



wwPDB EM Validation Summary Report ⓘ

Aug 6, 2026 – 07:51 AM JST

PDB ID : 23CP / pdb_000023cp
EMDB ID : EMD-68865
Title : Cryo-EM structure of RSC complex from Chaetomium thermophilum
Authors : Ma, S.S.; Liu, M.D.; Shen, Q.T.; Chen, Y.
Deposited on : 2026-02-01
Resolution : 3.12 Å(reported)

This is a wwPDB EM Validation Summary 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:

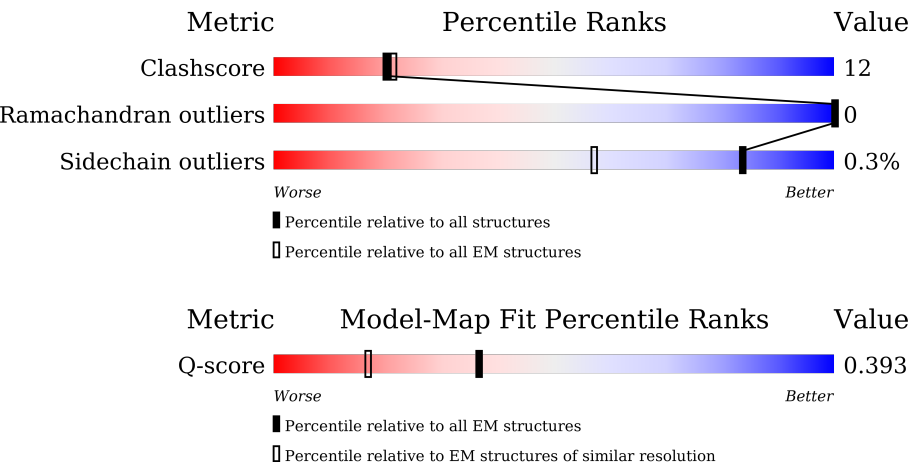
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.12 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	14478 (2.62 - 3.62)

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	29%14%56%
5	R	763	44%10%46%
6	S	607	5%58%8%34%
7	T	534	29%7%65%
8	V	990	29%12%59%
9	U	991	9%6%85%

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 25978 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	161	Total	C	N	O	S	0	0
			1321	824	262	226	9		

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	478	Total	C	N	O	S	0	0
			3758	2347	667	723	21		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	O	354	Total	C	N	O	S	0	0
			2890	1815	514	543	18		

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	376	Total	C	N	O	S	0	0
			3064	1937	547	571	9		

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	338	Total	C	N	O	S	0	0
			2750	1759	495	486	10		

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 Putative chromatin structure-remodeling complex protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	R	413	Total	C	N	O	S	0	0
			3289	2091	565	618	15		

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	269	MET	-	initiating methionine	UNP G0S909
R	444	ILE	ASN	conflict	UNP G0S909
R	601	GLU	ASP	conflict	UNP G0S909
R	741	THR	SER	conflict	UNP G0S909
R	1026	HIS	-	expression tag	UNP G0S909
R	1027	HIS	-	expression tag	UNP G0S909
R	1028	HIS	-	expression tag	UNP G0S909
R	1029	HIS	-	expression tag	UNP G0S909
R	1030	HIS	-	expression tag	UNP G0S909
R	1031	HIS	-	expression tag	UNP G0S909

- Molecule 6 is a protein called Putative chromatin structure-remodeling complex protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	S	399	Total	C	N	O	S	0	0
			3184	2014	565	593	12		

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S	6	ASP	ASN	conflict	UNP G0S475
S	272	ILE	THR	conflict	UNP G0S475
S	600	ASP	-	expression tag	UNP G0S475
S	601	TYR	-	expression tag	UNP G0S475
S	602	LYS	-	expression tag	UNP G0S475
S	603	ASP	-	expression tag	UNP G0S475
S	604	ASP	-	expression tag	UNP G0S475
S	605	ASP	-	expression tag	UNP G0S475
S	606	ASP	-	expression tag	UNP G0S475
S	607	LYS	-	expression tag	UNP G0S475

- Molecule 7 is a protein called Rsc7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	T	189	Total	C	N	O	S	0	0
			1514	954	269	285	6		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
T	527	ASP	-	expression tag	UNP G0S6N5
T	528	TYR	-	expression tag	UNP G0S6N5
T	529	LYS	-	expression tag	UNP G0S6N5
T	530	ASP	-	expression tag	UNP G0S6N5
T	531	ASP	-	expression tag	UNP G0S6N5
T	532	ASP	-	expression tag	UNP G0S6N5
T	533	ASP	-	expression tag	UNP G0S6N5
T	534	LYS	-	expression tag	UNP G0S6N5

- Molecule 8 is a protein called Rsc58.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	V	407	Total	C	N	O	S	0	0
			3070	1916	530	614	10		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
V	300	GLU	ASP	conflict	UNP G0S281
V	612	HIS	PRO	conflict	UNP G0S281
V	985	HIS	-	expression tag	UNP G0S281

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Chain	Residue	Modelled	Actual	Comment	Reference
V	986	HIS	-	expression tag	UNP G0S281
V	987	HIS	-	expression tag	UNP G0S281
V	988	HIS	-	expression tag	UNP G0S281
V	989	HIS	-	expression tag	UNP G0S281
V	990	HIS	-	expression tag	UNP G0S281

- Molecule 9 is a protein called Rsc1.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	U	150	Total	C	N	O	S	0	0
			1135	696	220	218	1		

