



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 11:28 AM UTC

PDB ID : 9L45 / pdb_00009l45
EMDB ID : EMD-62806
Title : ATR-ATRIP bound with VE-822
Authors : Wang, G.
Deposited on : 2024-12-19
Resolution : 3.95 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
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

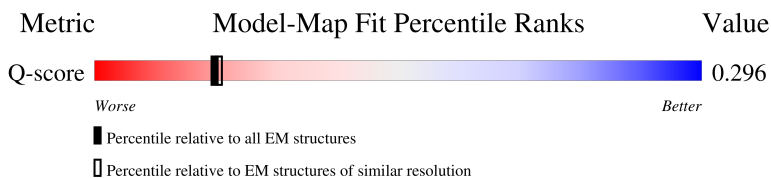
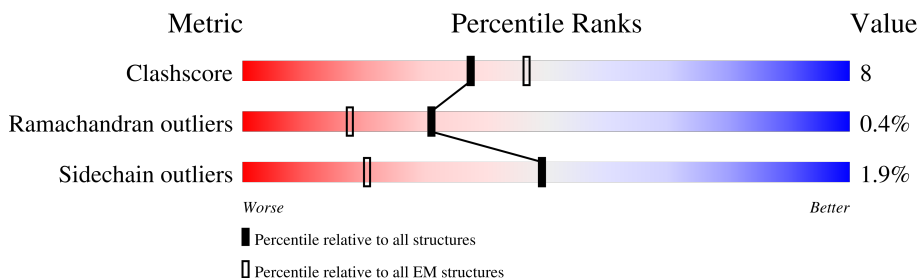
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.95 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	7707 (3.45 - 4.45)

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

Mol	Chain	Length	Quality of chain
1	A	2644	 6% 81% 12% 7%
1	B	2644	 12% 84% 9% 6%
2	C	791	 10% 41% 6% 52%
2	D	791	 15% 38% 8% 54%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 54714 atoms, of which 21335 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.

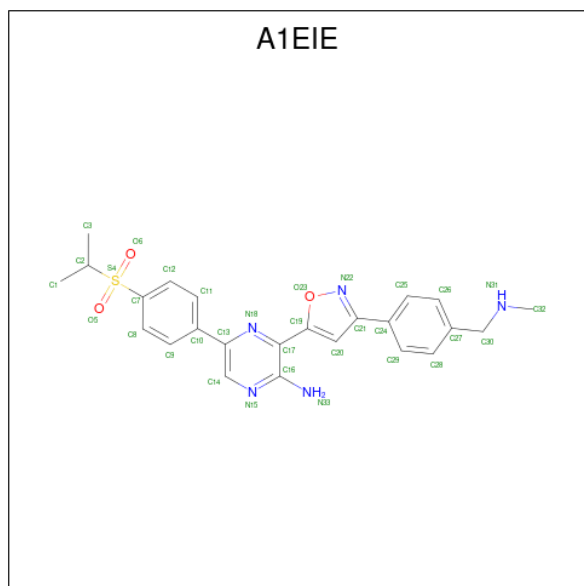
- Molecule 1 is a protein called Serine/threonine-protein kinase ATR.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	2459	Total	C	H	N	O	S	0	0
			24402	8972	9737	2768	2875	50		
1	B	2489	Total	C	H	N	O	S	0	0
			23559	8802	9100	2729	2890	38		

- Molecule 2 is a protein called ATR-interacting protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	D	366	Total	C	H	N	O	S	0	0
			3198	1203	1195	388	399	13		
2	C	380	Total	C	H	N	O	S	0	0
			3409	1258	1291	407	441	12		

- Molecule 3 is VE-822 (CCD ID: A1EIE) (formula: $C_{24}H_{25}N_5O_3S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						AltConf
3	A	1	Total	C	H	N	O	S	0
			36	24	3	5	3	1	
3	B	1	Total	C	H	N	O	S	0
			36	24	3	5	3	1	
3	B	1	Total	C	H	N	O	S	0
			36	24	3	5	3	1	
3	B	1	Total	C	H	N	O	S	0
			36	24	3	5	3	1	

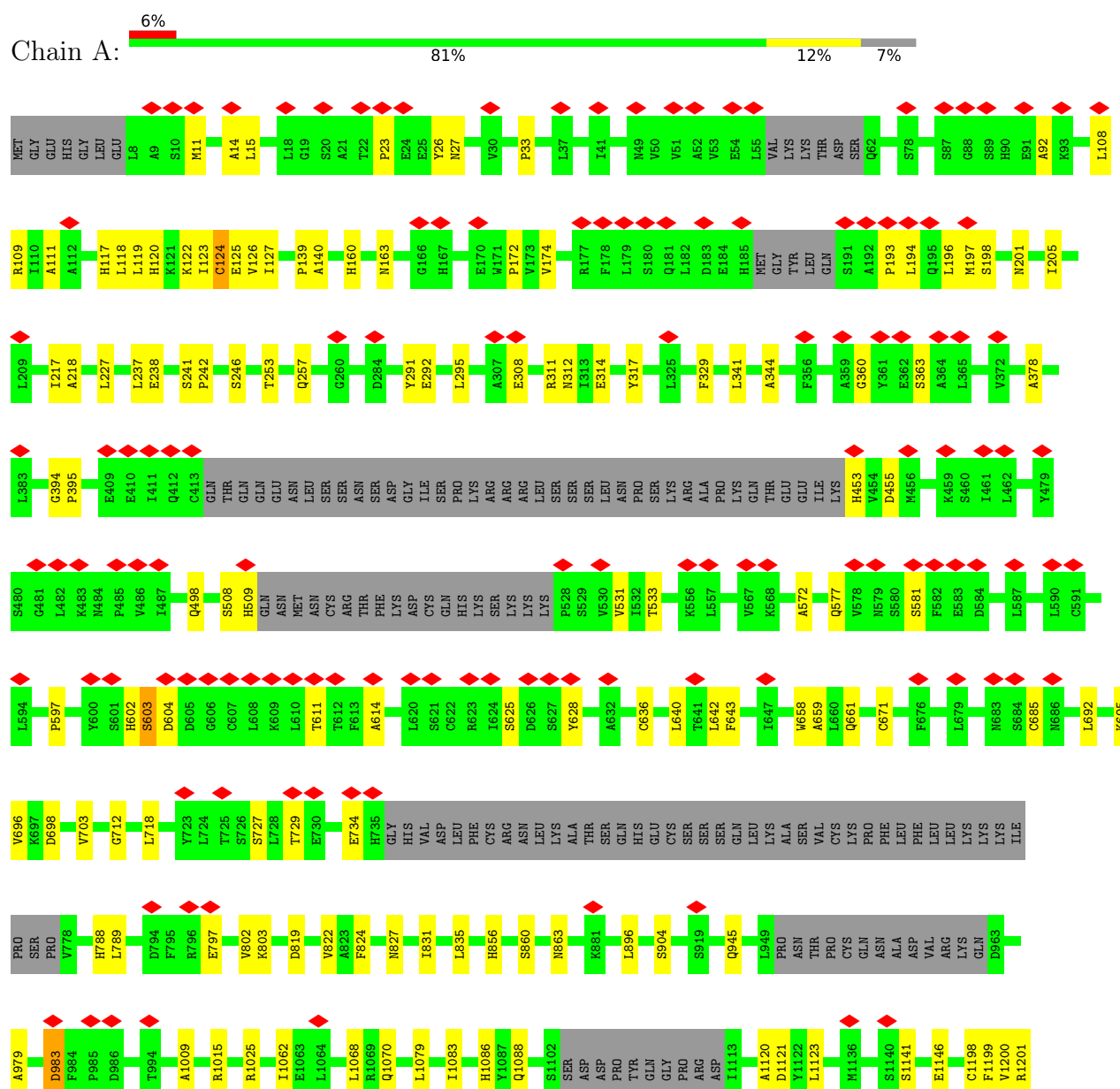
- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

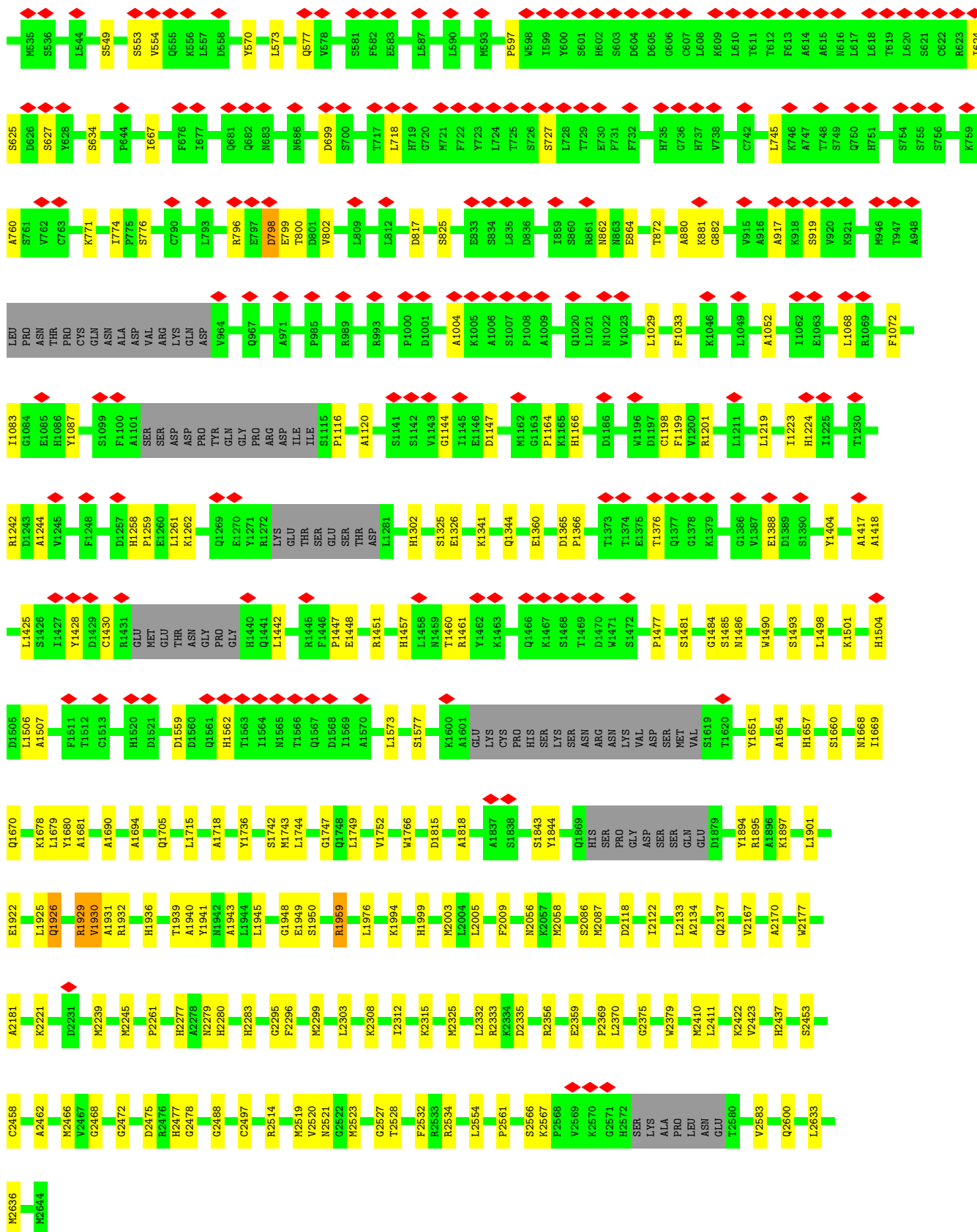
Mol	Chain	Residues	Atoms		AltConf
4	D	1	Total	Zn	0
			1	1	
4	C	1	Total	Zn	0
			1	1	

3 Residue-property plots

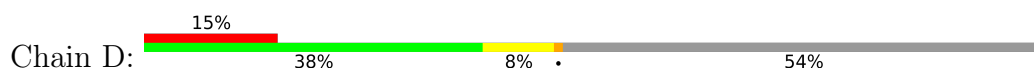
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Serine/threonine-protein kinase ATR



