



wwPDB EM Validation Summary Report ⓘ

Mar 28, 2026 – 07:02 PM UTC

PDB ID : 6U5V / pdb_00006u5v
EMDB ID : EMD-20657
Title : Electron cryomicroscopy Structure of C. albicans FAS in the Apo state
Authors : Lou, J.W.; Mazhab-Jafari, M.T.
Deposited on : 2019-08-28
Resolution : 2.80 Å (reported)
Based on initial model : 2UV8

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.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

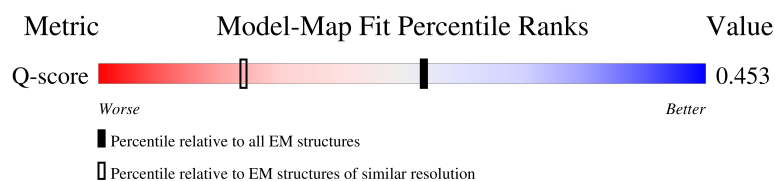
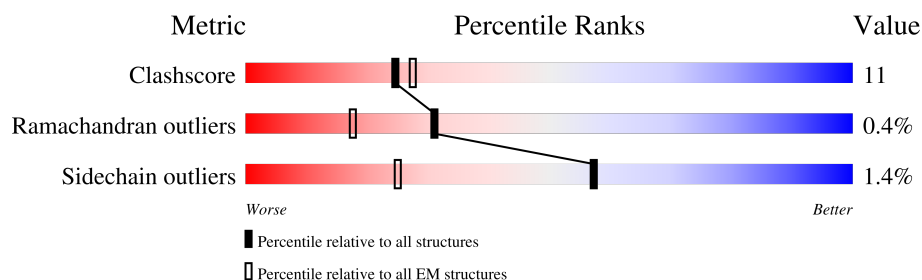
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.80 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	11806 (2.30 - 3.30)

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	1885	
2	B	2037	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	FMN	B	2101	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 28187 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 Fatty acid synthase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1596	Total	C	N	O	S	0	0
			12096	7645	2057	2349	45		

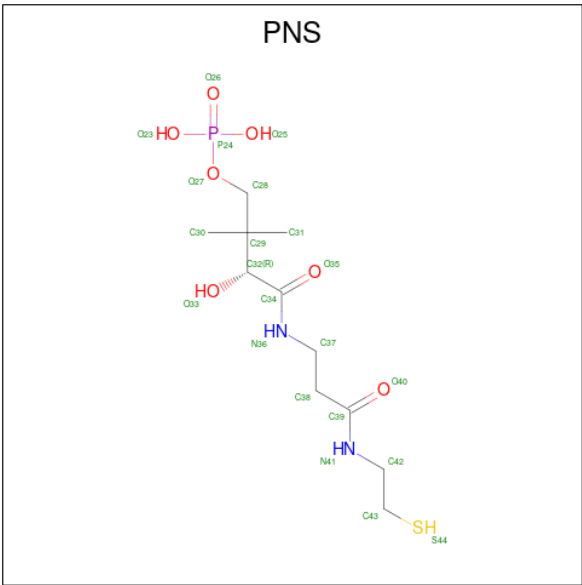
There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	350	VAL	SER	conflict	UNP P43098
A	351	ASP	ARG	conflict	UNP P43098
A	353	ASN	LYS	conflict	UNP P43098
A	354	LYS	GLN	conflict	UNP P43098
A	357	ALA	LEU	conflict	UNP P43098
A	814	THR	PRO	conflict	UNP P43098
A	1067	LYS	GLN	conflict	UNP P43098
A	1124	VAL	ILE	conflict	UNP P43098
A	1445	GLU	LYS	conflict	UNP P43098
A	1743	SER	ASN	conflict	UNP P43098

- Molecule 2 is a protein called Fatty acid synthase subunit beta.