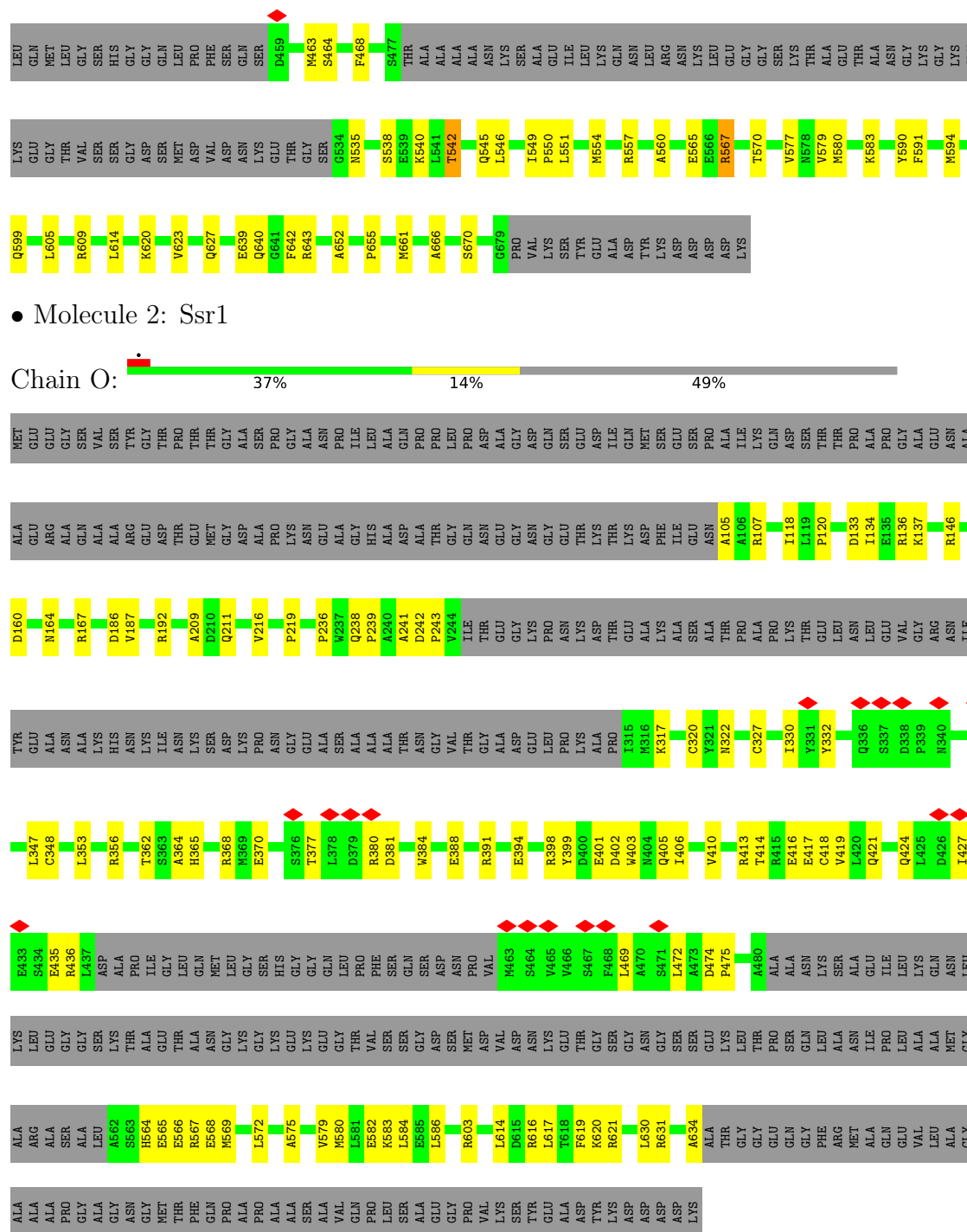
There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
U	294	GLY	ASP	conflict	UNP G0SB54
U	300	ASP	ASN	conflict	UNP G0SB54
U	363	HIS	TYR	conflict	UNP G0SB54
U	984	ASP	-	expression tag	UNP G0SB54
U	985	TYR	-	expression tag	UNP G0SB54
U	986	LYS	-	expression tag	UNP G0SB54
U	987	ASP	-	expression tag	UNP G0SB54
U	988	ASP	-	expression tag	UNP G0SB54
U	989	ASP	-	expression tag	UNP G0SB54
U	990	ASP	-	expression tag	UNP G0SB54
U	991	LYS	-	expression tag	UNP G0SB54

- Molecule 10 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
10	N	1	Total	Zn	0
			1	1	
10	O	1	Total	Zn	0
			1	1	
10	S	1	Total	Zn	0
			1	1	





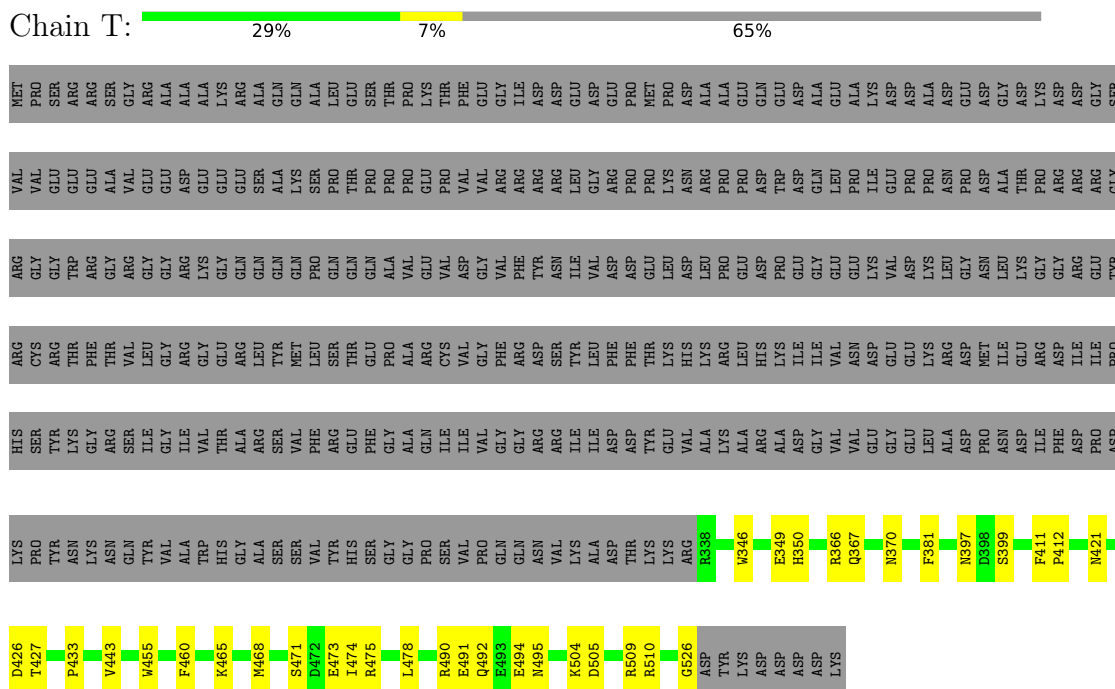
• Molecule 2: Ssr1

Chain O: 37% 14% 49%

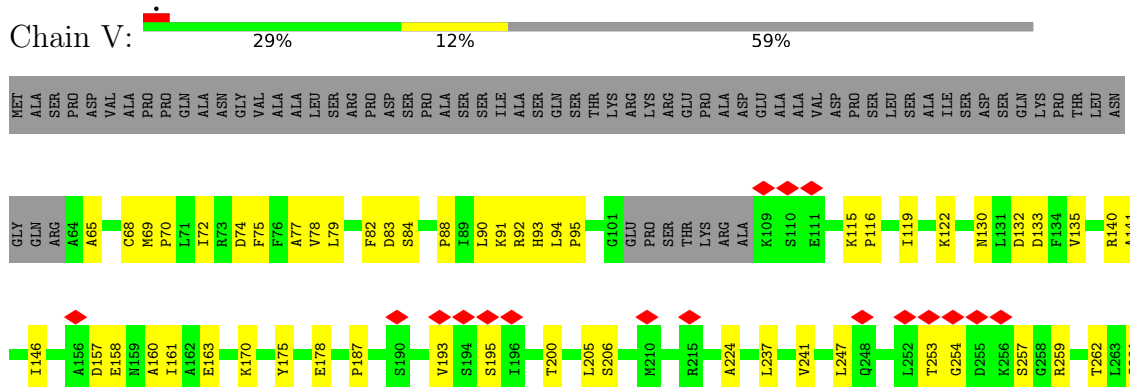
• Molecule 3: DM2 domain-containing protein