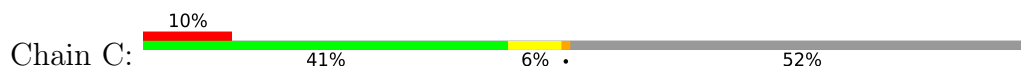


• Molecule 2: ATR-interacting protein

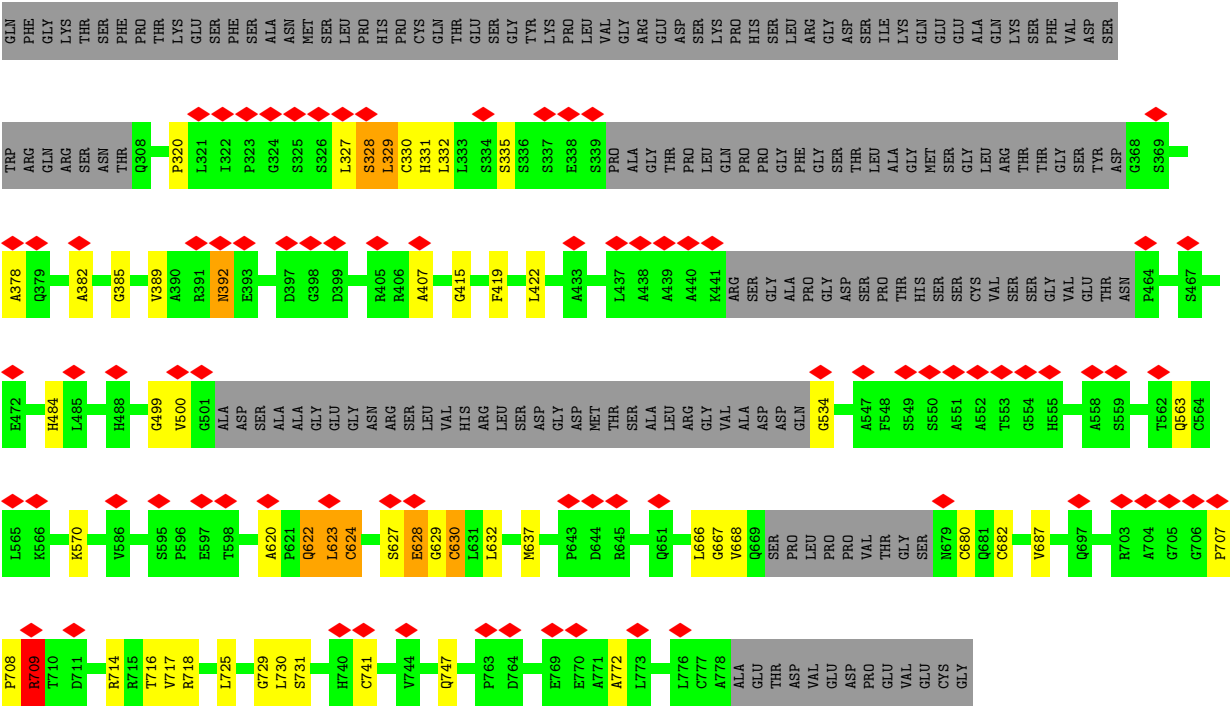


A704	G705	G706	G707	D711	Q712	V724	L727	H728	S731	Q732	K733	D734	K735	L736	M739	H740	C741	V742	L745	H746	Q747	F748	G754	L758	I759	L762	P763	D764	E770	A771	A772	L773	L776	CYS	ALA	ALA	GLU	THR	ASP	VAL	GLU	ASP	PRO	GLU	VAL	GLY	CYS	GLY																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
Q618	L619	A620	P621	Q622	L623	C624	S625	H626	S627	E628	G629	C630	L631	L632	L633	L634	L635	V636	M637	Y638	I639	P643	D644	R645	V646	A647	L648	E649	L666	G667	V668	Q669	S670	PRO	LEU	PRO	PRO	VAL	THR	GLY	SER	ASN	S594	S595	S596	E597	Q681	C682	N683	V686	R696	Q697	W698	L699	T700	V701	R702	R703																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																													
ARG	GLY	VAL	ALA	ASP	ASP	Q533	L538	L546	A547	F548	S549	S550	A551	A552	T553	G554	H555	L556	Q557	A558	S559	V560	L561	K566	K570	L571	A572	R582	F583	Q584	C585	V586	PRO	LEU	PRO	PRO	VAL	THR	GLY	SER	ASN	S594	S595	S596	E597	Q681	C682	N683	V686	R696	Q697	W698	L699	T700	V701	R702	R703																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														
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S369	F370	S371	L372	S373	A374	L375	R376	E377	A378	Q379	A390	R391	S395	R396	D397	G398	D399	P400	A401	E402	G403	G404	R405	R406	L410	C411	Q412	G415	A416	V417	L420	V423	Q424	F425	F426	I427	Q428	L429	H430	C431	Q432	A433	L434	Q435	L437	ALA	ALA	ALA	LYS	ARG	SER	GLY																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
TRP	ARG	GLN	ARG	SER	THR	ASN	G309	I311	Q319	P320	L321	I322	P323	G324	S325	S326	L327	S328	L329	C330	H331	L332	L333	S337	GLU	SER	PRO	ALA	GLY	THR	GLY	GLY	PHE	GLY	THR	LEU	ALA	GLY	MET	SER	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	

• Molecule 2: ATR-interacting protein



PHE	SER	LYS	LYS	LEU	GLN	SER	LEU	LEU	GLN	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	66141	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)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.595	Depositor
Minimum map value	-0.747	Depositor
Average map value	0.007	Depositor
Map value standard deviation	0.067	Depositor
Recommended contour level	0.255	Depositor
Map size (Å)	308.16, 308.16, 308.16	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	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: A1EIE, ZN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.46	21/14824 (0.1%)	0.55	22/20386 (0.1%)
1	B	0.40	10/14600 (0.1%)	0.52	13/20134 (0.1%)
2	C	0.56	3/2126 (0.1%)	0.87	12/2926 (0.4%)
2	D	0.52	0/2011	0.97	7/2774 (0.3%)
All	All	0.45	34/33561 (0.1%)	0.60	54/46220 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	3
2	C	0	2
2	D	0	1
All	All	0	8

All (34) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1594	HIS	ND1-CE1	5.40	1.38	1.32
1	B	1224	HIS	ND1-CE1	5.39	1.38	1.32
1	B	2437	HIS	ND1-CE1	5.38	1.38	1.32
1	A	2572	HIS	ND1-CE1	5.33	1.37	1.32
1	A	160	HIS	ND1-CE1	5.33	1.37	1.32
1	A	1086	HIS	ND1-CE1	5.29	1.37	1.32
1	A	1504	HIS	ND1-CE1	5.24	1.37	1.32
1	B	257	GLN	CD-OE1	5.22	1.33	1.23
1	A	788	HIS	ND1-CE1	5.22	1.37	1.32
1	A	1486	ASN	CG-OD1	5.18	1.33	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	1302	HIS	ND1-CE1	5.14	1.37	1.32
2	C	484	HIS	ND1-CE1	5.14	1.37	1.32
1	A	2517	HIS	ND1-CE1	5.14	1.37	1.32
1	B	2137	GLN	CD-OE1	5.13	1.33	1.23
1	B	1705	GLN	CD-OE1	5.12	1.33	1.23
1	A	1987	ASN	CG-OD1	5.12	1.33	1.23
1	A	1542	GLN	CD-OE1	5.10	1.33	1.23
1	B	2056	ASN	CG-OD1	5.09	1.33	1.23
1	A	1541	ASN	CG-OD1	5.08	1.33	1.23
1	A	1672	HIS	ND1-CE1	5.08	1.37	1.32
2	C	392	ASN	CG-OD1	5.07	1.33	1.23
1	A	1590	GLN	CD-OE1	5.06	1.33	1.23
1	A	1594	HIS	CD2-NE2	-5.06	1.32	1.37
1	B	1486	ASN	CG-OD1	5.05	1.33	1.23
1	A	2080	ASN	CG-OD1	5.04	1.33	1.23
1	A	312	ASN	CG-OD1	5.04	1.33	1.23
1	A	2227	ASN	CG-OD1	5.04	1.33	1.23
1	A	863	ASN	CG-OD1	5.04	1.33	1.23
1	B	2600	GLN	CD-OE1	5.04	1.33	1.23
1	A	1545	GLN	CD-OE1	5.03	1.33	1.23
1	A	1938	GLN	CD-OE1	5.03	1.33	1.23
1	B	2437	HIS	CD2-NE2	-5.02	1.32	1.37
1	A	163	ASN	CG-OD1	5.01	1.33	1.23
2	C	563	GLN	CD-OE1	5.01	1.33	1.23

All (54) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	708	PRO	N-CA-CB	-17.19	85.20	103.25
2	D	680	CYS	CB-CA-C	-17.01	77.78	110.10
1	B	1930	VAL	N-CA-C	-10.98	102.77	113.53
2	C	628	GLU	N-CA-C	-10.59	96.55	110.53
2	D	682	CYS	CB-CA-C	-10.27	93.74	110.79
2	D	634	LEU	N-CA-C	-8.78	101.71	111.28
1	B	1669	ILE	CA-C-N	-8.40	106.90	121.52
1	B	1669	ILE	C-N-CA	-8.40	106.90	121.52
2	C	630	CYS	CB-CA-C	8.33	123.89	109.65
1	B	1669	ILE	N-CA-C	7.53	122.32	112.76
1	A	124	CYS	N-CA-C	-7.44	101.94	111.02
2	C	328	SER	CA-C-O	-7.36	112.75	120.99
1	B	1670	GLN	CB-CA-C	7.21	118.46	109.16
2	C	622	GLN	O-C-N	-6.78	113.41	122.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	484	HIS	CB-CG-CD2	-6.71	122.48	131.20
1	A	1086	HIS	CB-CG-CD2	-6.70	122.50	131.20
1	A	2517	HIS	CB-CG-CD2	-6.68	122.51	131.20
1	B	2437	HIS	CB-CG-CD2	-6.67	122.53	131.20
1	A	1672	HIS	CB-CG-CD2	-6.65	122.55	131.20
2	C	624	CYS	N-CA-CB	6.62	119.83	110.36
1	A	2312	ILE	CA-C-O	-6.61	116.46	121.68
1	A	1594	HIS	CB-CG-CD2	-6.56	122.68	131.20
1	A	160	HIS	CB-CG-CD2	-6.54	122.70	131.20
1	A	2572	HIS	CB-CG-CD2	-6.53	122.71	131.20
1	B	1224	HIS	CB-CG-CD2	-6.51	122.74	131.20
1	A	788	HIS	CB-CG-CD2	-6.51	122.74	131.20
1	B	1302	HIS	CB-CG-CD2	-6.49	122.76	131.20
1	A	1504	HIS	CB-CG-CD2	-6.41	122.87	131.20
1	A	2640	TRP	N-CA-C	-6.24	104.48	111.28
2	D	331	HIS	N-CA-C	-6.15	104.84	112.90
2	C	630	CYS	CA-CB-SG	6.07	128.36	114.40
1	B	1477	PRO	N-CA-C	-6.07	99.97	112.47
2	D	370	PHE	CA-C-O	-6.04	113.94	121.50
2	C	630	CYS	N-CA-C	-5.95	101.48	110.28
2	D	681	GLN	N-CA-C	-5.85	105.97	113.23
1	B	2312	ILE	CA-C-O	-5.76	114.95	121.75
2	C	484	HIS	CB-CG-ND1	5.76	131.34	122.70
1	A	1672	HIS	CB-CG-ND1	5.76	131.34	122.70
1	A	2380	VAL	CA-C-O	-5.73	115.05	121.98
1	A	2494	ASP	CA-CB-CG	5.71	118.31	112.60
1	A	160	HIS	CB-CG-ND1	5.70	131.25	122.70
1	A	1086	HIS	CB-CG-ND1	5.69	131.23	122.70
1	A	2572	HIS	CB-CG-ND1	5.64	131.16	122.70
1	B	2437	HIS	CB-CG-ND1	5.61	131.12	122.70
1	A	788	HIS	CB-CG-ND1	5.61	131.11	122.70
1	A	1594	HIS	CB-CG-ND1	5.59	131.09	122.70
1	A	2517	HIS	CB-CG-ND1	5.59	131.08	122.70
1	B	1224	HIS	CB-CG-ND1	5.58	131.07	122.70
1	B	1302	HIS	CB-CG-ND1	5.58	131.07	122.70
1	A	1504	HIS	CB-CG-ND1	5.54	131.00	122.70
2	D	621	PRO	N-CA-C	-5.19	106.02	113.75
2	C	630	CYS	CA-C-O	-5.13	115.42	121.16
1	A	124	CYS	N-CA-CB	5.06	117.51	109.82
2	C	714	ARG	N-CA-C	-5.05	105.22	111.33

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	2496	ASN	Mainchain
1	A	797	GLU	Peptide
1	B	1929	ARG	Sidechain
1	B	1959	ARG	Sidechain
1	B	796	ARG	Sidechain
2	C	622	GLN	Mainchain
2	C	709	ARG	Sidechain
2	D	629	GLY	Mainchain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	14665	9737	9833	195	0
1	B	14459	9100	9181	152	0
2	C	2118	1291	1311	38	0
2	D	2003	1195	1203	36	0
3	A	33	3	0	0	0
3	B	99	9	0	5	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
All	All	33379	21335	21528	414	0