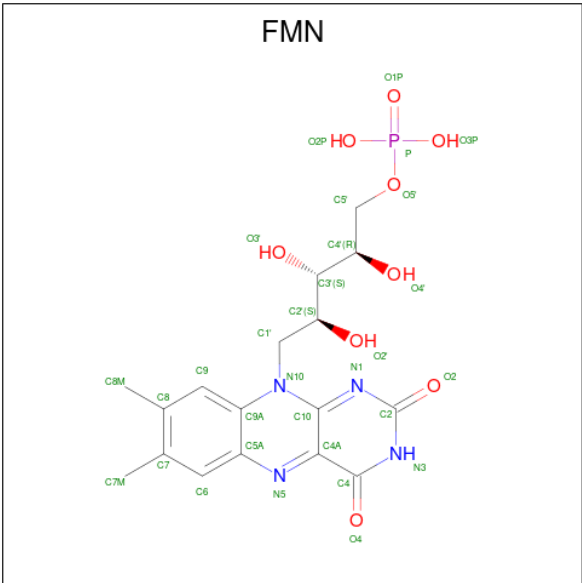
Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	2033	Total	C	N	O	S	1	0
			16054	10290	2665	3045	54		

- Molecule 3 is 4'-PHOSPHOPANTETHEINE (CCD ID: PNS) (formula: C₁₁H₂₃N₂O₇PS).



Mol	Chain	Residues	Atoms				AltConf
3	A	1	Total	C	O	P	0
			6	2	3	1	

- Molecule 4 is FLAVIN MONONUCLEOTIDE (CCD ID: FMN) (formula: C₁₇H₂₁N₄O₉P) (labeled as "Ligand of Interest" by depositor).