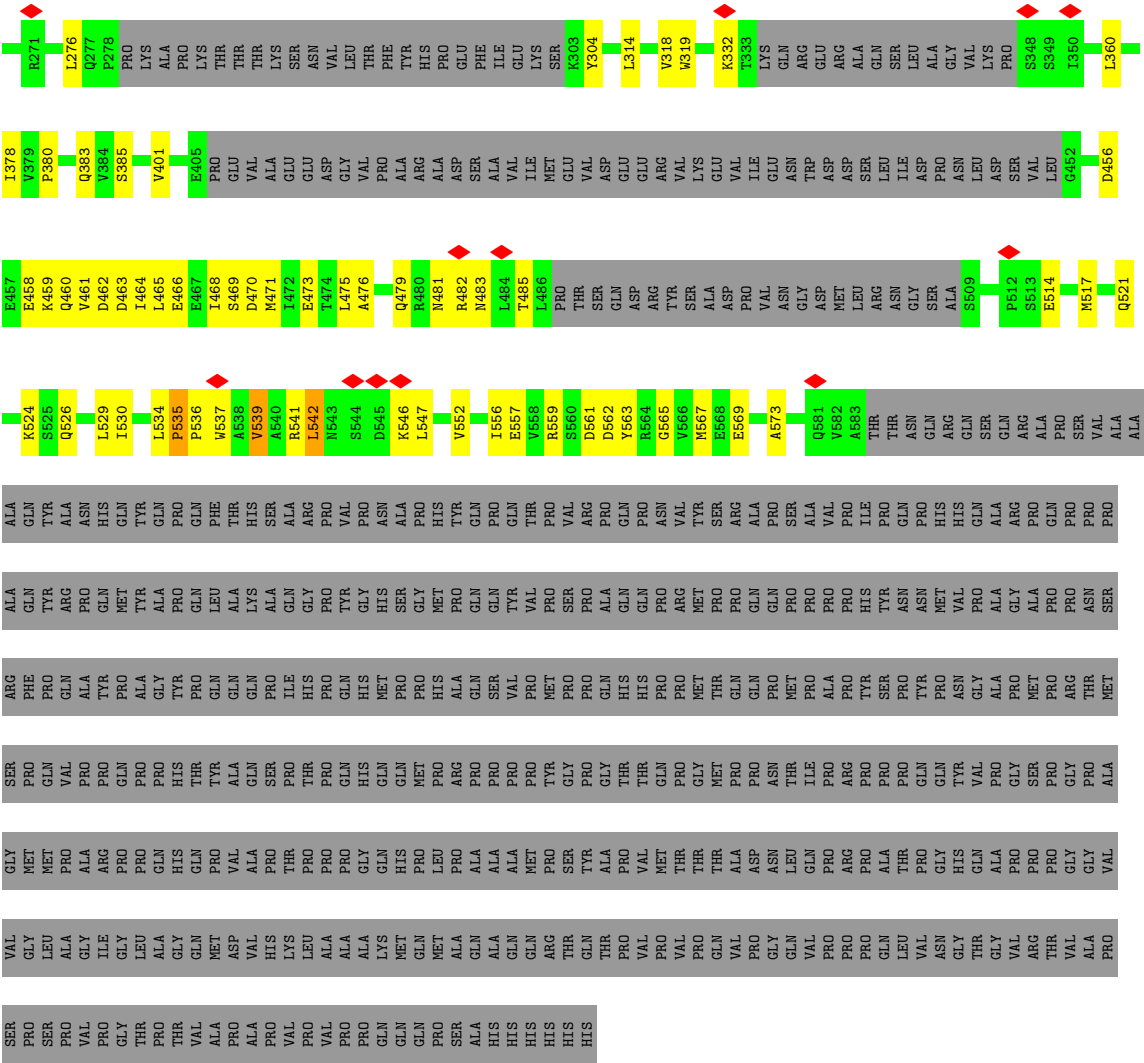
Chain P: 48% 20% 31%

- Molecule 7: Rsc7



- Molecule 8: Rsc58





E844	E951	E845	E952	E846	E953	E847	E954	E848	E955	E849	E956	E850	E957	E851	E958	E852	E959	E853	E960	E854	E961	E855	E962	E856	E963	E857	E964	E858	E965	E859	E966	E860	E967	E861	E968	E862	E969	E863	E970	E864	E971	E865	E972	E866	E973	E867	E974	E868	E975	E869	E976	E870	E977	E871	E978	E872	E979	E873	E980	E874	E981	E875	E982	E876	E983	E877	E984	E878	E985	E879	E986	E880	E987	E881	E988	E882	E989	E883	E990	E884	E991	E885	E992	E886	E993	E887	E994	E888	E995	E889	E996	E890	E997	E891	E998	E892	E999	E893	E900	E894	E901	E895	E902	E896	E903	E897	E904	E898	E905	E899	E906	E900	E907	E901	E908	E902	E909	E903	E910	E904	E911	E905	E912	E906	E913	E907	E914	E908	E915	E909	E916	E910	E917	E911	E918	E912	E919	E913	E920	E914	E921	E915	E922	E916	E923	E917	E924	E918	E925	E919	E926	E920	E927	E921	E928	E922	E929	E923	E930	E924	E931	E925	E932	E926	E933	E927	E934	E928	E935	E929	E936	E930	E937	E931	E938	E932	E939	E933	E940	E934	E941	E935	E942	E936	E943	E937	E944	E938	E945	E939	E946	E940	E947	E941	E948	E942	E949	E943	E950	E944	E951	E945	E952	E946	E953	E947	E954	E948	E955	E949	E956	E950	E957	E951	E958	E952	E959	E953	E960	E954	E961	E955	E962	E956	E963	E957	E964	E958	E965	E959	E966	E960	E967	E961	E968	E962	E969	E963	E970	E964	E971	E965	E972	E966	E973	E967	E974	E968	E975	E969	E976	E970	E977	E971	E978	E972	E979	E973	E980	E974	E981	E975	E982	E976	E983	E977	E984	E978	E985	E979	E986	E980	E987	E981	E988	E982	E989	E983	E990	E984	E991	E985	E992	E986	E993	E987	E994	E988	E995	E989	E996	E990	E997	E991	E998	E992	E999	E993	E900	E994	E995	E996	E997	E998	E999	E900	E901	E902	E903	E904	E905	E906	E907	E908	E909	E910	E911	E912	E913	E914	E915	E916	E917	E918	E919	E920	E921	E922	E923	E924	E925	E926	E927	E928	E929	E930	E931	E932	E933	E934	E935	E936	E937	E938	E939	E940	E941	E942	E943	E944	E945	E946	E947	E948	E949	E950	E951	E952	E953	E954	E955	E956	E957	E958	E959	E960	E961	E962	E963	E964	E965	E966	E967	E968	E969	E970	E971	E972	E973	E974	E975	E976	E977	E978	E979	E980	E981	E982	E983	E984	E985	E986	E987	E988	E989	E990	E991	E992	E993	E994	E995	E996	E997	E998	E999	E900	E901	E902	E903	E904	E905	E906	E907	E908	E909	E910	E911	E912	E913	E914	E915	E916	E917	E918	E919	E920	E921	E922	E923	E924	E925	E926	E927	E928	E929	E930	E931	E932	E933	E934	E935	E936	E937	E938	E939	E940	E941	E942	E943	E944	E945	E946	E947	E948	E949	E950	E951	E952	E953	E954	E955	E956	E957	E958	E959	E960	E961	E962	E963	E964	E965	E966	E967	E968	E969	E970	E971	E972	E973	E974	E975	E976	E977	E978	E979	E980	E981	E982	E983	E984	E985	E986	E987	E988	E989	E990	E991	E992	E993	E994	E995	E996	E997	E998	E999	E900	E901	E902	E903	E904	E905	E906	E907	E908	E909	E910	E911	E912	E913	E914	E915	E916	E917	E918	E919	E920	E921	E922	E923	E924	E925	E926	E927	E928	E929	E930	E931	E932	E933	E934	E935	E936	E937	E938	E939	E940	E941	E942	E943	E944	E945	E946	E947	E948	E949	E950	E951	E952	E953	E954	E955	E956	E957	E958	E959	E960	E961	E962	E963	E964	E965	E966	E967	E968	E969	E970	E971	E972	E973	E974	E975	E976	E977	E978	E979	E980	E981	E982	E983	E984	E985	E986	E987	E988	E989	E990	E991	E992	E993	E994	E995	E996	E997	E998	E999	E900	E901	E902	E903	E904	E905	E906	E907	E908	E909	E910	E911	E912	E913	E914	E915	E916	E917	E918	E919	E920	E921	E922	E923	E924	E925	E926	E927	E928	E929	E930	E931	E932	E933	E934	E935	E936	E937	E938	E939	E940	E941	E942	E943	E944	E945	E946	E947	E948	E949	E950	E951	E952	E953	E954	E955	E956	E957	E958	E959	E960	E961	E962	E963	E964	E965	E966	E967	E968	E969	E970	E971	E972	E973	E974	E975	E976	E977	E978	E979	E980	E981	E982	E983	E984	E985	E986	E987	E988	E989	E990	E991	E992	E993	E994	E995	E996	E997	E998	E999	E900	E901	E902	E903	E904	E905	E906	E907	E908	E909	E910	E911	E912	E913	E914	E915	E916	E917	E918	E919	E920	E921	E922	E923	E924	E925	E926	E927	E928	E929	E930	E931	E932	E933	E934	E935	E936	E937	E938	E939	E940	E941	E942	E943	E944	E945	E946	E947	E948	E949	E950	E951	E952	E953	E954	E955	E956	E957	E958	E959	E960	E961	E962	E963	E964	E965	E966	E967	E968	E969	E970	E971	E972	E973	E974	E975	E976	E977	E978	E979	E980	E981	E982	E983	E984	E985	E986	E987	E988	E989	E990	E991	E992	E993	E994	E995	E996	E997	E998	E999	E900	E901	E902	E903	E904	E905	E906	E907	E908	E909	E910	E911	E912	E913	E914	E915	E916	E917	E918	E919	E920	E921	E922	E923	E924	E925	E926	E927	E928	E929	E930	E931	E932	E933	E934	E935	E936	E937	E938	E939	E940	E941	E942	