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

All (414) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:378:ALA:HB1	2:C:422:LEU:HA	1.36	1.05
1:A:896:LEU:HA	1:A:904:SER:HA	1.57	0.85
1:B:1430:CYS:HA	1:B:1442:LEU:CB	2.10	0.82
1:B:281:VAL:HA	1:B:333:VAL:CB	2.10	0.80
2:C:630:CYS:CB	2:C:682:CYS:HB3	2.11	0.80
1:A:1141:SER:CB	1:A:1411:SER:HA	2.13	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:729:GLY:C	2:C:731:SER:H	1.92	0.78
1:B:1715:LEU:HA	1:B:1718:ALA:HB3	1.66	0.77
2:D:629:GLY:O	2:D:682:CYS:SG	2.43	0.77
2:C:378:ALA:HB1	2:C:422:LEU:CA	2.15	0.76
1:B:2239:MET:HE3	1:B:2296:PHE:CB	2.16	0.76
1:A:2370:LEU:H	1:A:2375:GLY:HA2	1.52	0.74
1:A:109:ARG:HA	1:A:194:LEU:HA	1.69	0.73
1:B:2356:ARG:O	1:B:2359:GLU:N	2.22	0.72
1:A:498:GLN:HA	1:A:572:ALA:HB1	1.71	0.72
1:B:1004:ALA:HA	1:B:1052:ALA:HB2	1.70	0.72
2:C:382:ALA:HA	2:C:419:PHE:HA	1.70	0.71
1:A:172:PRO:HA	1:A:196:LEU:O	1.90	0.71
1:B:1418:ALA:HB1	1:B:1457:HIS:CB	2.21	0.71
1:B:1945:LEU:HA	3:B:2703:A1EIE:C30	2.22	0.70
1:B:172:PRO:HA	1:B:196:LEU:O	1.90	0.70
2:D:624:CYS:HA	2:D:630:CYS:HB3	1.76	0.68
1:B:2468:GLY:O	1:B:2472:GLY:N	2.27	0.67
1:B:1404:TYR:CB	1:B:1417:ALA:HB3	2.24	0.67
2:C:729:GLY:C	2:C:731:SER:N	2.52	0.67
1:A:1429:ASP:O	1:A:1439:GLY:HA3	1.95	0.67
2:D:620:ALA:HA	2:D:623:LEU:HD12	1.76	0.66
1:A:2356:ARG:O	1:A:2359:GLU:N	2.28	0.66
1:B:2058:MET:HE2	1:B:2058:MET:N	2.11	0.65
1:B:727:SER:CB	1:B:745:LEU:HA	2.27	0.65
1:B:2370:LEU:H	1:B:2375:GLY:HA2	1.61	0.65
1:A:2181:ALA:HB2	1:A:2369:PRO:O	1.95	0.64
2:C:687:VAL:CB	2:C:741:CYS:SG	2.86	0.64
1:A:253:THR:O	1:A:257:GLN:HG3	1.97	0.64
2:D:629:GLY:O	2:D:630:CYS:HB2	1.98	0.64
1:A:14:ALA:HB1	1:A:33:PRO:CB	2.29	0.63
1:A:625:SER:O	1:A:628:TYR:N	2.31	0.63
1:B:1498:LEU:O	1:B:1501:LYS:N	2.30	0.63
1:B:341:LEU:O	1:B:344:ALA:HB3	1.99	0.63
1:A:455:ASP:HA	1:A:533:THR:H	1.64	0.63
1:A:1784:TRP:CD1	1:A:1812:LYS:HZ2	2.16	0.63
2:C:331:HIS:O	2:C:335:SER:N	2.31	0.63
1:B:1999:HIS:CD2	1:B:2003:MET:HE2	2.34	0.62
1:B:140:ALA:HA	2:D:668:VAL:HA	1.80	0.62
1:A:1478:ILE:O	1:A:1484:GLY:HA3	1.99	0.62
1:B:1715:LEU:HA	1:B:1718:ALA:CB	2.30	0.62
2:C:378:ALA:CB	2:C:422:LEU:HA	2.23	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:630:CYS:HB2	2:C:682:CYS:HB3	1.82	0.61
2:D:733:LYS:O	2:D:734:ASP:C	2.43	0.61
1:A:498:GLN:HA	1:A:572:ALA:CB	2.29	0.61
1:B:89:SER:O	1:B:90:HIS:C	2.42	0.61
1:A:2468:GLY:O	1:A:2472:GLY:N	2.33	0.61
1:A:1985:PRO:O	1:A:1987:ASN:N	2.30	0.61
2:D:680:CYS:HB3	2:D:682:CYS:N	2.14	0.61
1:B:1504:HIS:CB	1:B:1507:ALA:HB3	2.30	0.61
1:B:597:PRO:HA	1:B:625:SER:CB	2.30	0.60
1:B:1481:SER:O	1:B:1485:SER:N	2.34	0.60
1:A:394:GLY:HA3	1:A:734:GLU:CB	2.31	0.60
1:B:1559:ASP:O	1:B:1562:HIS:N	2.33	0.60
1:A:23:PRO:HA	1:A:26:TYR:CB	2.32	0.60
1:A:11:MET:O	1:A:15:LEU:N	2.33	0.60
1:A:509:HIS:CB	1:A:531:VAL:HA	2.31	0.60
1:A:597:PRO:HA	1:A:625:SER:CB	2.32	0.59
1:B:1694:ALA:HA	3:B:2701:A1EIE:C9	2.33	0.59
1:B:1258:HIS:O	1:B:1262:LYS:N	2.35	0.59
1:B:198:SER:O	1:B:202:LEU:N	2.35	0.59
1:A:122:LYS:O	1:A:125:GLU:N	2.36	0.59
1:B:2118:ASP:O	1:B:2122:ILE:HG13	2.03	0.59
1:B:2295:GLY:O	1:B:2315:LYS:N	2.36	0.59
1:B:1940:ALA:HB1	1:B:1943:ALA:HB3	1.85	0.59
1:A:945:GLN:CB	1:A:1009:ALA:HB1	2.33	0.58
1:A:124:CYS:O	1:A:125:GLU:C	2.45	0.58
1:A:1079:LEU:O	1:A:1083:ILE:N	2.36	0.58
1:B:1258:HIS:H	1:B:1261:LEU:CB	2.16	0.58
1:A:140:ALA:HA	2:C:668:VAL:O	2.03	0.58
1:B:1004:ALA:CA	1:B:1052:ALA:HB2	2.32	0.58
1:A:1146:GLU:OE1	1:A:1146:GLU:N	2.36	0.57
1:B:1376:THR:HG23	1:B:1376:THR:O	2.04	0.57
2:C:385:GLY:HA2	2:C:415:GLY:HA2	1.86	0.57
1:B:1219:LEU:O	1:B:1223:ILE:N	2.35	0.57
2:D:603:VAL:O	2:D:606:ALA:HB3	2.05	0.57
1:A:14:ALA:HB1	1:A:33:PRO:HA	1.87	0.57
1:A:602:HIS:O	1:A:603:SER:C	2.48	0.56
1:A:2306:LEU:HB2	1:A:2309:PRO:HG3	1.86	0.56
2:C:729:GLY:O	2:C:731:SER:N	2.38	0.56
1:A:1088:GLN:CD	1:A:1088:GLN:H	2.14	0.56
2:D:582:ARG:C	2:D:584:GLN:N	2.64	0.56
1:A:1454:LEU:O	1:A:1458:LEU:N	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1448:GLU:HA	1:B:1451:ARG:CB	2.36	0.56
1:B:2466:MET:HE2	1:B:2466:MET:HA	1.88	0.56
2:C:623:LEU:HD12	2:C:624:CYS:N	2.21	0.56
1:A:174:VAL:HA	1:A:194:LEU:O	2.06	0.56
1:A:1347:ASN:O	1:A:1350:ALA:HB3	2.06	0.56
1:A:14:ALA:HB1	1:A:33:PRO:CA	2.36	0.55
1:A:1447:PRO:O	1:A:1448:GLU:C	2.49	0.55
1:B:771:LYS:O	1:B:774:ILE:N	2.39	0.55
2:D:734:ASP:O	2:D:736:LEU:N	2.38	0.55
1:A:2371:ASN:N	1:A:2374:CYS:O	2.40	0.55
1:A:2369:PRO:HA	1:A:2375:GLY:HA3	1.87	0.55
1:B:2303:LEU:O	1:B:2308:LYS:HA	2.06	0.55
1:B:1029:LEU:O	1:B:1033:PHE:N	2.41	0.54
2:C:628:GLU:O	2:C:629:GLY:C	2.50	0.54
1:A:124:CYS:O	1:A:127:ILE:N	2.41	0.54
1:A:2435:ILE:O	1:A:2438:GLU:N	2.38	0.54
1:A:685:CYS:CB	1:A:718:LEU:HA	2.38	0.54
2:C:331:HIS:O	2:C:332:LEU:C	2.50	0.54
1:A:198:SER:O	1:A:201:ASN:N	2.39	0.53
1:A:1280:ASP:O	1:A:1283:THR:N	2.37	0.53
1:B:93:LYS:O	1:B:94:GLY:C	2.50	0.53
2:C:320:PRO:HA	2:C:328:SER:CB	2.39	0.53
2:C:329:LEU:O	2:C:330:CYS:C	2.52	0.53
1:A:727:SER:C	1:A:729:THR:H	2.15	0.52
1:A:2553:VAL:O	1:A:2556:THR:OG1	2.26	0.52
1:A:692:LEU:O	1:A:696:VAL:N	2.41	0.52
1:A:712:GLY:HA2	1:A:789:LEU:CB	2.40	0.52
1:A:2395:LYS:O	1:A:2398:GLY:N	2.41	0.52
1:B:880:ALA:C	1:B:882:GLY:H	2.18	0.52
1:B:2466:MET:HE2	1:B:2466:MET:CA	2.40	0.52
1:A:111:ALA:HB1	1:A:205:ILE:HA	1.91	0.52
2:D:582:ARG:C	2:D:584:GLN:H	2.18	0.52
1:A:2058:MET:O	1:A:2061:GLN:N	2.42	0.52
1:B:1116:PRO:O	1:B:1120:ALA:N	2.42	0.52
1:B:1068:LEU:O	1:B:1072:PHE:N	2.43	0.51
1:B:1657:HIS:O	1:B:1660:SER:OG	2.23	0.51
1:A:602:HIS:O	1:A:604:ASP:N	2.43	0.51
1:A:1198:CYS:O	1:A:1199:PHE:C	2.53	0.51
1:A:1407:TYR:CB	1:A:1414:GLN:HA	2.41	0.51
2:C:499:GLY:HA3	2:C:534:GLY:HA2	1.93	0.51
1:A:831:ILE:O	1:A:835:LEU:N	2.34	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1517:MET:HE3	1:A:1521:ASP:CB	2.41	0.51
1:B:2466:MET:HE2	1:B:2466:MET:N	2.26	0.51
1:A:227:LEU:CB	2:C:407:ALA:HB1	2.41	0.51
2:D:614:ALA:N	2:D:623:LEU:HD11	2.25	0.51
1:A:341:LEU:HA	1:A:344:ALA:HB3	1.92	0.51
2:D:582:ARG:O	2:D:584:GLN:N	2.43	0.51
1:A:237:LEU:O	1:A:238:GLU:C	2.55	0.50
1:A:2072:PHE:HB3	1:A:2090:MET:HE3	1.93	0.50
1:A:329:PHE:C	1:A:378:ALA:HB2	2.37	0.50
1:A:822:VAL:C	1:A:824:PHE:H	2.19	0.50
1:B:2422:LYS:O	1:B:2423:VAL:C	2.54	0.50
1:B:1198:CYS:O	1:B:1199:PHE:C	2.55	0.49
1:B:2475:ASP:HB3	1:B:2497:CYS:SG	2.52	0.49
1:A:1280:ASP:O	1:A:1281:LEU:C	2.55	0.49
1:A:1403:ALA:O	1:A:1406:ALA:HB3	2.12	0.49
1:B:1715:LEU:CA	1:B:1718:ALA:HB3	2.41	0.49
2:D:734:ASP:O	2:D:735:LYS:C	2.54	0.49
2:C:716:THR:O	2:C:717:VAL:C	2.55	0.49
1:A:659:ALA:HB3	1:A:671:CYS:CB	2.42	0.49
1:B:93:LYS:C	1:B:95:SER:N	2.69	0.49
1:A:1403:ALA:O	1:A:1407:TYR:N	2.45	0.49
2:D:412:GLN:HA	2:D:490:GLY:H	1.77	0.49
1:B:798:ASP:C	1:B:800:THR:H	2.20	0.49
1:B:2566:SER:OG	1:B:2567:LYS:N	2.45	0.49
2:D:390:ALA:O	2:D:391:ARG:C	2.55	0.49
1:B:2181:ALA:HB2	1:B:2369:PRO:O	2.13	0.49
1:B:1678:LYS:O	1:B:1681:ALA:HB3	2.12	0.48
1:A:23:PRO:O	1:A:26:TYR:N	2.47	0.48
1:A:611:THR:CB	1:A:614:ALA:HB2	2.43	0.48
1:A:1362:GLY:O	1:A:1364:ILE:N	2.45	0.48
1:A:329:PHE:O	1:A:378:ALA:HB2	2.13	0.48
1:B:1144:GLY:O	1:B:1147:ASP:N	2.46	0.48
1:B:798:ASP:O	1:B:800:THR:N	2.46	0.48
1:B:124:CYS:O	1:B:125:GLU:C	2.56	0.48
1:B:1164:PRO:C	1:B:1166:HIS:H	2.22	0.48
2:D:432:GLN:O	2:D:433:ALA:C	2.57	0.48
1:A:2316:GLY:O	1:A:2319:GLY:N	2.38	0.48
2:C:500:VAL:N	2:C:534:GLY:HA2	2.28	0.48
1:B:1749:LEU:O	1:B:1752:VAL:N	2.46	0.48
1:B:760:ALA:CB	1:B:802:VAL:HA	2.43	0.47
1:B:2561:PRO:HA	1:B:2583:VAL:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1645:SER:OG	1:A:1650:ALA:O	2.31	0.47
2:C:499:GLY:CA	2:C:534:GLY:HA2	2.44	0.47
1:A:1657:HIS:O	1:A:1660:SER:OG	2.28	0.47
2:C:620:ALA:O	2:C:623:LEU:HD23	2.14	0.47
2:D:432:GLN:O	2:D:435:GLN:N	2.48	0.47
1:A:360:GLY:HA2	1:A:363:SER:O	2.14	0.47
1:A:1279:THR:O	1:A:1280:ASP:C	2.57	0.47
1:A:2604:LYS:O	1:A:2606:ARG:N	2.48	0.47
2:D:373:SER:C	2:D:375:LEU:H	2.23	0.47
1:A:1429:ASP:C	1:A:1439:GLY:HA3	2.39	0.47
1:A:108:LEU:O	1:A:111:ALA:HB3	2.15	0.47
1:A:856:HIS:O	1:A:860:SER:N	2.35	0.46
1:A:2615:SER:O	1:A:2618:GLY:N	2.49	0.46
1:B:233:GLY:O	1:B:248:ALA:HB1	2.15	0.46
2:C:666:LEU:HD23	2:C:666:LEU:C	2.41	0.46
1:B:862:ASN:HD21	1:B:864:GLU:CB	2.29	0.46
1:B:1365:ASP:O	1:B:1366:PRO:C	2.58	0.46
1:B:2332:LEU:O	1:B:2335:ASP:N	2.49	0.46
1:A:1442:LEU:O	1:A:1445:ARG:N	2.40	0.46
1:B:798:ASP:C	1:B:800:THR:N	2.73	0.46
1:A:692:LEU:O	1:A:695:LYS:N	2.48	0.46
1:B:760:ALA:HB1	1:B:802:VAL:HA	1.98	0.46
1:B:1843:SER:O	1:B:1844:TYR:C	2.58	0.46
1:A:1015:ARG:HA	1:A:1025:ARG:CB	2.45	0.46
1:B:1506:LEU:HD23	1:B:1506:LEU:C	2.41	0.46
2:D:727:LEU:O	2:D:731:SER:N	2.49	0.46
1:A:1760:HIS:HA	1:A:1763:ARG:O	2.16	0.45
1:A:329:PHE:CB	1:A:378:ALA:HB2	2.45	0.45
1:A:1285:LEU:O	1:A:1286:GLN:C	2.59	0.45
1:A:2530:GLY:O	1:A:2531:LEU:C	2.58	0.45
1:A:802:VAL:O	1:A:803:LYS:C	2.58	0.45
1:A:1455:GLU:HA	1:A:1458:LEU:CB	2.47	0.45
1:A:1860:LEU:HD23	1:A:1860:LEU:C	2.41	0.45
1:B:2523:MET:HE1	1:B:2532:PHE:CD1	2.51	0.45
2:D:554:GLY:H	2:D:557:GLN:CB	2.29	0.45
1:A:117:HIS:O	1:A:120:HIS:N	2.49	0.45
1:B:2527:GLY:O	1:B:2528:THR:C	2.59	0.45
1:A:625:SER:C	1:A:628:TYR:H	2.24	0.45
1:B:634:SER:CB	1:B:667:ILE:HA	2.47	0.45
1:B:1447:PRO:O	1:B:1451:ARG:N	2.50	0.45