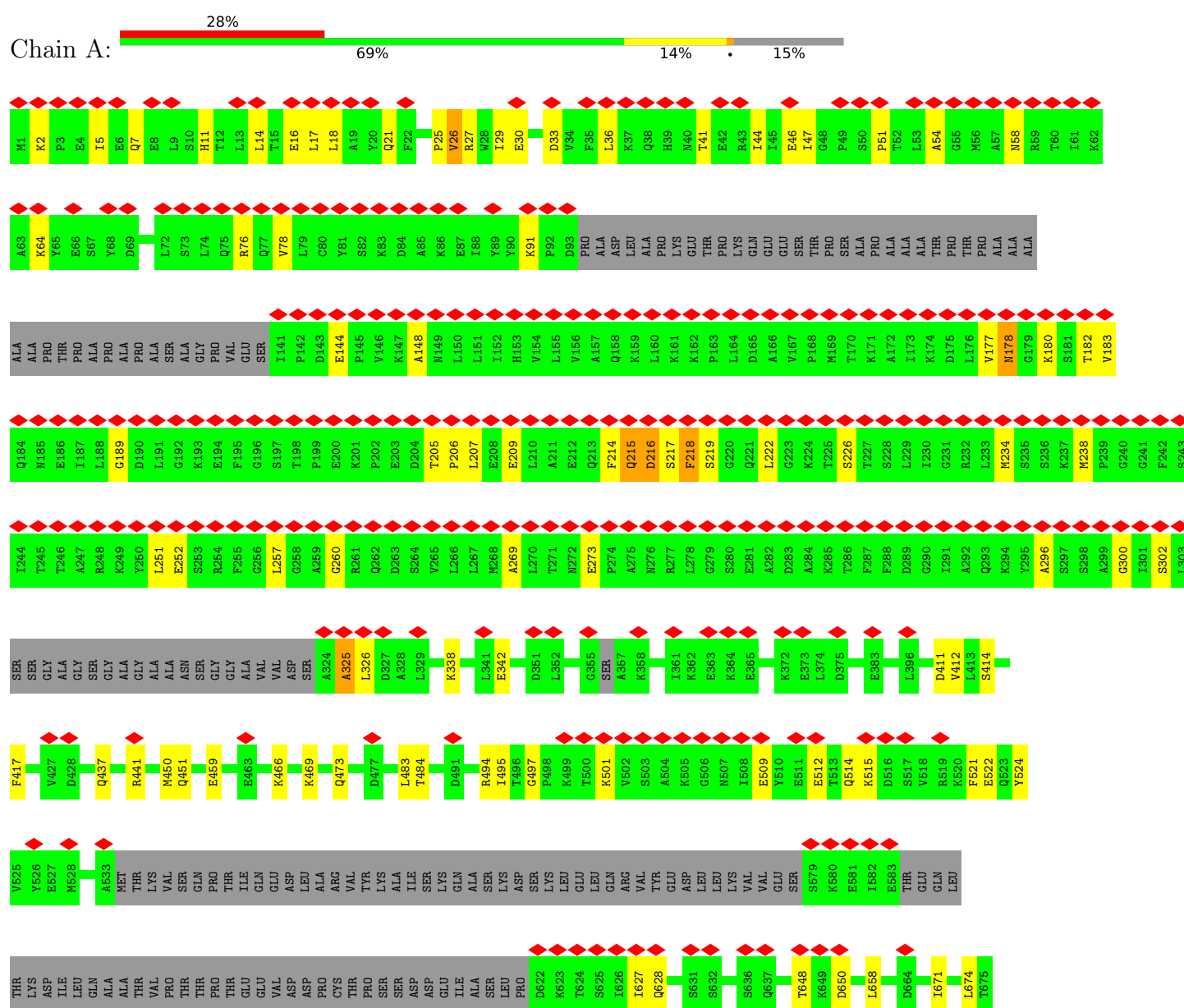


Mol	Chain	Residues	Atoms					AltConf
4	B	1	Total	C	N	O	P	0
			31	17	4	9	1	

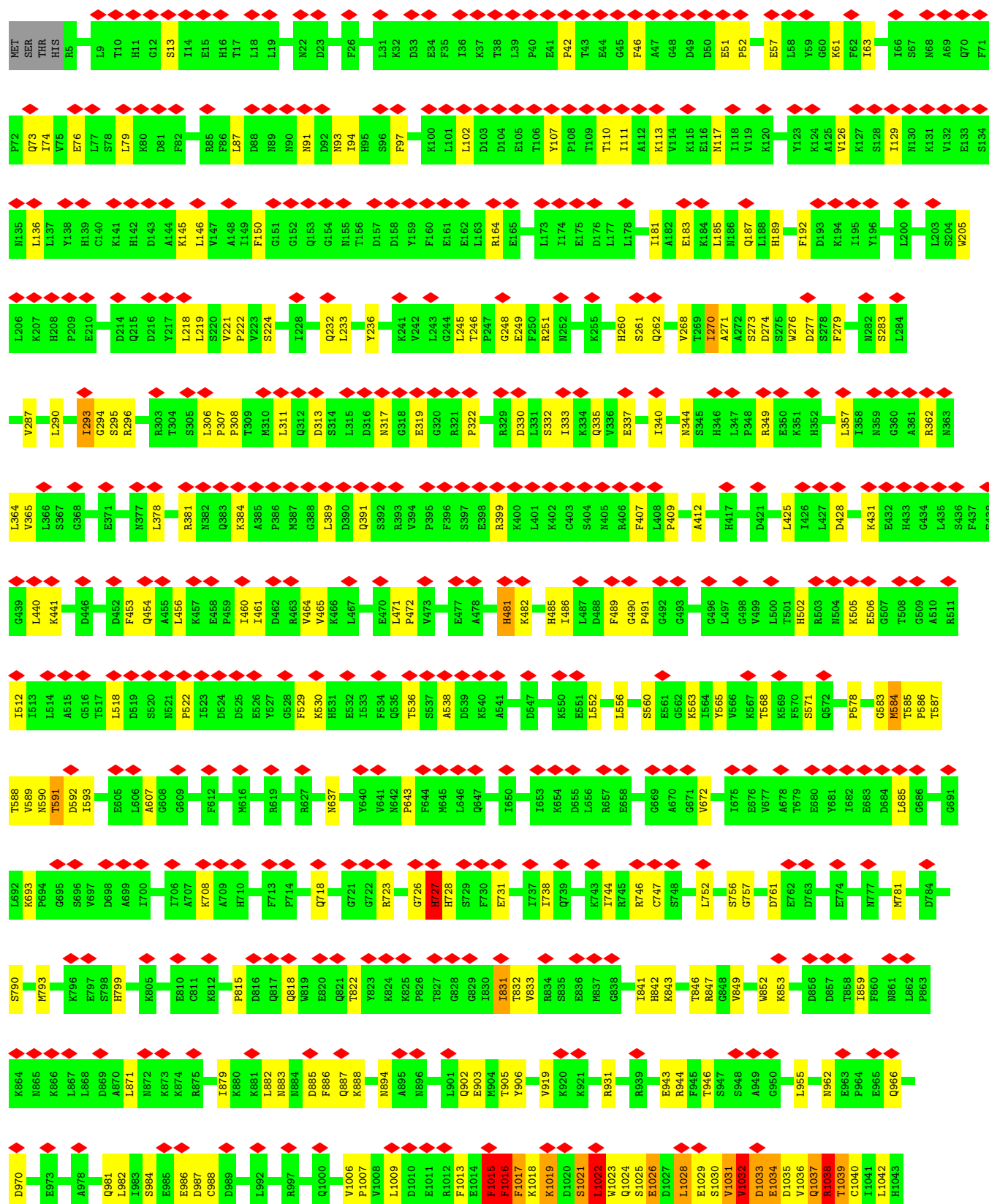
3 Residue-property plots

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.

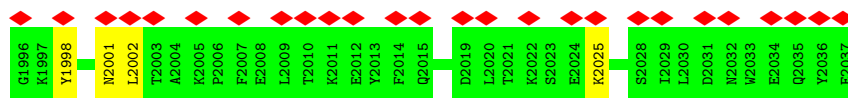
• Molecule 1: Fatty acid synthase subunit alpha