E943	E944	E945	E946	E947	E948	E949	E950	E951	E952	E953	E954	E955	E956	E957	E958	E959	E960	E961	E962	E963	E964	E965	E966	E967	E968	E969	E970	E971	E972	E973	E974	E975	E976	E977	E978	E979	E980	E981	E982	E983	E984	E985	E986	E987	E988	E989	E990	E991	E992	E993	E994	E995	E996	E997	E998	E999	E900	E901	E902	E903	E904	E905	E906	E907	E908	E909	E910	E911	E912	E913	E914	E915	E916	E917	E918	E919	E920	E921	E922	E923	E924	E925	E926	E927	E928	E929	E930	E931	E932	E933	E934	E935	E936	E937	E938	E939	E940	E941	E942	E943	E944	E945	E946	E947	E948	E949	E950	E951	E952	E953	E954	E955	E956	E957	E958	E959	E960	E961	E962	E963	E964	E965	E966	E967	E968	E969	E970	E971	E972	E973	E974	E975	E976	E977	E978	E979	E980	E981	E982	E983	E984	E985	E986	E987	E988	E989	E990	E991	E992	E993	E994	E995	E996	E997	E998	E999	E900	E901	E902	E903	E904	E905	E906	E907	E908	E909	E910	E911	E912	E913	E914	E915	E916	E917	E918	E919	E920	E921	E922	E923	E924	E925	E926	E927	E928	E929	E930	E931	E932	E933	E934	E935	E936	E937	E938	E939	E940	E941	E942	E943	E944	E945	E946	E947	E948	E949	E950	E951	E952	E953	E954	E955	E956	E957	E958	E959	E960	E961	E962	E963	E964	E965	E966	E967	E968	E969	E970	E971	E972	E973	E974	E975	E976	E977	E978	E979	E980	E981	E982	E983	E984	E985	E986	E987	E988	E989	E990	E991	E992	E993	E994	E995	E996	E997	E998	E999	E900	E901	E902	E903	E904	E905	E906	E907	E908	E909	E910	E911	E912	E913	E914	E915	E916	E917	E918	E919	E920	E921	E922	E923	E924	E925	E926	E927	E928	E929	E930	E931	E932	E933	E934	E935	E936	E937	E938	E939	E940	E941	E942	E943	E944	E945	E946	E947	E948	E949	E950	E951	E952	E953	E954	E955	E956	E957	E958	E959	E960	E961	E962	E963	E964	E965	E966	E967	E968	E969	E970	E971	E972	E973	E974	E975	E976	E977	E978	E979	E980	E981	E982	E983	E984	E985	E986	E987	E988	E989	E990	E991	E992	E993	E994	E995	E996	E997	E998	E999	E900	E901	E902	E903	E904	E905	E906	E907	E908	E909	E910	E911	E912	E913	E914	E915	E916	E917	E918	E919	E920	E921	E922	E923	E924	E925	E926	E927	E928	E929	E930	E931	E932	E933	E934	E935	E936	E937	E938	E939	E940	E941	E942	E943	E944	E945	E946	E947	E948	E949	E950	E951	E952	E953	E954	E955	E956	E957	E958	E959	E960	E961	E962	E963	E964	E965	E966	E967	E968	E969	E970	E971	E972	E973	E974	E975	E976	E977	E978	E979	E980	E981	E982	E983	E984	E985	E986	E987	E988	E989	E990	E991	E992	E993	E994	E995	E996	E997	E998	E999	E900	E901	E902	E903	E904	E905	E906	E907	E908	E909	E910	E911	E912	E913	E914	E915	E916	E917	E918	E919	E920	E921	E922	E923	E924	E925	E926	E927	E928	E929	E930	E931	E932	E933	E934	E935	E936	E937	E938	E939	E940	E941	E942	E943	E944	E945	E946	E947	E948	E949	E950	E951	E952	E953	E954	E955	E956	E957	E958	E959	E960	E961	E962	E963	E964	E965	E966	E967	E968	E969	E970	E971	E972	E973	E974	E975	E976	E977	E978	E979	E980	E981	E982	E983	E984	E985	E986	E987	E988	E989	E990	E991	E992	E993	E994	E995	E996	E997	E998	E999	E900	E901	E902	E903	E904	E905	E906	E907	E908	E909	E910	E911	E912	E913	E914	E915	E916	E917	E918	E919	E920	E921	E922	E923	E924	E925	E926	E927	E928	E929	E930	E931	E932	E933	E934	E935	E936	E937	E938	E939	E940	E941	E942	E943	E944	E945	E946	E947	E948	E949	E950	E951	E952	E953	E954	E955	E956	E957	E958	E959	E960	E961	E962	E963	E964	E965	E966	E967	E968	E969	E970	E971	E972	E973	E974	E975	E976	E977	E978	E979	E980	E981	E982	E983	E984	E985	E986	E987	E988	E989	E990	E991	E992	E993	E994	E995	E996	E997	E998	E999	E900	E901	E902	E903	E904	E905	E906	E907	E908	E909	E910	E911	E912	E913	E914	E915	E916	E917	E918	E919	E920	E921	E922	E923	E924	E925	E926	E927	E928	E929	E930	E931	E932	E933	E934	E935	E936	E937	E938	E939	E940	E94
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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	250420	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	1.887	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.028	Depositor
Recommended contour level	0.11	Depositor
Map size (Å)	432.00003, 432.00003, 432.00003	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08, 1.08, 1.08	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.32	0/1336	0.57	0/1774
2	N	0.23	0/3834	0.44	4/5197 (0.1%)
2	O	0.20	0/2952	0.42	0/3999
3	P	0.28	4/3125 (0.1%)	0.46	2/4220 (0.0%)
4	Q	0.41	6/2820 (0.2%)	0.58	4/3821 (0.1%)
5	R	0.18	1/3350 (0.0%)	0.36	0/4548
6	S	0.20	2/3271 (0.1%)	0.36	2/4452 (0.0%)
7	T	0.13	0/1556	0.31	0/2122
8	V	0.28	2/3122 (0.1%)	0.52	2/4243 (0.0%)
9	U	0.36	2/1150 (0.2%)	0.53	1/1552 (0.1%)
All	All	0.26	17/26516 (0.1%)	0.45	15/35928 (0.0%)

