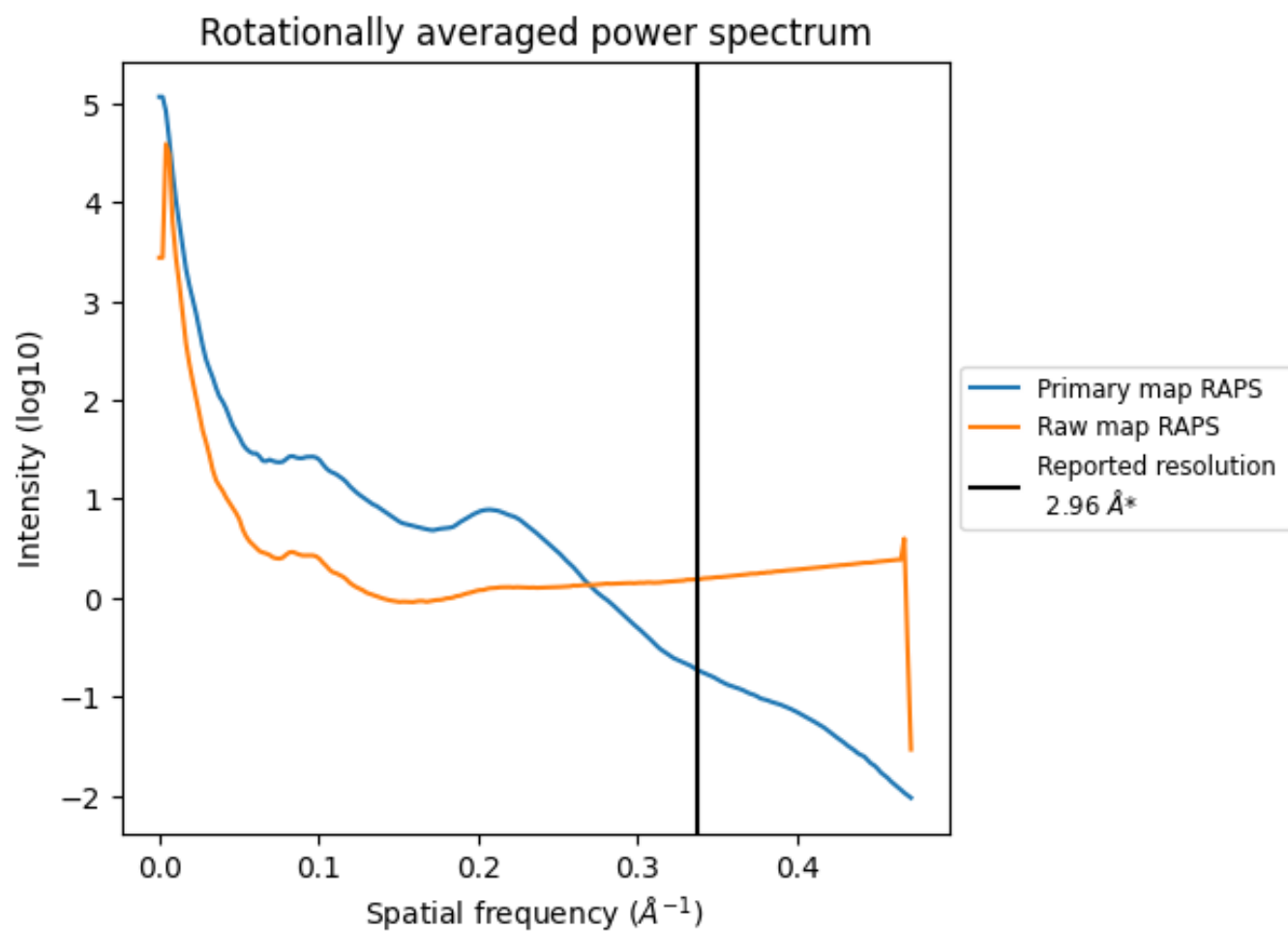
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 121 nm^3 ; this corresponds to an approximate mass of 109 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