2:C:680:CYS:SG	2:C:682:CYS:N	2.87	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:508:SER:O	1:A:509:HIS:C	2.60	0.45
1:B:1815:ASP:CG	1:B:1818:ALA:HB3	2.41	0.45
1:B:2277:HIS:C	1:B:2279:ASN:H	2.25	0.45
1:A:636:CYS:O	1:A:640:LEU:N	2.45	0.45
1:A:2477:HIS:O	1:A:2478:GLY:C	2.57	0.45
1:A:123:ILE:O	1:A:124:CYS:C	2.55	0.44
1:B:140:ALA:HB2	2:D:667:GLY:O	2.17	0.44
2:C:725:LEU:HA	2:C:772:ALA:HB1	1.99	0.44
1:B:198:SER:O	1:B:199:MET:C	2.60	0.44
1:B:880:ALA:C	1:B:882:GLY:N	2.75	0.44
1:B:1360:GLU:OE1	1:B:1360:GLU:HA	2.16	0.44
1:B:1945:LEU:HA	3:B:2703:A1EIE:N31	2.32	0.44
1:B:2520:VAL:O	1:B:2521:ASN:C	2.59	0.44
1:A:1405:LEU:C	1:A:1405:LEU:HD23	2.43	0.44
1:B:1922:GLU:O	1:B:1926:GLN:N	2.47	0.44
1:B:452:LYS:O	1:B:530:VAL:HA	2.18	0.44
1:B:1573:LEU:O	1:B:1577:SER:OG	2.29	0.44
1:A:1454:LEU:O	1:A:1457:HIS:N	2.50	0.44
1:B:1941:TYR:C	1:B:1943:ALA:H	2.26	0.44
1:A:1907:LEU:O	1:A:1908:LEU:C	2.60	0.44
1:A:1088:GLN:CD	1:A:1088:GLN:N	2.76	0.44
1:B:570:TYR:O	1:B:573:LEU:N	2.51	0.44
1:B:1259:PRO:C	1:B:1262:LYS:H	2.26	0.44
1:A:14:ALA:CB	1:A:33:PRO:HA	2.48	0.44
1:B:917:ALA:C	1:B:919:SER:H	2.26	0.44
1:B:624:ILE:O	1:B:627:SER:N	2.50	0.44
1:A:1389:ASP:O	1:A:1392:PHE:N	2.51	0.43
1:A:2370:LEU:H	1:A:2375:GLY:CA	2.26	0.43
1:B:1931:ALA:O	1:B:1932:ARG:C	2.61	0.43
1:A:453:HIS:HA	1:A:531:VAL:H	1.83	0.43
1:A:2225:LEU:HD23	1:A:2225:LEU:C	2.42	0.43
1:B:2299:MET:CA	1:B:2299:MET:HE2	2.48	0.43
1:A:824:PHE:O	1:A:827:ASN:N	2.51	0.43
1:A:2073:GLY:CA	1:A:2090:MET:HE1	2.47	0.43
1:B:1679:LEU:O	1:B:1680:TYR:C	2.62	0.43
2:C:382:ALA:CA	2:C:419:PHE:HA	2.45	0.43
1:A:698:ASP:CB	1:A:703:VAL:HB	2.48	0.43
1:A:1120:ALA:O	1:A:1121:ASP:C	2.60	0.43
1:A:1146:GLU:N	1:A:1146:GLU:CD	2.76	0.43
1:A:2383:THR:HA	1:A:2483:PHE:O	2.19	0.43
1:A:1864:ILE:O	1:A:1865:LYS:C	2.61	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:182:LEU:O	1:B:183:ASP:C	2.62	0.43
1:B:549:SER:O	1:B:553:SER:N	2.50	0.43
1:A:329:PHE:CA	1:A:378:ALA:HB2	2.48	0.43
1:A:1645:SER:O	1:A:1648:SER:N	2.51	0.43
1:A:1831:ILE:O	1:A:1832:VAL:C	2.61	0.43
2:D:417:VAL:HA	2:D:420:LEU:CD1	2.48	0.43
2:C:385:GLY:HA2	2:C:415:GLY:CA	2.49	0.43
1:A:117:HIS:O	1:A:118:LEU:C	2.62	0.43
1:A:2058:MET:HA	1:A:2061:GLN:CB	2.49	0.43
1:B:573:LEU:O	1:B:577:GLN:N	2.49	0.43
1:A:394:GLY:O	1:A:395:PRO:C	2.61	0.43
1:B:2410:MET:HE3	1:B:2411:LEU:O	2.18	0.43
1:B:2633:LEU:O	1:B:2636:MET:N	2.49	0.43
1:A:819:ASP:O	1:A:822:VAL:O	2.35	0.42
1:B:470:ALA:HB2	1:B:496:VAL:CB	2.48	0.42
1:B:2453:SER:OG	1:B:2488:GLY:HA3	2.19	0.42
2:D:666:LEU:C	2:D:666:LEU:HD23	2.44	0.42
1:A:1651:TYR:O	1:A:1654:ALA:HB3	2.19	0.42
1:A:642:LEU:O	1:A:643:PHE:C	2.63	0.42
1:B:2086:SER:O	1:B:2087:MET:C	2.61	0.42
1:B:2332:LEU:O	1:B:2333:ARG:C	2.61	0.42
1:B:2477:HIS:O	1:B:2478:GLY:C	2.62	0.42
2:D:742:VAL:HA	2:D:745:LEU:CB	2.49	0.42
1:A:1895:ARG:CZ	1:A:2357:ARG:NH2	2.83	0.42
1:A:1964:TRP:O	1:A:1965:SER:C	2.63	0.42
1:B:825:SER:CB	1:B:872:THR:HA	2.49	0.42
1:B:1744:LEU:O	1:B:1747:GLY:N	2.52	0.42
1:A:979:ALA:O	1:A:983:ASP:N	2.49	0.42
1:A:1062:ILE:HD12	1:A:1062:ILE:HA	1.83	0.42
1:A:1350:ALA:O	1:A:1351:ARG:C	2.62	0.42
1:B:1341:LYS:HA	1:B:1341:LYS:HD3	1.87	0.42
1:B:2279:ASN:O	1:B:2283:HIS:HB2	2.19	0.42
1:B:2133:LEU:HD23	1:B:2133:LEU:HA	1.79	0.42
2:C:709:ARG:H	2:C:709:ARG:HG2	1.42	0.42
1:A:1907:LEU:O	1:A:1910:LEU:N	2.52	0.42
1:A:1944:LEU:O	1:A:1947:ALA:HB3	2.18	0.42
1:A:2259:LEU:HD12	1:A:2259:LEU:HA	1.82	0.42
1:B:1425:LEU:HA	1:B:1428:TYR:O	2.19	0.42
1:B:1484:GLY:HA2	1:B:1490:TRP:HA	2.01	0.42
1:B:1690:ALA:HA	3:B:2701:A1EIE:C3	2.49	0.42
2:D:410:LEU:O	2:D:411:CYS:C	2.63	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:566:LYS:O	2:D:570:LYS:HG2	2.19	0.42
1:A:292:GLU:O	1:A:295:LEU:N	2.53	0.42
1:A:1694:ALA:HA	3:B:2703:A1EIE:C9	2.50	0.42
1:A:2073:GLY:HA2	1:A:2090:MET:HE1	2.02	0.42
1:B:380:LEU:HD23	1:B:380:LEU:C	2.44	0.42
1:B:1742:SER:OG	1:B:1743:MET:N	2.52	0.42
1:B:1894:TYR:O	1:B:1895:ARG:C	2.62	0.42
1:B:1325:SER:O	1:B:1326:GLU:C	2.62	0.42
1:B:1736:TYR:CD1	1:B:1766:TRP:HZ3	2.38	0.42
1:A:193:PRO:O	1:A:194:LEU:C	2.63	0.41
1:A:218:ALA:HA	2:C:718:ARG:HH22	1.85	0.41
1:A:1120:ALA:O	1:A:1123:LEU:N	2.53	0.41
1:A:1198:CYS:O	1:A:1201:ARG:N	2.53	0.41
1:A:1358:LEU:HD23	1:A:1358:LEU:HA	1.76	0.41
1:A:2097:TYR:CD2	1:A:2122:ILE:HD12	2.55	0.41
1:A:2560:ASP:OD1	1:A:2562:LEU:N	2.53	0.41
1:B:1242:ARG:C	1:B:1244:ALA:H	2.28	0.41
1:B:1341:LYS:O	1:B:1344:GLN:N	2.44	0.41
1:B:1736:TYR:CE1	1:B:1766:TRP:HZ3	2.37	0.41
1:B:2462:ALA:HB2	1:B:2532:PHE:CD1	2.55	0.41
1:A:119:LEU:O	1:A:120:HIS:C	2.61	0.41
1:A:1480:LEU:HA	1:A:1480:LEU:HD23	1.77	0.41
1:A:1703:LYS:HB3	1:A:1703:LYS:HE2	1.80	0.41
1:A:2058:MET:O	1:A:2059:GLU:C	2.64	0.41
1:A:2120:GLY:O	1:A:2124:LYS:HG3	2.19	0.41
1:B:380:LEU:HD21	1:B:469:LYS:CB	2.50	0.41
1:B:776:SER:CB	1:B:817:ASP:HB2	2.50	0.41
1:B:1897:LYS:O	1:B:1901:LEU:HD12	2.19	0.41
1:B:1949:GLU:O	1:B:1950:SER:C	2.61	0.41
1:B:2005:LEU:HD11	1:B:2009:PHE:CE1	2.55	0.41
1:A:1912:LYS:HD2	1:A:1912:LYS:HA	1.71	0.41
1:A:2198:LEU:O	1:A:2202:ILE:HG12	2.20	0.41
1:A:2382:ASN:O	1:A:2484:ASP:HA	2.20	0.41
1:A:2550:LEU:O	1:A:2553:VAL:HG22	2.20	0.41
1:A:2597:GLN:O	1:A:2600:GLN:N	2.53	0.41
2:D:680:CYS:HB3	2:D:682:CYS:H	1.84	0.41
1:A:455:ASP:HA	1:A:533:THR:N	2.32	0.41
1:A:1985:PRO:C	1:A:1987:ASN:H	2.25	0.41
1:B:89:SER:CB	1:B:92:ALA:HB3	2.50	0.41
1:B:2221:LYS:HE3	1:B:2245:MET:CB	2.50	0.41
2:C:747:GLN:H	2:C:747:GLN:CD	2.28	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1068:LEU:C	1:A:1070:GLN:N	2.79	0.41
1:A:2359:GLU:HG3	1:A:2359:GLU:O	2.21	0.41
1:B:1198:CYS:O	1:B:1201:ARG:N	2.54	0.41
1:B:1651:TYR:O	1:B:1654:ALA:HB3	2.21	0.41
1:B:2167:VAL:O	1:B:2170:ALA:N	2.53	0.41
1:B:2325:MET:HB2	1:B:2379:TRP:CE3	2.55	0.41
1:A:217:ILE:HD12	1:A:217:ILE:HA	1.87	0.41
1:A:241:SER:O	1:A:242:PRO:C	2.64	0.41
1:A:1379:LYS:HZ1	1:A:1839:PHE:C	2.28	0.41
1:A:1778:ALA:O	1:A:1781:LEU:N	2.54	0.41
1:A:1951:ARG:O	1:A:1952:LEU:C	2.63	0.41
1:B:89:SER:O	1:B:92:ALA:N	2.54	0.41
1:B:1404:TYR:CB	1:B:1417:ALA:CB	2.98	0.41
2:C:389:VAL:O	2:C:392:ASN:OD1	2.38	0.41
2:C:499:GLY:HA3	2:C:534:GLY:CA	2.50	0.41
2:C:707:PRO:HG2	2:C:709:ARG:HH22	1.85	0.41
1:A:246:SER:CB	1:A:291:TYR:HA	2.51	0.41
1:A:2224:GLU:O	1:A:2228:LYS:N	2.54	0.41
1:B:1259:PRO:O	1:B:1262:LYS:N	2.53	0.41
1:B:1936:HIS:O	1:B:1939:THR:N	2.42	0.41
1:B:1948:GLY:O	1:B:1949:GLU:C	2.64	0.41
1:B:2134:ALA:HB2	1:B:2280:HIS:CE1	2.56	0.41
2:D:698:TRP:O	2:D:701:VAL:HG12	2.20	0.41
1:A:27:ASN:CB	1:A:92:ALA:HB2	2.50	0.41
1:A:120:HIS:O	1:A:123:ILE:N	2.52	0.41
1:A:124:CYS:O	1:A:126:VAL:N	2.54	0.41
1:A:1288:SER:CB	1:A:1307:LEU:HD13	2.51	0.41
1:A:1298:ASP:O	1:A:1302:HIS:ND1	2.42	0.41
1:A:1325:SER:O	1:A:1326:GLU:C	2.63	0.41
1:A:1528:LEU:HD23	1:A:1528:LEU:HA	1.83	0.41
1:A:1644:ALA:O	1:A:1645:SER:C	2.63	0.41
1:A:1759:VAL:HG13	1:A:1766:TRP:HE3	1.86	0.41
1:A:1843:SER:O	1:A:1844:TYR:C	2.64	0.41
1:A:2018:SER:HA	1:A:2045:TYR:OH	2.21	0.41
1:A:2302:ILE:HG21	1:A:2308:LYS:HD3	2.02	0.41
1:A:2441:LEU:HD23	1:A:2441:LEU:HA	1.90	0.41
1:B:380:LEU:HD23	1:B:380:LEU:O	2.21	0.41
1:B:2534:ARG:NE	1:B:2534:ARG:HA	2.35	0.41
1:A:1893:SER:OG	1:A:1895:ARG:HG2	2.21	0.41
1:B:1976:LEU:HD22	1:B:2005:LEU:HD23	2.03	0.41
1:B:1994:LYS:H	1:B:1994:LYS:HD3	1.87	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:218:ALA:HA	2:C:718:ARG:NH2	2.36	0.40
1:A:314:GLU:O	1:A:317:TYR:N	2.54	0.40
1:A:1348:SER:O	1:A:1349:GLN:C	2.63	0.40
1:A:1741:LYS:NZ	1:A:1741:LYS:HB3	2.36	0.40
1:B:2458:CYS:SG	1:B:2523:MET:HG2	2.61	0.40
1:A:11:MET:HA	1:A:14:ALA:HB3	2.03	0.40
1:A:139:PRO:HB2	2:C:667:GLY:O	2.22	0.40
1:A:308:GLU:O	1:A:311:ARG:N	2.49	0.40
1:A:577:GLN:O	1:A:581:SER:HA	2.20	0.40
1:A:658:TRP:O	1:A:661:GLN:N	2.55	0.40
1:A:822:VAL:C	1:A:824:PHE:N	2.79	0.40
1:A:1376:THR:O	1:A:1377:GLN:C	2.63	0.40
1:B:93:LYS:O	1:B:96:CYS:N	2.55	0.40
1:B:227:LEU:N	1:B:227:LEU:HD23	2.36	0.40
1:B:1976:LEU:HD12	1:B:1976:LEU:HA	1.78	0.40
1:B:2177:TRP:CZ2	1:B:2261:PRO:HD3	2.56	0.40
1:B:2514:ARG:O	1:B:2519:MET:HE1	2.21	0.40
1:A:2145:LEU:HD22	1:A:2160:LEU:HD12	2.02	0.40
1:A:2272:SER:OG	1:A:2273:ILE:N	2.54	0.40
1:A:2341:PHE:CE2	1:A:2345:ILE:HD11	2.56	0.40
1:A:2615:SER:O	1:A:2616:ILE:C	2.64	0.40
2:D:754:GLY:O	2:D:758:LEU:HD13	2.21	0.40
1:A:2243:PHE:C	1:A:2245:MET:H	2.28	0.40
1:A:2370:LEU:HD22	1:A:2370:LEU:HA	1.96	0.40
1:A:2605:THR:HB	1:A:2607:ASN:OD1	2.22	0.40
1:B:93:LYS:O	1:B:95:SER:N	2.55	0.40
1:B:1388:GLU:H	1:B:1388:GLU:HG3	1.72	0.40
2:D:333:LEU:O	2:D:379:GLN:HA	2.21	0.40
2:D:405:ARG:HB3	2:D:406:ARG:NH2	2.37	0.40
2:D:632:LEU:O	2:D:633:LEU:CB	2.68	0.40
2:D:728:HIS:CG	2:D:772:ALA:HA	2.56	0.40
2:D:741:CYS:O	2:D:742:VAL:C	2.64	0.40
2:C:637:MET:HE3	2:C:637:MET:HB3	1.77	0.40
1:A:197:MET:HG2	1:A:197:MET:O	2.22	0.40
1:A:1198:CYS:O	1:A:1200:VAL:N	2.54	0.40
1:B:1083:ILE:O	1:B:1087:TYR:HA	2.21	0.40
1:B:1742:SER:O	1:B:1743:MET:C	2.63	0.40
1:B:2554:LEU:HA	1:B:2554:LEU:HD23	1.88	0.40
2:D:319:GLN:O	2:D:320:PRO:C	2.64	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	2429/2644 (92%)	2300 (95%)	126 (5%)	3 (0%)	48	81
1	B	2463/2644 (93%)	2345 (95%)	109 (4%)	9 (0%)	30	65
2	C	370/791 (47%)	346 (94%)	19 (5%)	5 (1%)	9	39
2	D	356/791 (45%)	327 (92%)	25 (7%)	4 (1%)	11	44
All	All	5618/6870 (82%)	5318 (95%)	279 (5%)	21 (0%)	31	65