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	Q	109	PHE	C-N	8.40	1.45	1.33
3	P	451	ALA	C-N	-7.46	1.24	1.33
4	Q	108	TYR	C-N	7.46	1.44	1.33
4	Q	321	PRO	C-N	7.06	1.42	1.33
3	P	339	PHE	C-N	-6.94	1.24	1.33

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	P	452	PHE	N-CA-C	11.09	123.11	111.14
4	Q	109	PHE	CA-C-N	-7.23	111.88	122.65
4	Q	109	PHE	C-N-CA	-7.23	111.88	122.65
8	V	535	PRO	N-CA-C	6.63	118.78	110.70
2	N	567	ARG	N-CA-C	-6.07	106.85	114.56

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	1321	0	1360	44	0
2	N	3758	0	3653	116	0
2	O	2890	0	2804	121	0
3	P	3064	0	3018	100	0
4	Q	2750	0	2734	104	0
5	R	3289	0	3298	61	0
6	S	3184	0	3082	31	0
7	T	1514	0	1454	34	0
8	V	3070	0	3004	103	0
9	U	1135	0	1058	54	0
10	N	1	0	0	0	0
10	O	1	0	0	0	0
10	S	1	0	0	0	0
All	All	25978	0	25465	631	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 12.

The worst 5 of 631 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:N:642:PHE:CE2	2:O:634:ALA:HB3	1.72	1.22
2:N:642:PHE:CZ	2:O:634:ALA:HB3	1.76	1.19
2:O:603:ARG:HH12	5:R:981:ARG:HA	1.13	1.07
2:N:642:PHE:CE1	2:O:631:ARG:HA	1.95	1.00
2:N:642:PHE:CE2	2:O:634:ALA:CB	2.47	0.98

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	153/1595 (10%)	140 (92%)	13 (8%)	0	100	100
2	N	470/694 (68%)	450 (96%)	20 (4%)	0	100	100
2	O	346/694 (50%)	333 (96%)	13 (4%)	0	100	100
3	P	362/547 (66%)	339 (94%)	23 (6%)	0	100	100
4	Q	330/769 (43%)	316 (96%)	14 (4%)	0	100	100
5	R	405/763 (53%)	395 (98%)	10 (2%)	0	100	100
6	S	389/607 (64%)	375 (96%)	14 (4%)	0	100	100
7	T	187/534 (35%)	178 (95%)	9 (5%)	0	100	100
8	V	395/990 (40%)	366 (93%)	29 (7%)	0	100	100
9	U	148/991 (15%)	136 (92%)	12 (8%)	0	100	100
All	All	3185/8184 (39%)	3028 (95%)	157 (5%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	K	135/1356 (10%)	134 (99%)	1 (1%)	76	80
2	N	398/562 (71%)	396 (100%)	2 (0%)	81	83
2	O	312/562 (56%)	312 (100%)	0	100	100
3	P	330/462 (71%)	328 (99%)	2 (1%)	78	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	Q	290/598 (48%)	290 (100%)	0	100	100
5	R	358/655 (55%)	357 (100%)	1 (0%)	86	86
6	S	341/493 (69%)	340 (100%)	1 (0%)	86	86
7	T	165/457 (36%)	165 (100%)	0	100	100
8	V	331/836 (40%)	329 (99%)	2 (1%)	78	81
9	U	102/861 (12%)	102 (100%)	0	100	100
All	All	2762/6842 (40%)	2753 (100%)	9 (0%)	84	86

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
8	V	539	VAL
8	V	542	LEU
3	P	68	ARG
3	P	361	GLU
5	R	435	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
8	V	125	GLN
8	V	460	GLN
2	O	204	ASN
2	N	673	GLN
8	V	483	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

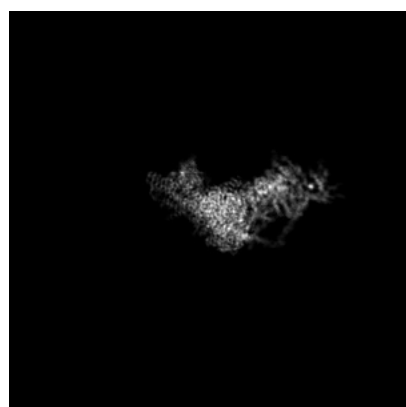
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-68865. These allow visual inspection of the internal detail of the map and identification of artifacts.

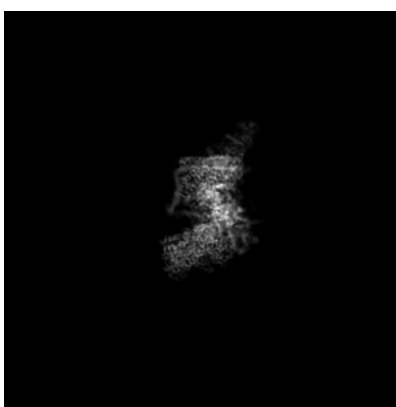
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

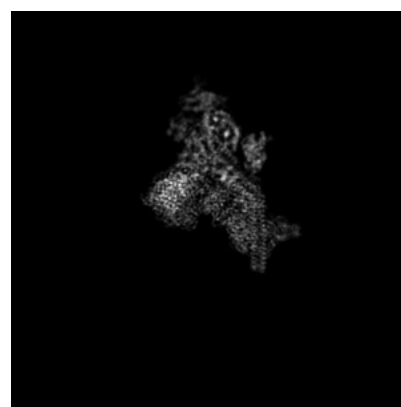
6.1.1 Primary map



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: 200



Y Index: 200



Z Index: 200

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: 242



Y Index: 214

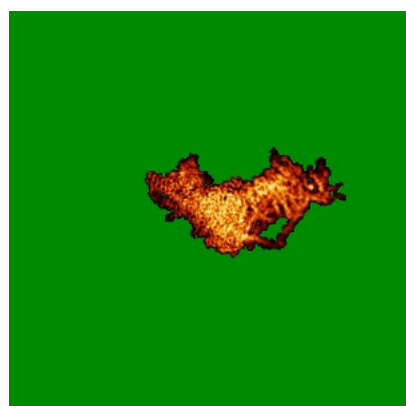


Z Index: 212

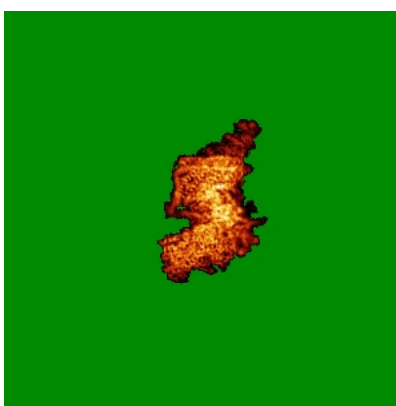
The images above show the largest variance slices of the map in three orthogonal directions.