GI044	PI045	VI046	AI047	SI048	SI052	KI053	VI054	DI055	EI056	DI060	GI068	KI075	EI076	EI077	YI078	AI079	GI080	DI081	EI082	SI083	KI084	EI089	KI094	KI095	PI096	AI097	SI098	SI100	AI101	TI102	SI103	VI104	NI105	TI106	TI107	DI108	GI109	NI110	QI111	EI115	TI116	TI117	SI118	EI119	LI120	PI121	NI122	KI123	QI124	LI127									
DI128	LI129	LI130	AI131	TI133	EI134	LI135	NI136	QI139	TI144	DI145	RI146	KI152	NI156	PI157	LI158	HI159	DI160	LI161	LI162	TI163	PI164	AI165	KI166	HI167	SI168	KI169	KI174	KI175	TI176	KI177	KI178	LI179	TI180	AI181	F1182	EI183	NI184	TI185	GI186	GI187	DI188	LI189	LI190	PI191	VI192	VI193	EI194	LI197	VI198	KI199	PI200	NI201							
TI202	EI209	HI210	TI211	TI212	AI213	DI214	TI215	NI216	PI221	F1222	YI224	KI225	DI230	EI237	TI238	MI239	EI240	EI244	TI245	TI246	KI247	GI256	SI257	SI258	VI259	PI260	SI262	MI263	DI264	TI265	NI266	VI267	EI268	KI269	AI270	TI271	TI272	GI273	DI274	EI275	DI276	TI277	TI278	SI279	SI280	QI281	TI282	NI283	SI284	HI288									
AI289	TI290	GI291	MI292	KI293	CI294	AI295	AI296	F1297	VI298	DI299	RI300	PI301	GI302	KI303	AI304	TI305	LI306	AI307	PI308	MI309	DI310	F1311	TI315	AI323	HI324	EI325	PI326	KI327	DI330	GI331	DI332	LI333	LI334	KI335	LI336	VI337	HI338	NI341	AI342	YI343	TI347	GI348	AI349	AI350	PI351	LI352	KI353	KI354	GI355	DI356	VI357	VI358	SI359						
AI362	EI363	TI364	LI368	NI369	QI370	PI371	SI372	GI373	KI374	LI375	GI380	EI385	GI386	KI387	QI395	F1396	RI399	GI400	EI401	YI402	MI403	DI404	NI407	KI411	EI414	TI415	PI416	YI417	QI418	VI419	AI420	F1421	KI422	SI423	AI424	KI425	DI426	LI427	AI428	VI429	LI430	RI431	EI434	HI437	LI438	EI439	KI440	DI441	VI442										
QI443	F1444	DI445	VI446	F1449	RI450	QI451	EI452	KI458	SI459	AI460	NI461	YI462	YI463	SI464	SI465	TI466	TI469	LI473	LI474	EI475	LI476	PI477	TI478	KI479	EI480	F1325	YI481	NI482	QI483	VI484	GI485	SI486	VI487	DI488	VI489	EI490	AI491	GI492	NI497	PI498	DI501	YI502	LI503	SI504	RI505	NI506	GI507	NI508	TI509	LI510	EI511	SI512	SI513	VI514					
LI515	F1516	EI517	NI518	AI519	LI520	PI521	LI522	SI523	SI524	GI525	EI526	EI527	LI528	TI529	SI530	KI531	GI534	EI537	DI545	YI546	NI547	YI548	LI549	HI550	VI551	SI552	RI553	YI554	KI560	TI564	LI565	NI566	MI569	YI570	TI575	RI576	EI580	EI581	VI582	AI583	AI584	NI585	NI586	VI587	AI588	AI589	RI590	AI593	F1594	DI597									
F1598	VI599	GI600	MI601	VI602	LI603	PI604	NI605	DI606	TI607	LI608	QI609	TI610	TI611	MI612	EI613	HI614	VI615	GI616	NI619	KI622	KI625	YI626	EI627	QI628	RI629	MI630	VI631	EI632	TI633	EI634	LI635	LI638	NI639	GI640	EI643	TI644	EI645	TI648	TI649	TI650	YI651	VI652	F1653	TI654	QI655	QI656	SI658	QI659	EI660	QI661	GI662	MI663							
GI664	MI665	EI666	TI667	YI668	NI669	SI670	SI671	EI672	VI673	AI674	TI675	EI676	DI682	RI683	VI686	NI687	NI688	YI689	TI693	LI694	DI695	LI696	YI697	QI698	NI699	NI700	PI701	NI702	EI703	RI714	RI717	DI718	NI719	YI720	TI721	GI722	MI723	EI726	TI727	TI728	GI729	EI730	DI731	GI732	AI733	LI734	KI735	SI736	EI737	KI738	LI739	F1740	KI741						
DI742	TI743	DI744	EI745	TI746	TI747	F1752	VI753	SI754	PI755	TI756	GI757	LI758	LI759	SI760	AI761	TI762	QI763	F1764	TI765	QI766	PI767	AI768	LI769	TI770	LI771	MI772	EI773	KI774	EI778	DI779	KI783	GI784	LI785	LI786	PI787	SI788	DI789	LI790	KI791	F1792	AI793	GI794	HI795	SI796	LI797	GI798	EI799	YI800	SI801	AI802	LI803	SI804	SI805	LI806	AI807	NI808			
PI811	LI812	EI813	SI814	LI815	VI816	DI817	YI818	YI819	RI822	GI823	MI824	TI825	MI826	QI827	VI828	AI829	YI830	PI831	RI832	DI833	EI834	LI835	LI836	YI837	SI838	NI839	YI840	GI841	MI842	YI843	AI844	VI845	PI847	SI848	RI849	VI850	SI851	AI852	TI853	F1854	DI855	DI856	SI857	YI858	LI859	RI860	F1861	VI862	YI863	DI864	EI865	YI866	NI868	KI869	TI870				
KI871	VI872	LI873	LI874	EI875	LI876	VI877	NI878	YI879	NI880	YI881	EI882	NI883	QI884	QI885	YI886	VI887	AI888	YI889	GI890	DI891	LI892	RI893	AI894	LI895	DI896	TI897	LI898	TI899	NI900	YI901	LI902	NI903	YI904	LI905	KI906	LI907	NI908	KI909	LI910	DI911	YI912	YI913	KI914	LI915	YI916	YI917	YI918	YI919	YI920	YI921	EI922	KI923	YI924	KI925	YI926	YI927	YI928	YI929	EI930
TI931	YI932	DI933	EI934	YI935	AI936	AI937	KI938	SI939	LI940	AI941	KI942	PI943	QI944	PI945	TI946	DI947	LI948	EI949	RI950	YI951	F1952	AI953	YI954	YI955	PI956	LI957	KI958	YI959	YI960	SI961	YI962	YI963	F1964	YI965	SI966	SI967	MI970	KI974	YI975	F1976	QI977	YI978	F1979	LI980	YI981	KI982	YI983	KI986	YI987	YI988	YI989	KI990	YI991	QI992	YI993				