All (21) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	603	SER
1	A	1986	GLU
1	B	90	HIS
1	B	1668	ASN
2	D	371	SER
2	D	583	PHE
2	D	426	PHE
2	D	735	LYS
2	C	623	LEU
2	C	730	LEU
1	B	799	GLU
2	C	632	LEU
1	B	94	GLY
1	B	699	ASP
1	B	1460	THR
1	A	983	ASP
1	B	881	LYS
1	B	1461	ARG
2	C	329	LEU
2	C	627	SER
1	B	554	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	A	717/2363 (30%)	708 (99%)	9 (1%)	61	72
1	B	621/2363 (26%)	613 (99%)	8 (1%)	61	72
2	C	91/678 (13%)	88 (97%)	3 (3%)	33	56
2	D	74/678 (11%)	65 (88%)	9 (12%)	5	21
All	All	1503/6082 (25%)	1474 (98%)	29 (2%)	49	67

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1594	HIS
1	A	1771	ASN
1	A	1983	CYS
1	A	2308	LYS
1	A	2311	LYS
1	A	2370	LEU
1	A	2372	ASP
1	A	2479	GLU
1	A	2638	LEU
1	B	718	LEU
1	B	798	ASP
1	B	1493	SER
1	B	1925	LEU
1	B	1926	GLN
1	B	1929	ARG
1	B	1930	VAL
1	B	1959	ARG
2	D	311	ILE
2	D	328	SER
2	D	373	SER
2	D	429	LEU
2	D	492	VAL
2	D	624	CYS
2	D	637	MET

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Mol	Chain	Res	Type
2	D	680	CYS
2	D	682	CYS
2	C	327	LEU
2	C	570	LYS
2	C	709	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1224	HIS
1	A	1258	HIS
1	A	1597	GLN
1	A	1987	ASN
1	A	2361	HIS
1	A	2559	HIS
1	A	2635	GLN
1	B	788	HIS
1	B	1349	GLN
1	B	1672	HIS
1	B	1677	GLN
1	B	1869	GLN
1	B	2137	GLN
1	B	2289	HIS
1	B	2559	HIS
1	B	2585	ASN
2	C	563	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	A1EIE	B	2701	-	36,36,36	0.41	1 (2%)	45,52,52	0.44	1 (2%)
3	A1EIE	B	2703	-	36,36,36	0.37	0	45,52,52	0.40	0
3	A1EIE	A	2701	-	36,36,36	0.40	0	45,52,52	0.52	1 (2%)
3	A1EIE	B	2702	-	36,36,36	0.38	0	45,52,52	0.52	1 (2%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	A1EIE	B	2701	-	-	14/27/27/27	0/4/4/4
3	A1EIE	B	2703	-	-	15/27/27/27	0/4/4/4
3	A1EIE	A	2701	-	-	8/27/27/27	0/4/4/4
3	A1EIE	B	2702	-	-	7/27/27/27	0/4/4/4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	2701	A1EIE	C30-N31	2.03	1.49	1.46

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	2701	A1EIE	C19-C17-N18	-2.54	110.10	115.55
3	B	2702	A1EIE	C19-C17-N18	-2.40	110.41	115.55
3	B	2701	A1EIE	C19-C17-N18	-2.15	110.95	115.55

There are no chirality outliers.

All (44) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	2701	A1EIE	N18-C17-C19-O23
3	A	2701	A1EIE	C1-C2-S4-C7
3	A	2701	A1EIE	C1-C2-S4-O5
3	A	2701	A1EIE	C1-C2-S4-O6
3	A	2701	A1EIE	C3-C2-S4-C7
3	A	2701	A1EIE	C3-C2-S4-O5
3	A	2701	A1EIE	C3-C2-S4-O6
3	B	2701	A1EIE	C16-C17-C19-C20
3	B	2701	A1EIE	C16-C17-C19-O23
3	B	2701	A1EIE	N18-C17-C19-C20
3	B	2701	A1EIE	N18-C17-C19-O23
3	B	2701	A1EIE	C1-C2-S4-C7
3	B	2701	A1EIE	C1-C2-S4-O5
3	B	2701	A1EIE	C1-C2-S4-O6
3	B	2701	A1EIE	C3-C2-S4-O6
3	B	2702	A1EIE	C1-C2-S4-C7
3	B	2702	A1EIE	C1-C2-S4-O6
3	B	2702	A1EIE	C3-C2-S4-C7
3	B	2702	A1EIE	C3-C2-S4-O5
3	B	2702	A1EIE	C3-C2-S4-O6
3	B	2702	A1EIE	C27-C30-N31-C32
3	B	2703	A1EIE	C16-C17-C19-C20
3	B	2703	A1EIE	C16-C17-C19-O23
3	B	2703	A1EIE	N18-C17-C19-C20
3	B	2703	A1EIE	N18-C17-C19-O23
3	B	2703	A1EIE	C1-C2-S4-C7
3	B	2703	A1EIE	C1-C2-S4-O5
3	B	2703	A1EIE	C1-C2-S4-O6
3	B	2703	A1EIE	C3-C2-S4-C7
3	B	2703	A1EIE	C3-C2-S4-O5
3	B	2703	A1EIE	C3-C2-S4-O6
3	B	2703	A1EIE	C27-C30-N31-C32
3	B	2701	A1EIE	C20-C21-C24-C25
3	B	2701	A1EIE	N22-C21-C24-C25
3	B	2701	A1EIE	N22-C21-C24-C29
3	B	2701	A1EIE	C20-C21-C24-C29
3	B	2703	A1EIE	C12-C7-S4-O5
3	B	2701	A1EIE	C3-C2-S4-C7
3	B	2703	A1EIE	C8-C7-S4-O5
3	A	2701	A1EIE	N18-C17-C19-C20
3	B	2702	A1EIE	C1-C2-S4-O5
3	B	2703	A1EIE	C12-C7-S4-C2

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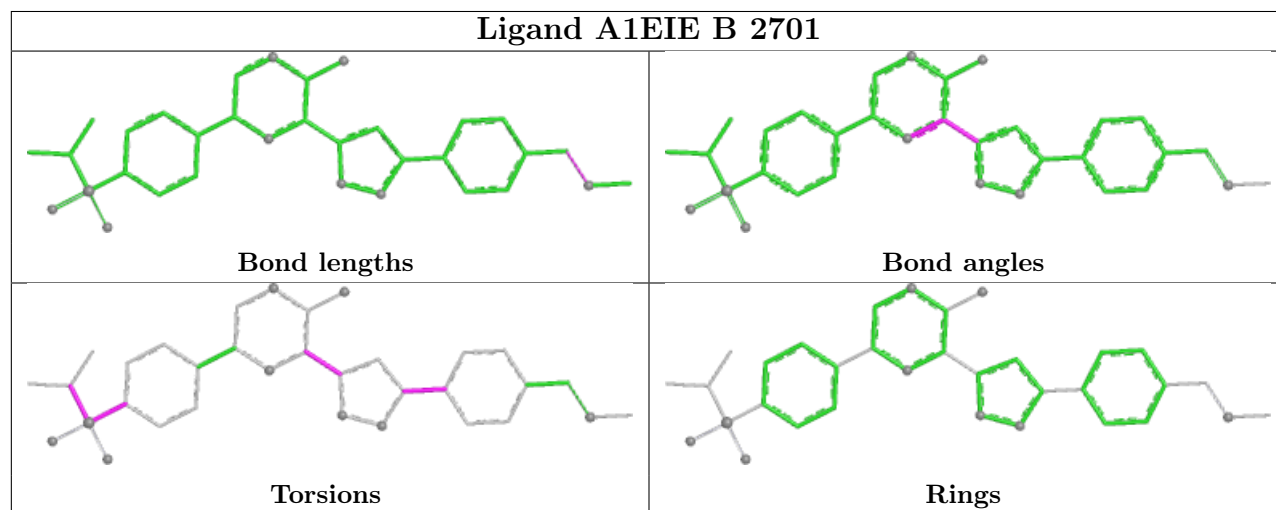
Mol	Chain	Res	Type	Atoms
3	B	2701	A1EIE	C12-C7-S4-O6
3	B	2703	A1EIE	C8-C7-S4-C2