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

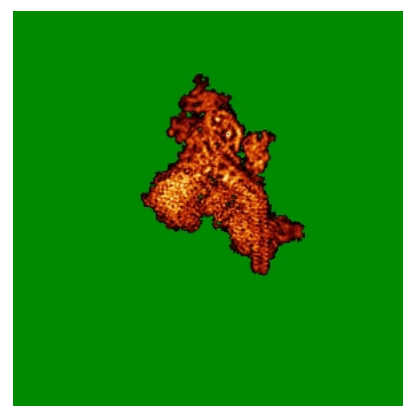
6.4.1 Primary map



X



Y

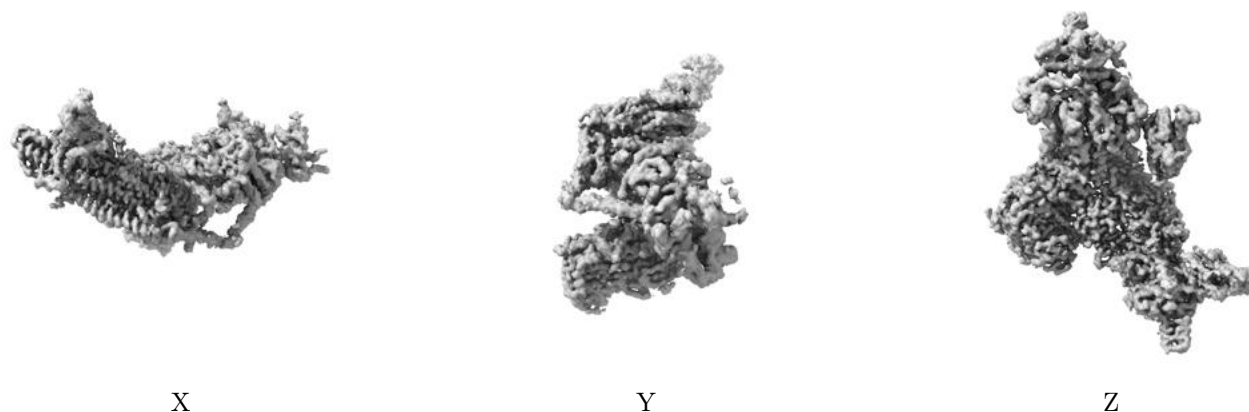


Z

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 0.11. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

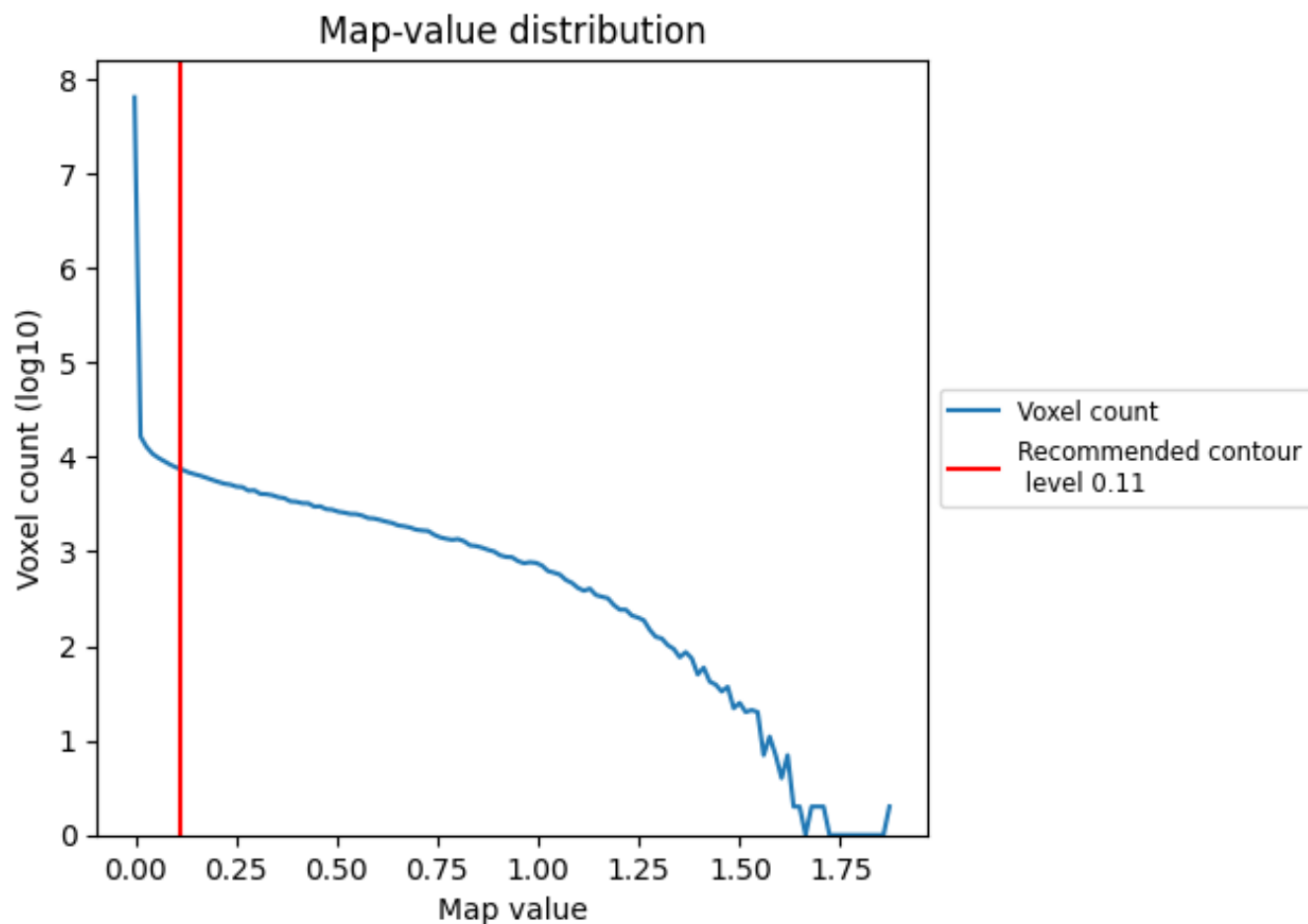
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