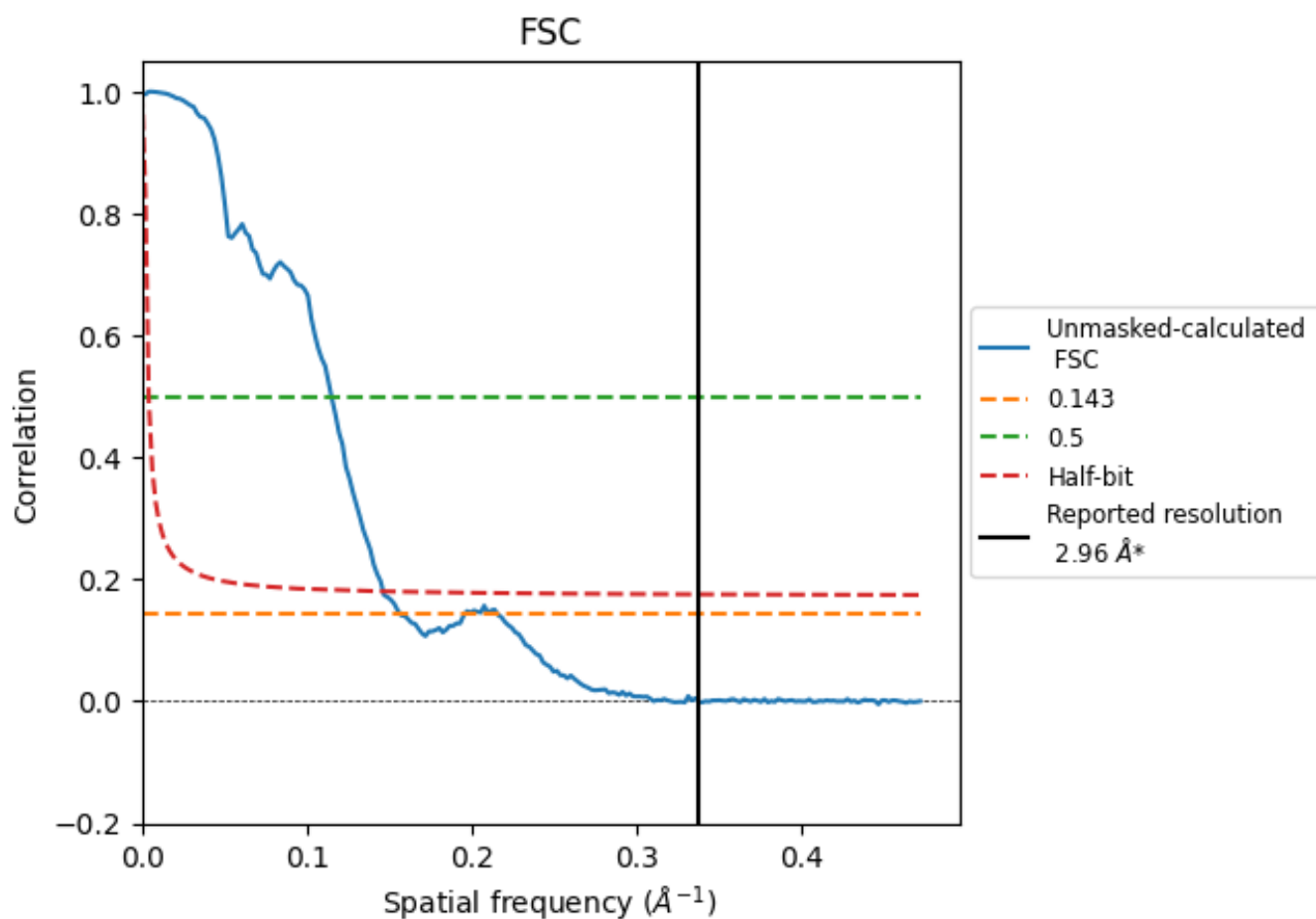


*Reported resolution corresponds to spatial frequency of 0.338 $\text{\AA}^{-1}$

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 0.338 Å⁻¹

8.2 Resolution estimates [i](#)

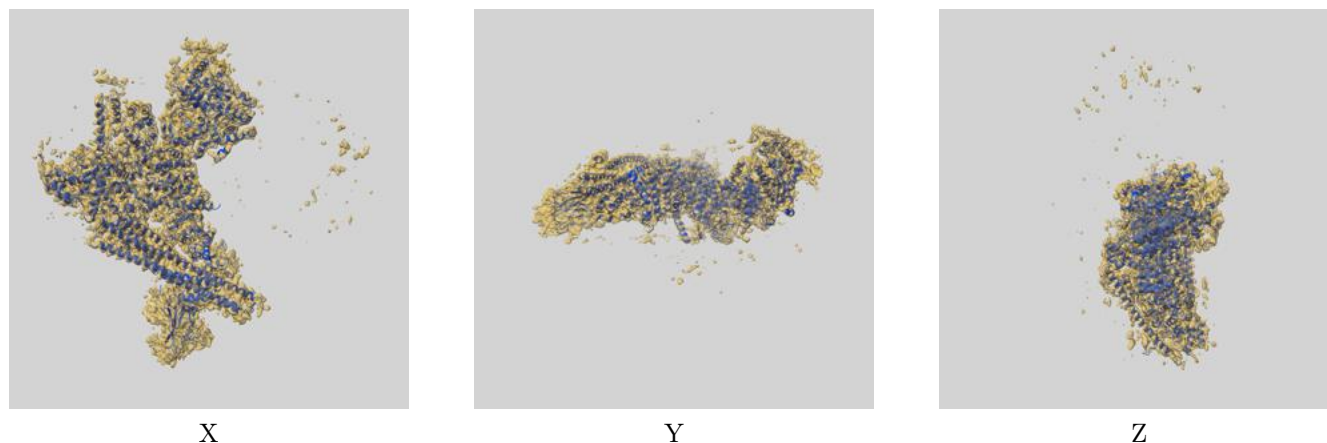
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.96	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.39	8.70	6.84