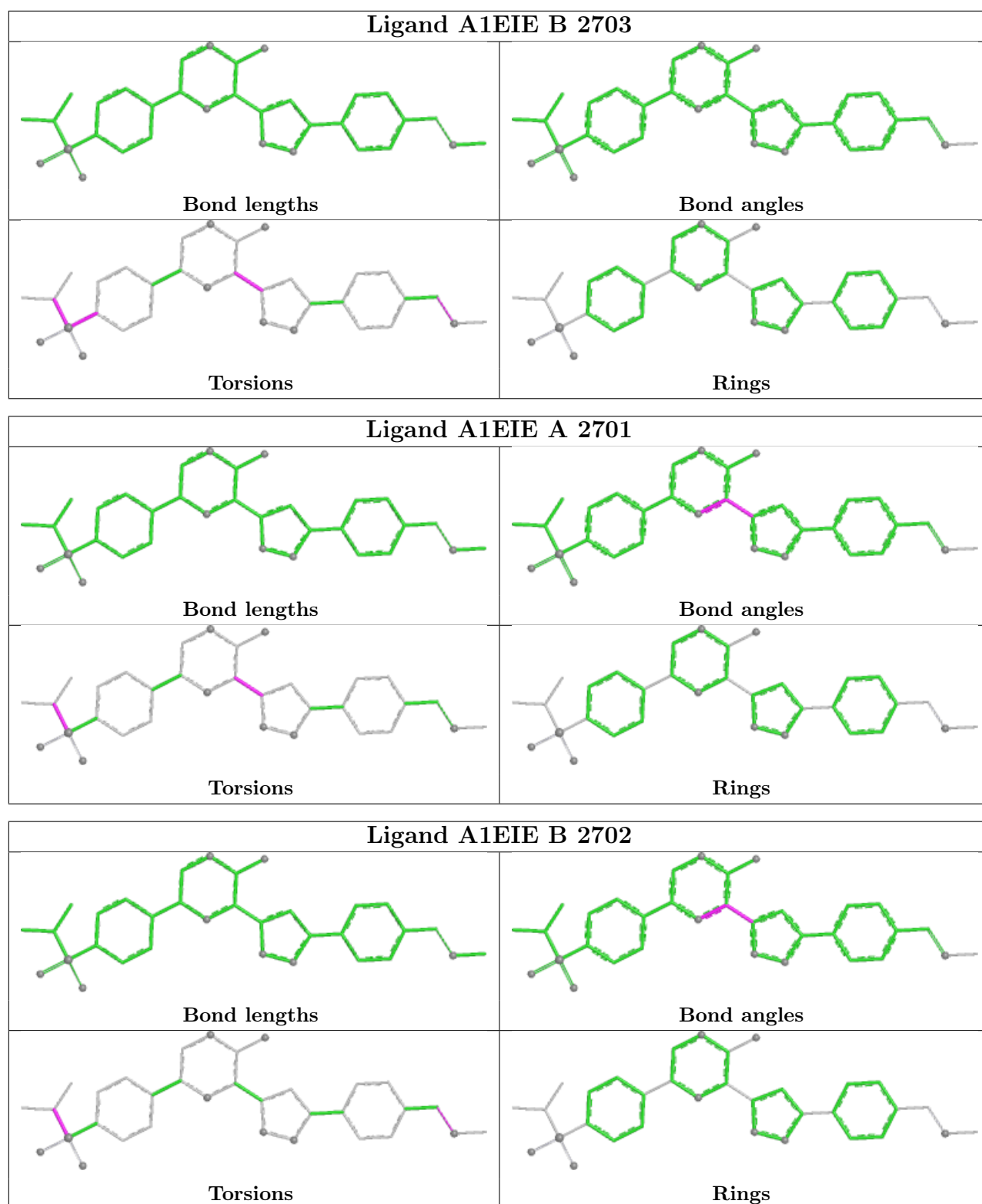
There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	2701	A1EIE	2	0
3	B	2703	A1EIE	3	0

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





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.

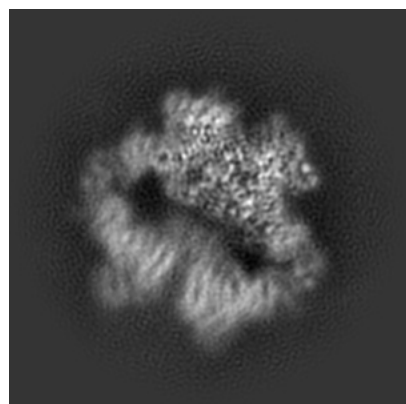
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62806. These allow visual inspection of the internal detail of the map and identification of artifacts.

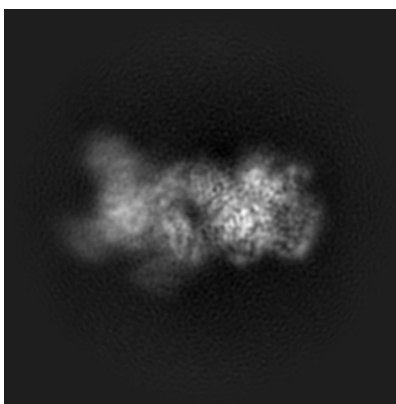
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

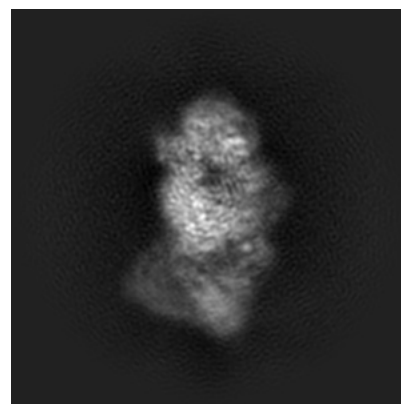
6.1.1 Primary map



X

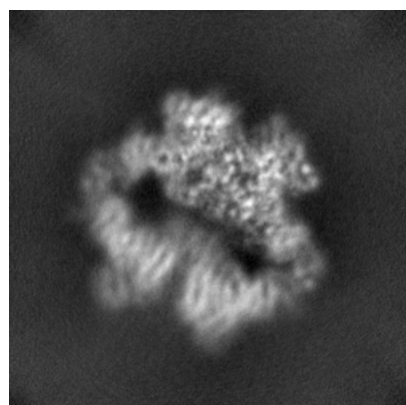


Y

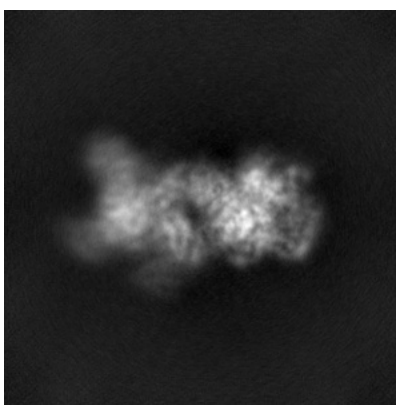


Z

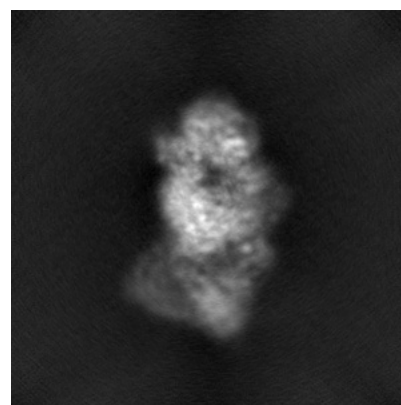
6.1.2 Raw map



X



Y

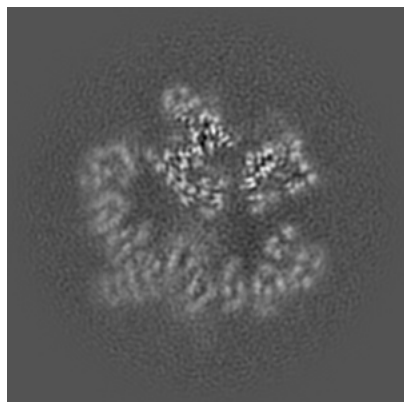


Z

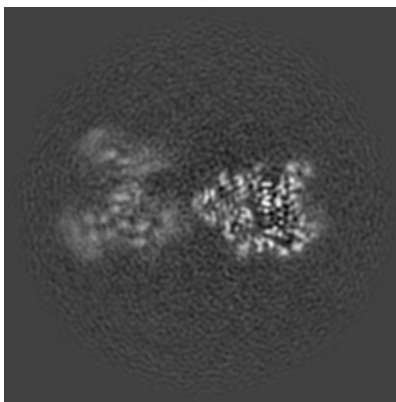
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

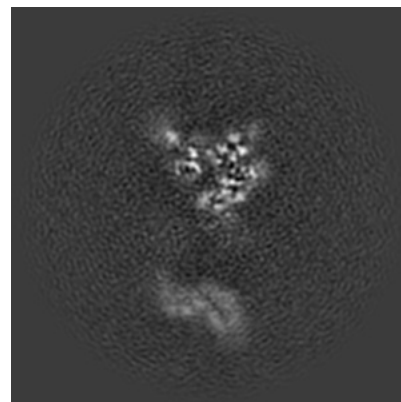
6.2.1 Primary map



X Index: 144

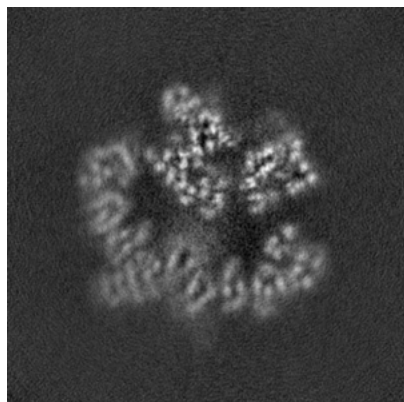


Y Index: 144

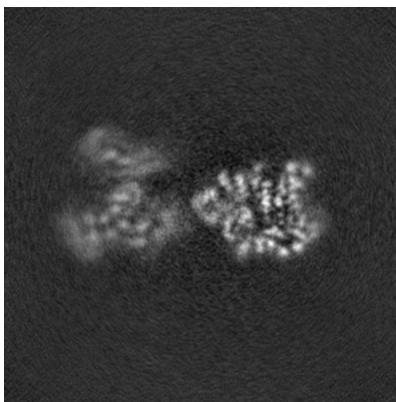


Z Index: 144

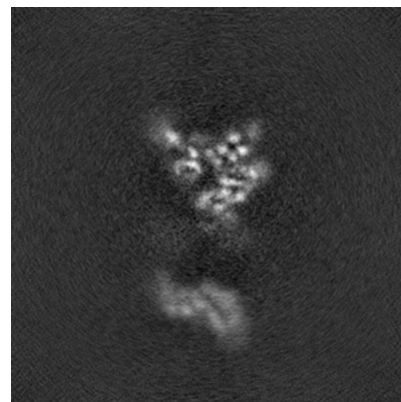
6.2.2 Raw map



X Index: 144



Y Index: 144

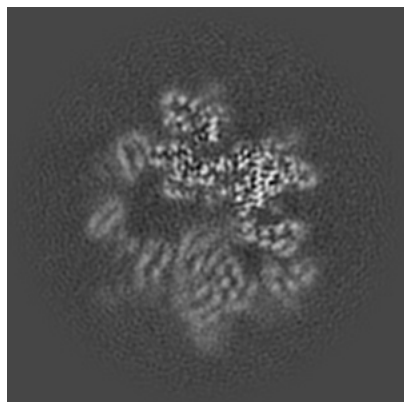


Z Index: 144

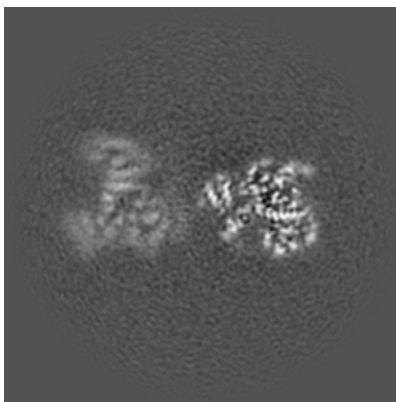
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

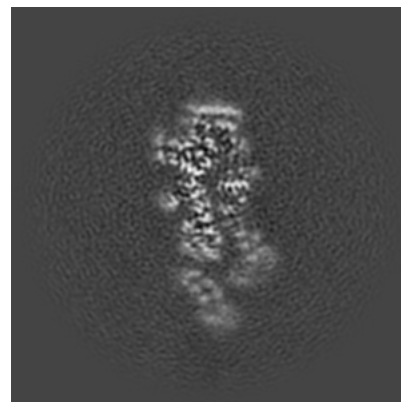
6.3.1 Primary map



X Index: 133

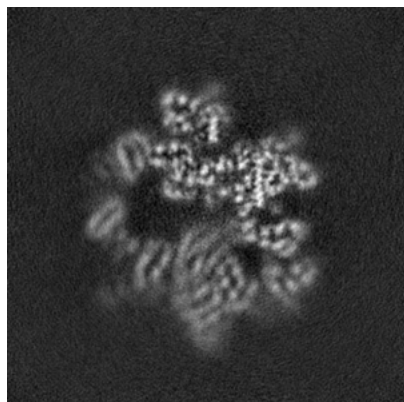


Y Index: 139

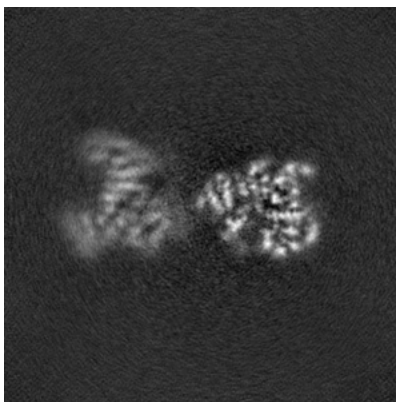


Z Index: 173

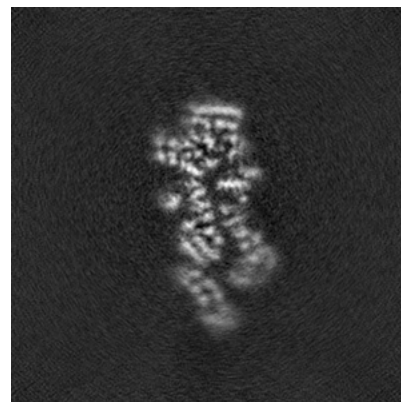
6.3.2 Raw map



X Index: 133



Y Index: 140

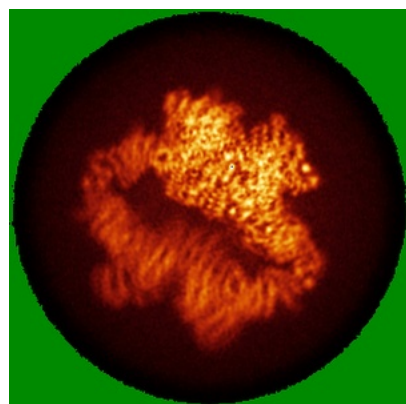


Z Index: 174

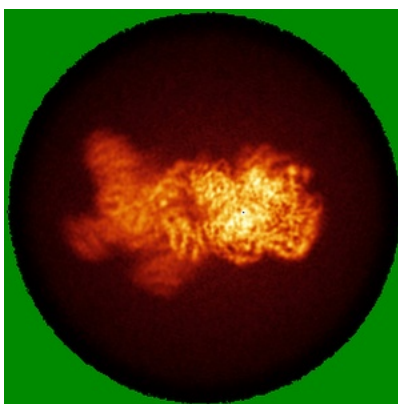
The images above show the largest variance slices of the map in three orthogonal directions.