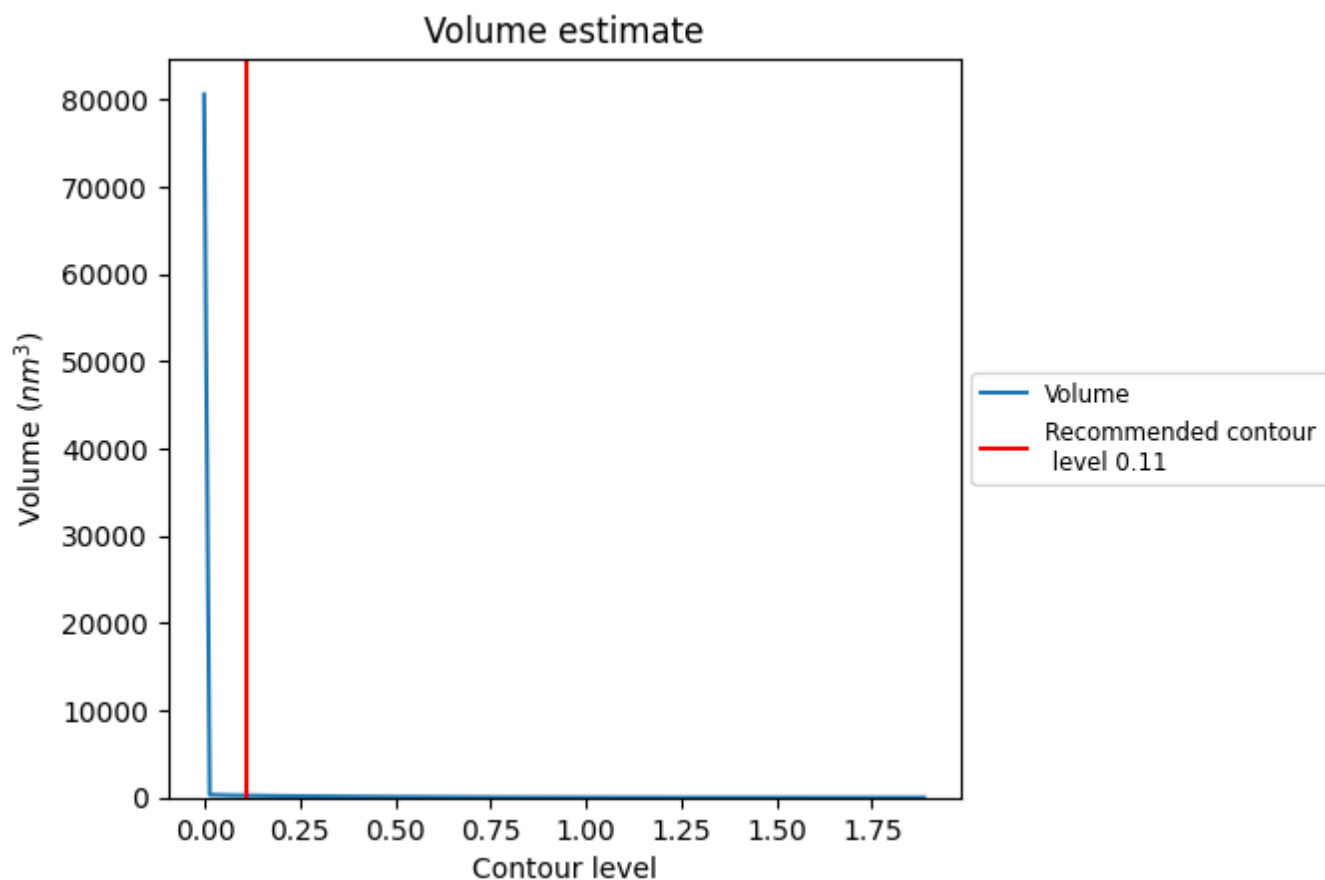
This section contains the results of statistical analysis of the map.

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.

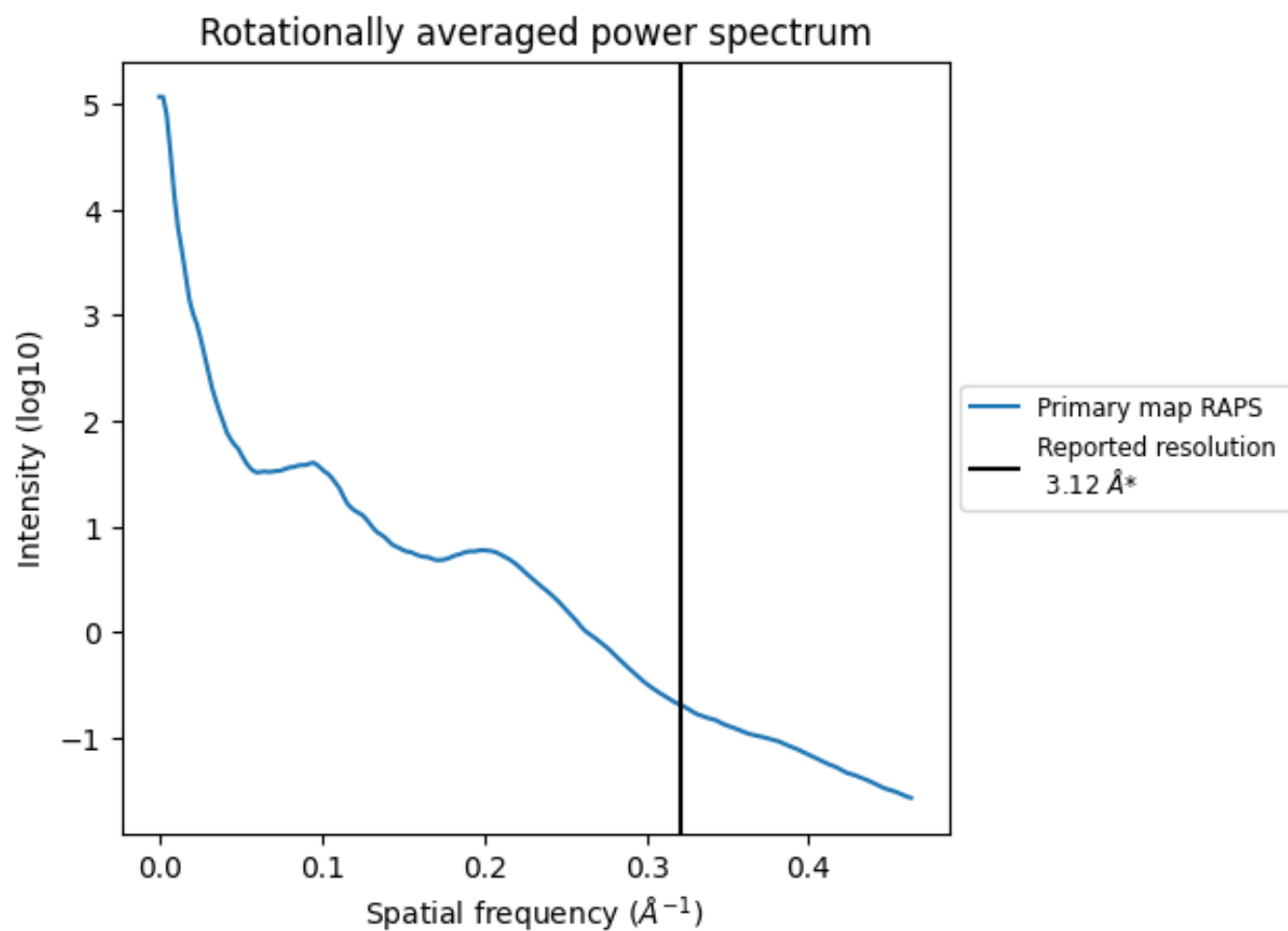
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 230 nm³; this corresponds to an approximate mass of 208 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 0.321 Å⁻¹