*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 6.39 differs from the reported value 2.96 by more than 10 %

9 Map-model fit [i](#)

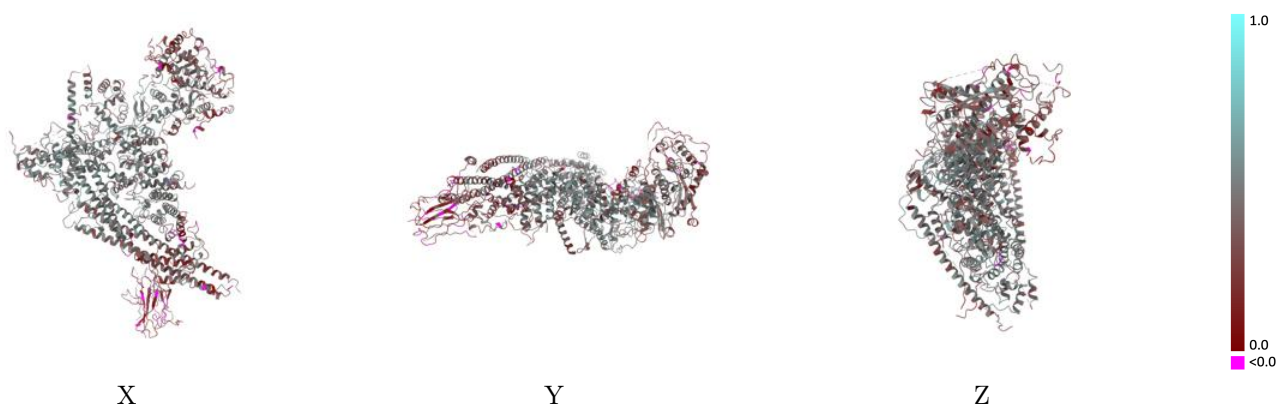
This section contains information regarding the fit between EMDB map EMD-68925 and PDB model 23FJ. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)



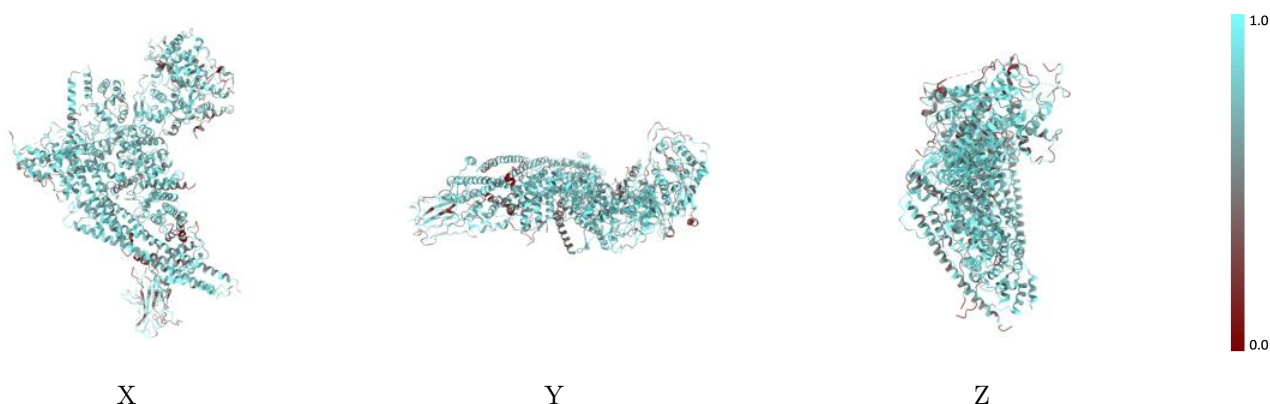
The images above show the 3D surface view of the map at the recommended contour level 0.201 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