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

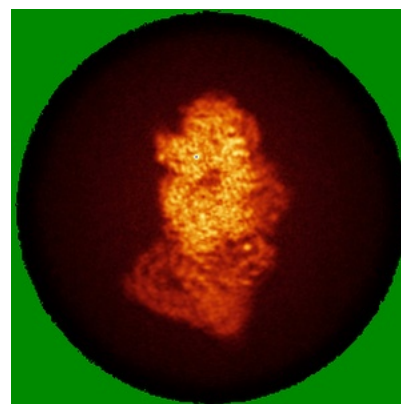
6.4.1 Primary map



X

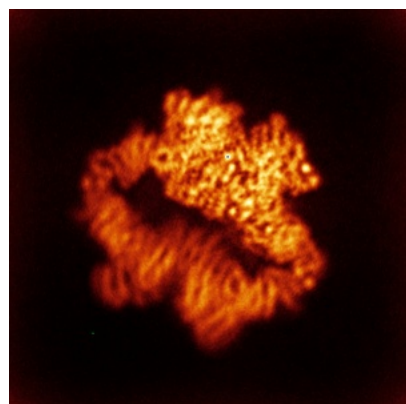


Y

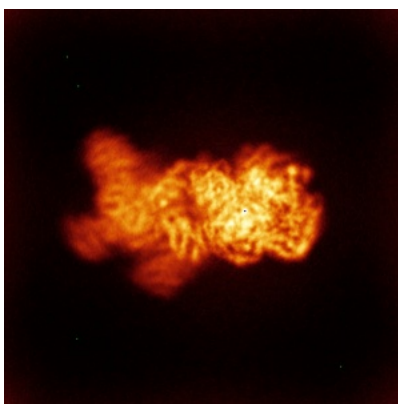


Z

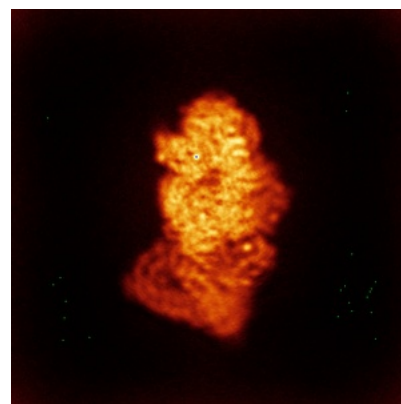
6.4.2 Raw map



X



Y

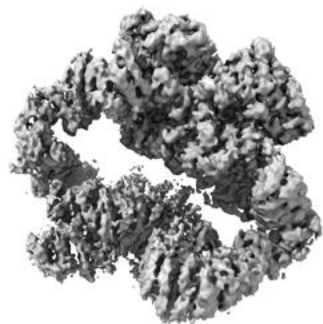


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



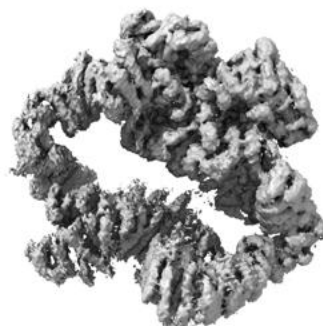
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.255. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X



Y



Z

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

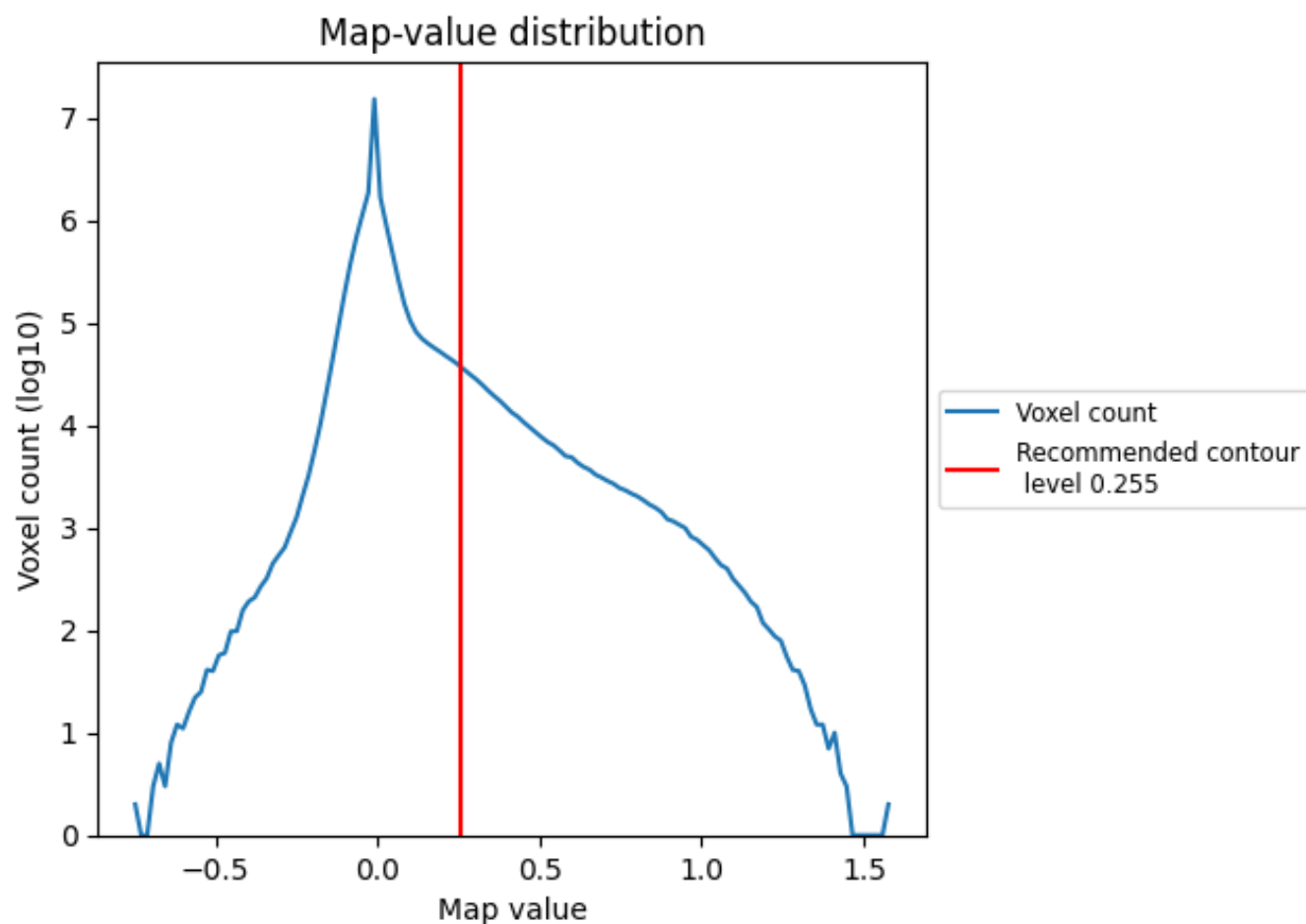
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

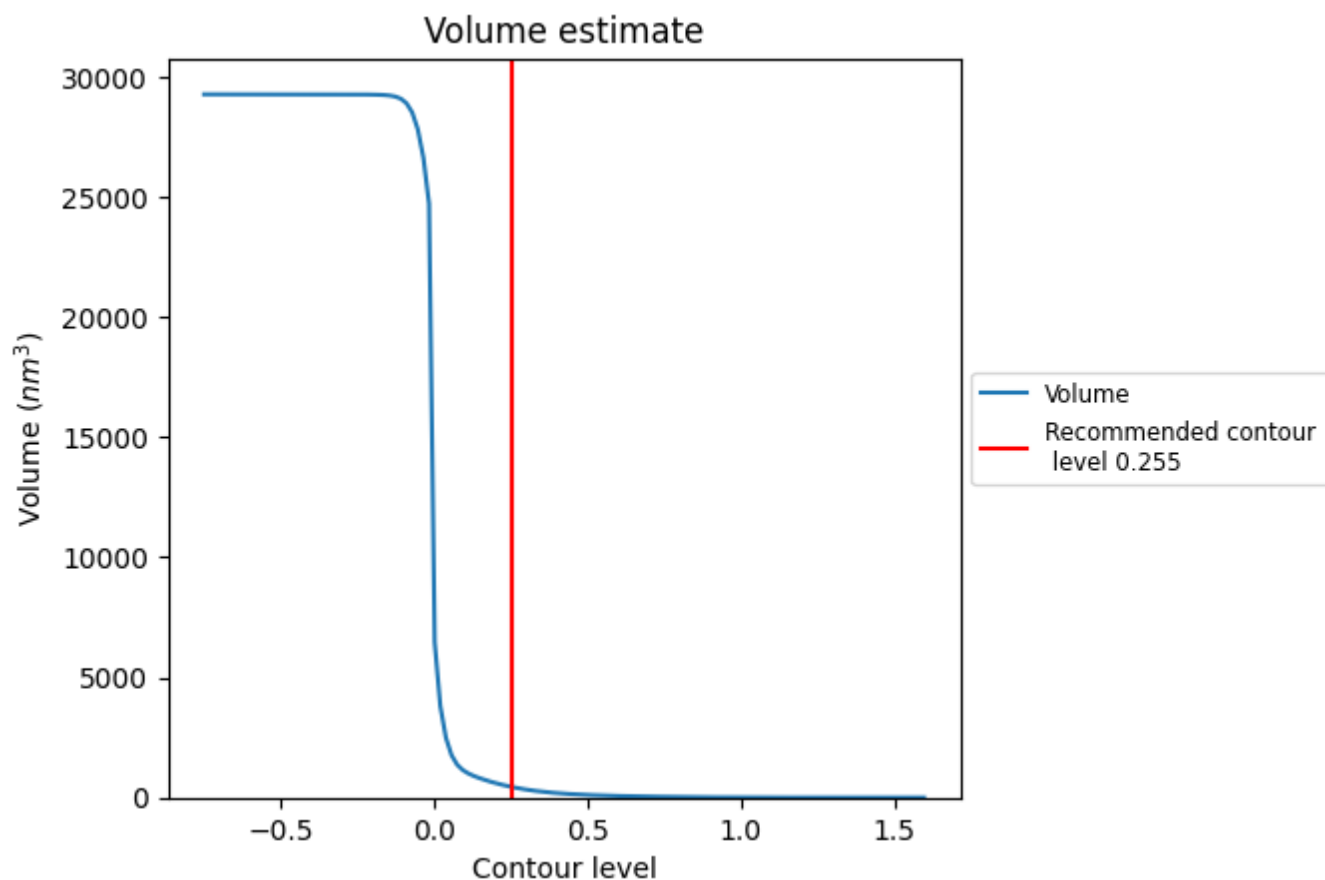
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