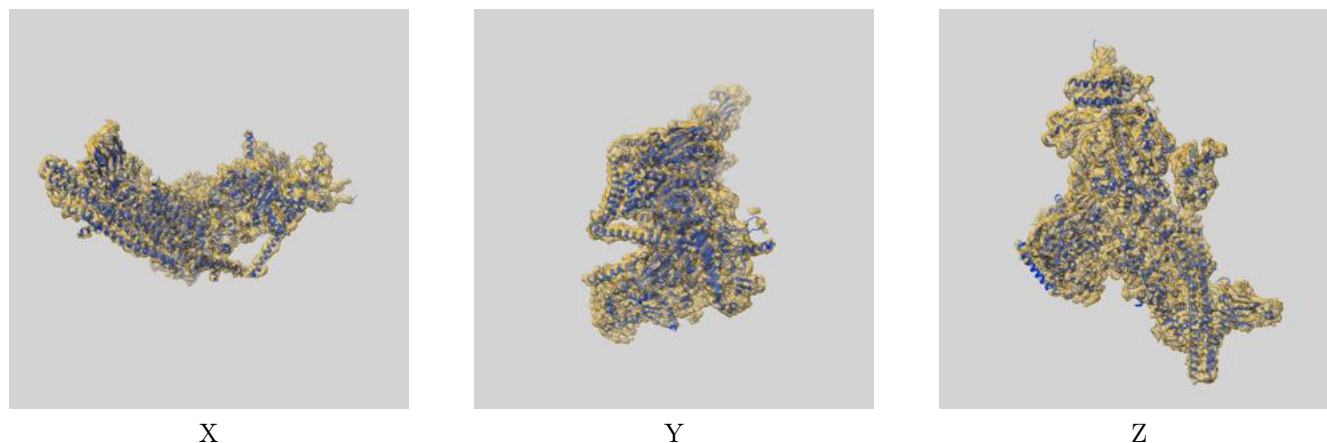
8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-68865 and PDB model 23CP. Per-residue inclusion information can be found in section [3](#) on page [10](#).

9.1 Map-model overlay [i](#)



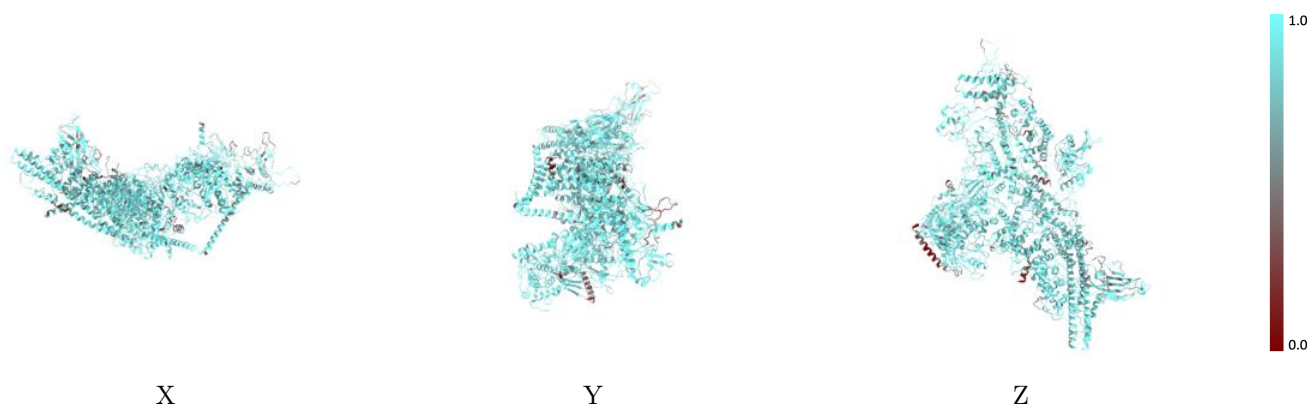
The images above show the 3D surface view of the map at the recommended contour level 0.11 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



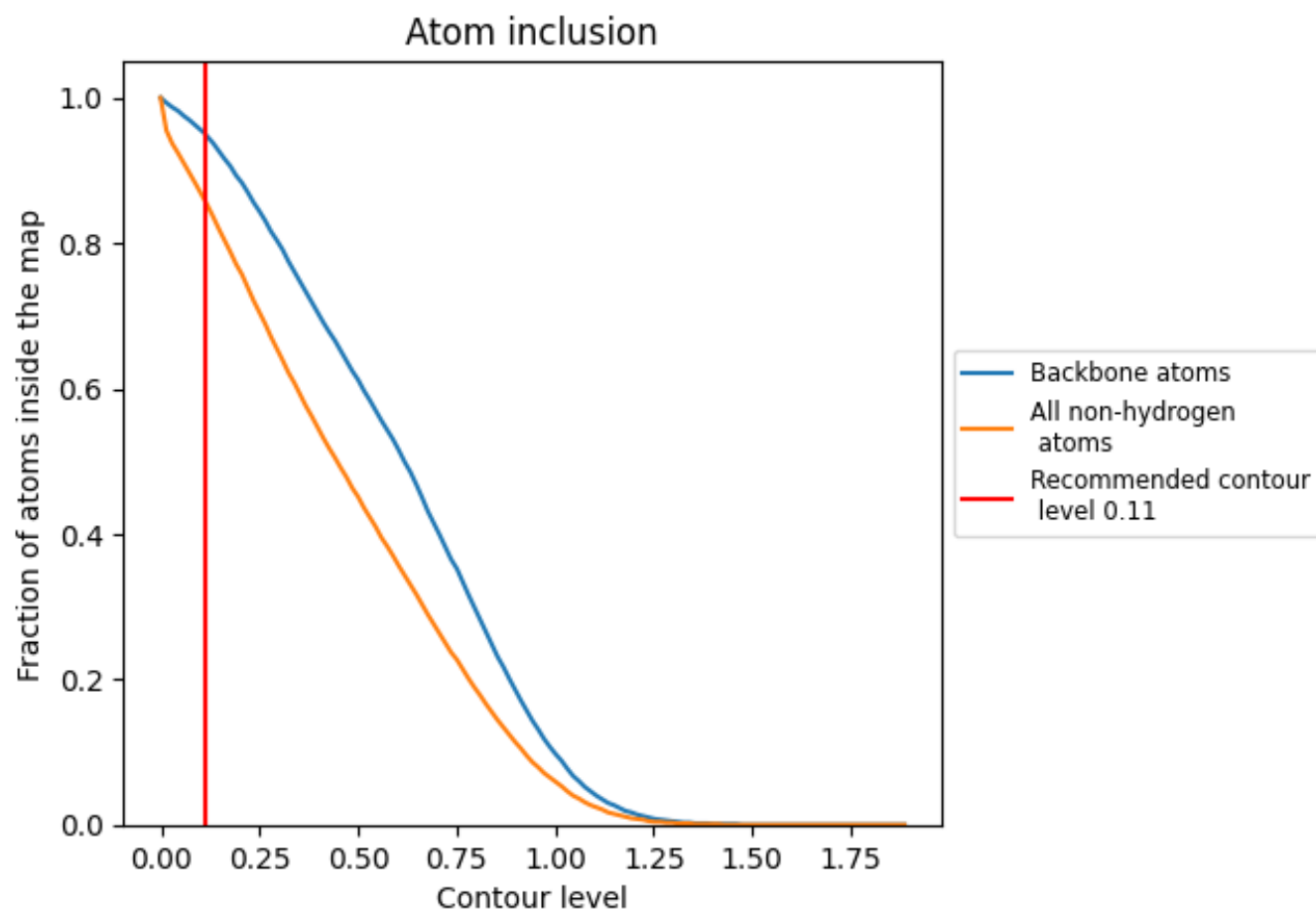
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.11).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 86% 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 (0.11) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8590	0.3930
K	0.7990	0.3260
N	0.8870	0.4190
O	0.8500	0.3820
P	0.8110	0.3750
Q	0.8620	0.3370
R	0.9190	0.4990
S	0.8560	0.4650
T	0.9360	0.4720
U	0.8500	0.2410
V	0.8100	0.2990

1.0

0.0

<0.0