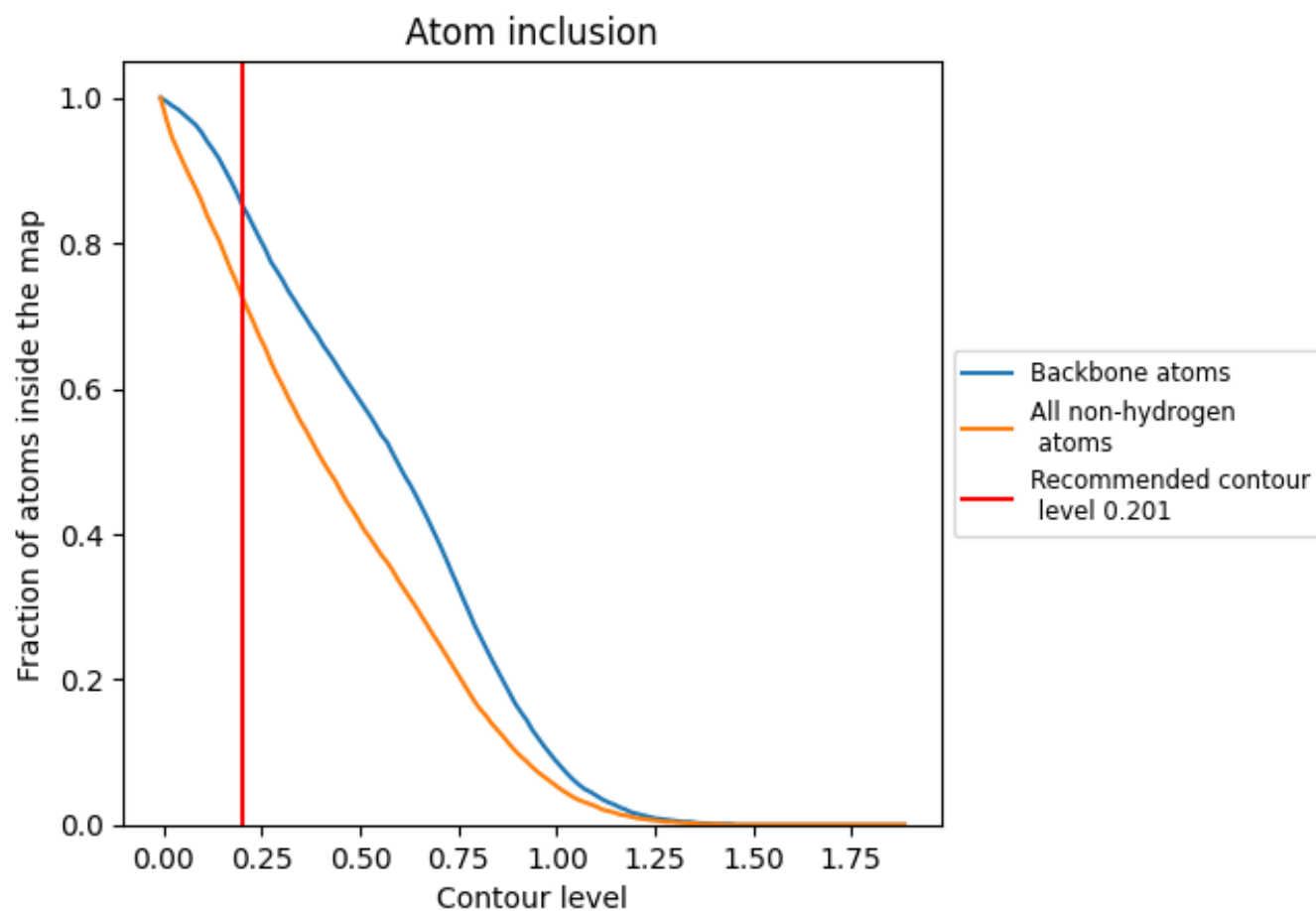
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.201).

9.4 Atom inclusion ⓘ



At the recommended contour level, 85% of all backbone atoms, 72% 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 (0.201) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7240	0.3970
K	0.6860	0.4410
N	0.8030	0.4400
O	0.7320	0.3890
P	0.6590	0.3120
Q	0.7300	0.3990
R	0.7620	0.4470
S	0.7050	0.3990
T	0.6740	0.3150
U	0.4940	0.2560

1.0

0.0

<0.0