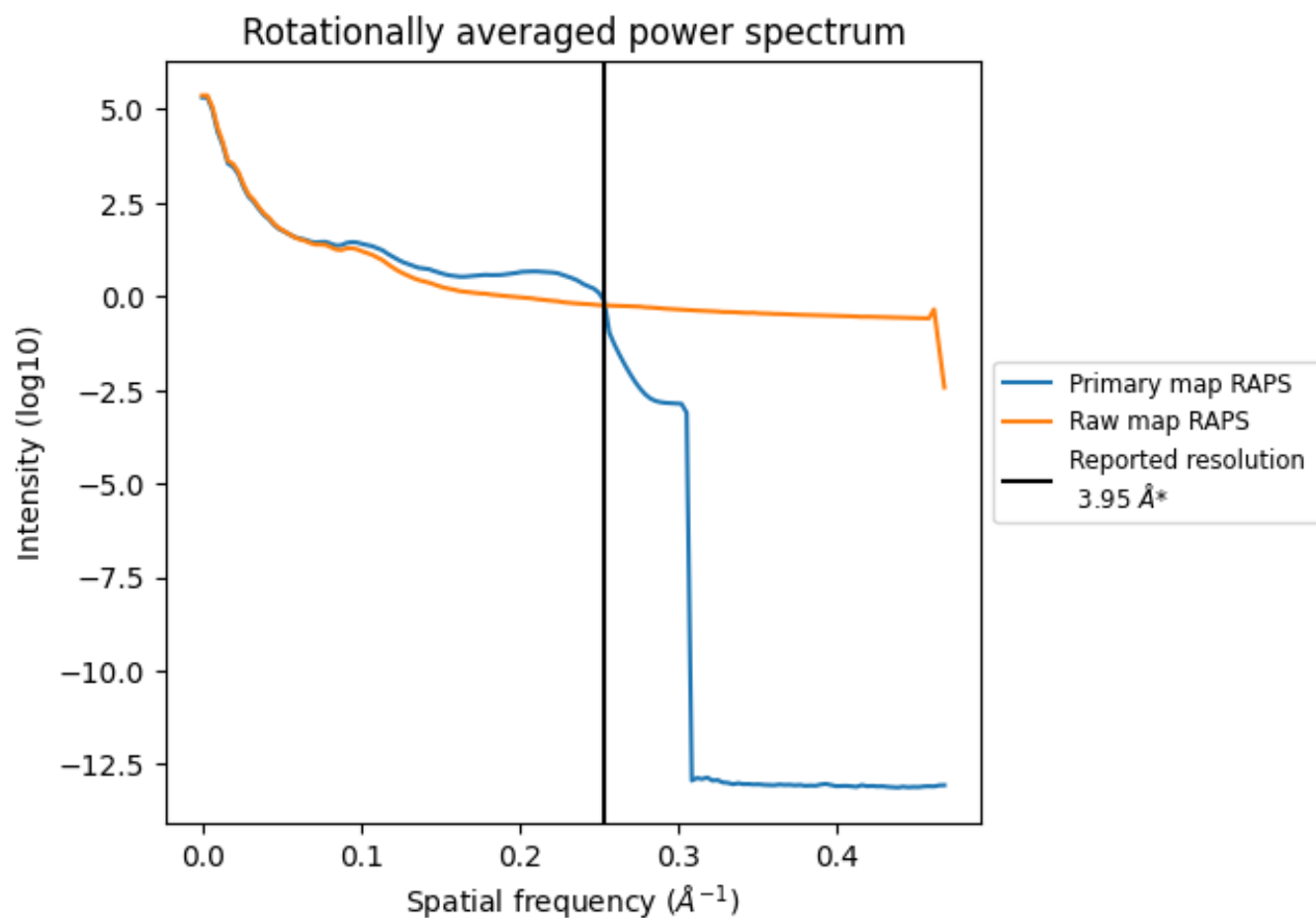
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 438 nm³; this corresponds to an approximate mass of 396 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 ⓘ

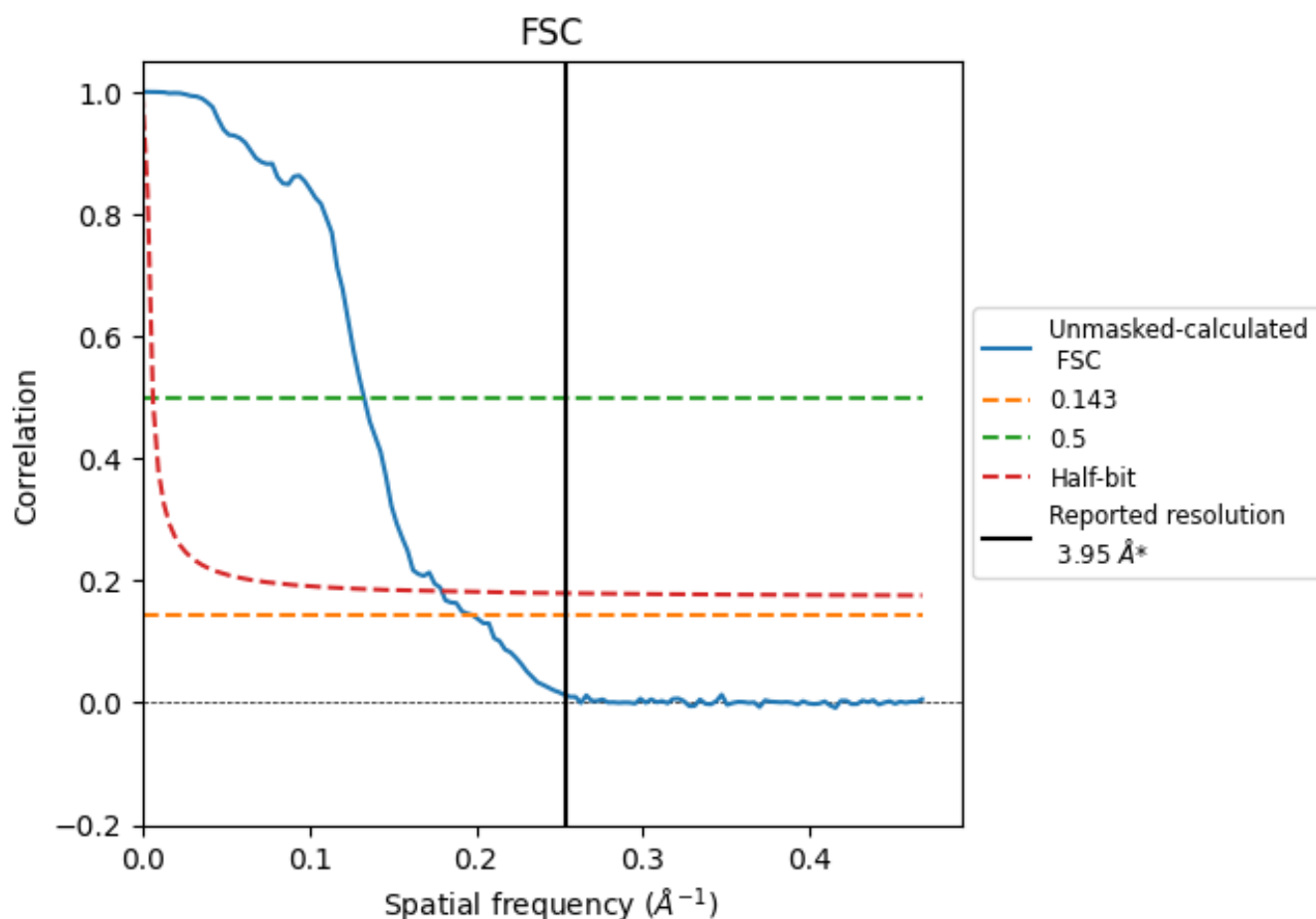


*Reported resolution corresponds to spatial frequency of 0.253 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.253 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

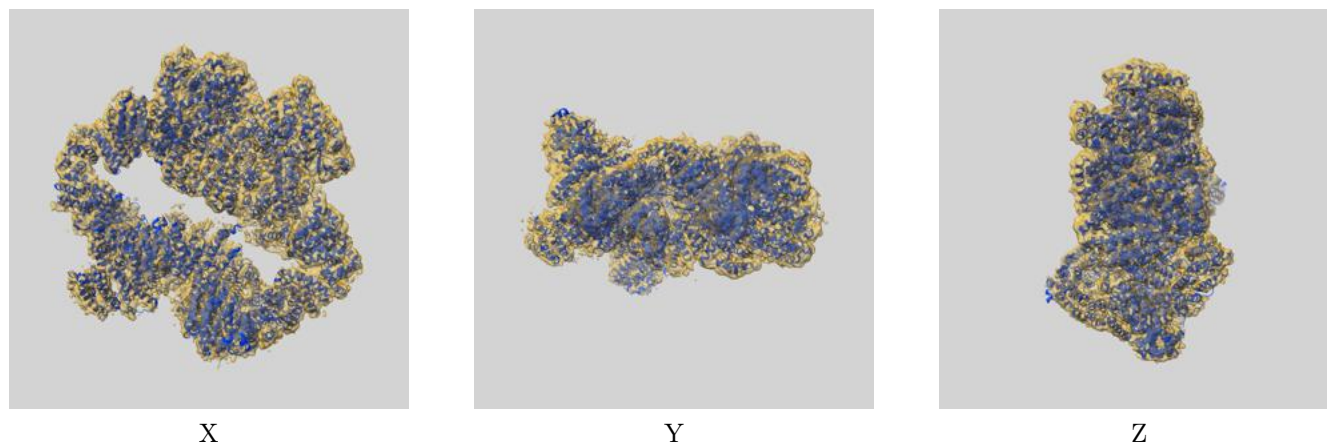
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.95	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	5.05	7.52	5.57

*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 5.05 differs from the reported value 3.95 by more than 10 %

9 Map-model fit [i](#)

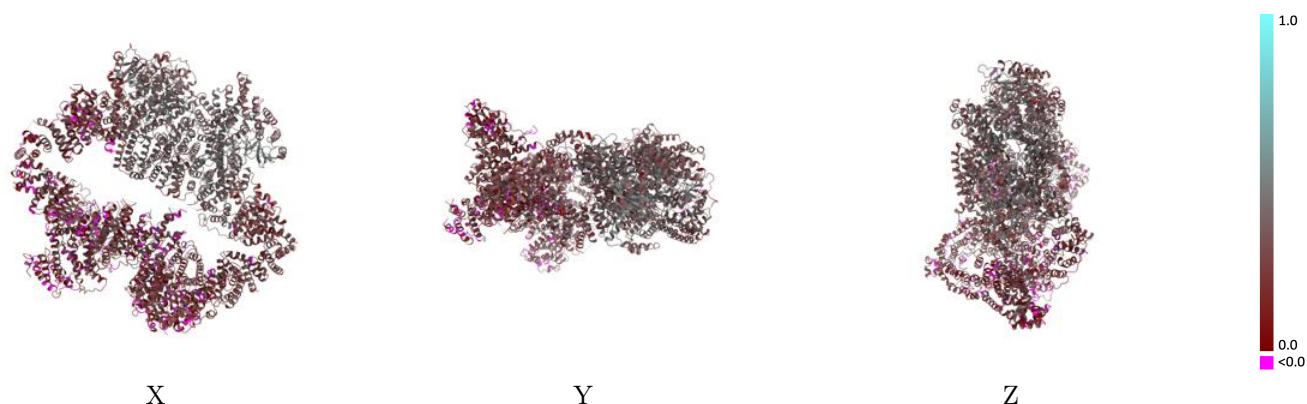
This section contains information regarding the fit between EMDB map EMD-62806 and PDB model 9L45. Per-residue inclusion information can be found in section 3 on page 5.

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.255 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

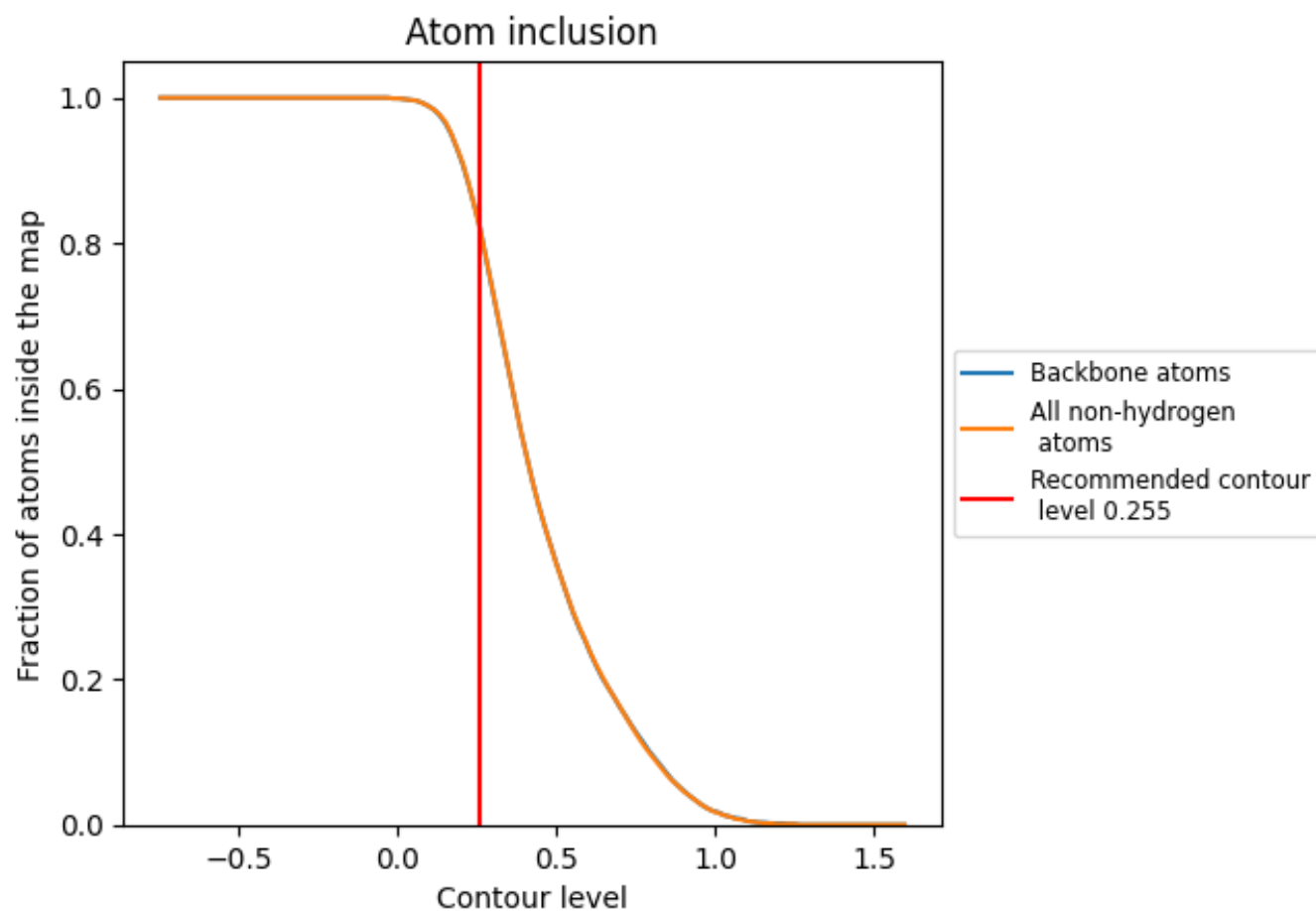


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 83% 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 (0.255) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8270	0.2960
A	0.8820	0.3240
B	0.8150	0.2950
C	0.7110	0.2070
D	0.6090	0.1930