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D3	Depositor
Number of particles used	92958	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE; CTFFIND4 within cryoSPARC2	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	43	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	2.505	Depositor
Minimum map value	-1.098	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.142	Depositor
Recommended contour level	0.744	Depositor
Map size ($\text{\AA}$)	373.12, 373.12, 373.12	wwPDB
Map dimensions	352, 352, 352	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.06, 1.06, 1.06	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: PNS, FMN

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	0.45	0/12322	0.71	2/16684 (0.0%)
2	B	0.43	13/16423 (0.1%)	0.70	16/22279 (0.1%)
All	All	0.44	13/28745 (0.0%)	0.70	18/38963 (0.0%)

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	1
2	B	0	3
All	All	0	4

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1792	PHE	C-O	-8.03	1.14	1.23
2	B	1529	THR	CA-C	-7.50	1.43	1.52
2	B	1792	PHE	CA-C	-7.01	1.44	1.52
2	B	1529	THR	C-O	-6.65	1.15	1.23
2	B	1527	GLU	N-CA	-6.65	1.38	1.46

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1529	THR	N-CA-C	11.44	125.91	110.35
2	B	1529	THR	CB-CA-C	-8.38	94.61	109.62
2	B	1528	LEU	N-CA-C	7.61	122.14	113.01
2	B	727[A]	HIS	CB-CA-C	7.20	120.52	110.16

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	727[B]	HIS	CB-CA-C	7.20	120.52	110.16

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1588	PRO	Peptide
2	B	1111	GLN	Peptide
2	B	1199	LYS	Peptide
2	B	481	HIS	Peptide

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	12096	0	11589	202	0
2	B	16054	0	16016	417	0
3	A	6	0	2	0	0
4	B	31	0	19	34	0
All	All	28187	0	27626	592	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

The worst 5 of 592 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:B:1007:PRO:HD2	2:B:1016:PHE:CE2	1.08	1.59
2:B:886:PHE:CE2	2:B:1017:PHE:CE1	1.83	1.58
2:B:886:PHE:CE2	2:B:1017:PHE:HE1	0.92	1.56
2:B:886:PHE:CZ	2:B:1017:PHE:CE1	1.93	1.54
2:B:1007:PRO:CD	2:B:1016:PHE:HE2	0.89	1.52

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	1586/1885 (84%)	1513 (95%)	64 (4%)	9 (1%)	21	51
2	B	2032/2037 (100%)	1924 (95%)	103 (5%)	5 (0%)	43	72
All	All	3618/3922 (92%)	3437 (95%)	167 (5%)	14 (0%)	31	60

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	218	PHE
2	B	591	THR
2	B	1032	VAL
1	A	178	ASN
2	B	1038	ARG

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	1221/1579 (77%)	1213 (99%)	8 (1%)	76	91
2	B	1780/1784 (100%)	1745 (98%)	35 (2%)	48	80
All	All	3001/3363 (89%)	2958 (99%)	43 (1%)	57	85

5 of 43 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	1032	VAL

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Mol	Chain	Res	Type
2	B	1527	GLU
2	B	1033	ASP
2	B	1039	THR
2	B	1529	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 59 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	335	GLN
2	B	1614	HIS
2	B	734	HIS
2	B	1585	ASN
2	B	1370	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

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
4	FMN	B	2101	-	33,33,33	6.45	22 (66%)	48,50,50	1.35	6 (12%)
3	PNS	A	1901	1	2,5,21	0.59	0	1,5,29	0.16	0

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
4	FMN	B	2101	-	-	5/18/18/18	0/3/3/3
3	PNS	A	1901	1	-	1/1/3/27	-

The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	2101	FMN	C6-C7	13.49	1.58	1.39
4	B	2101	FMN	C6-C5A	12.40	1.58	1.40
4	B	2101	FMN	C9-C9A	12.37	1.59	1.39
4	B	2101	FMN	C9-C8	11.90	1.55	1.39
4	B	2101	FMN	O4-C4	9.96	1.42	1.23

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	2101	FMN	C4'-C3'-C2'	-3.56	107.64	113.57
4	B	2101	FMN	C4A-C10-N10	3.07	120.87	116.48
4	B	2101	FMN	C10-C4A-N5	-2.77	119.16	124.81
4	B	2101	FMN	C4-N3-C2	-2.44	121.31	125.64
4	B	2101	FMN	C5A-C9A-N10	2.03	119.81	117.97

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

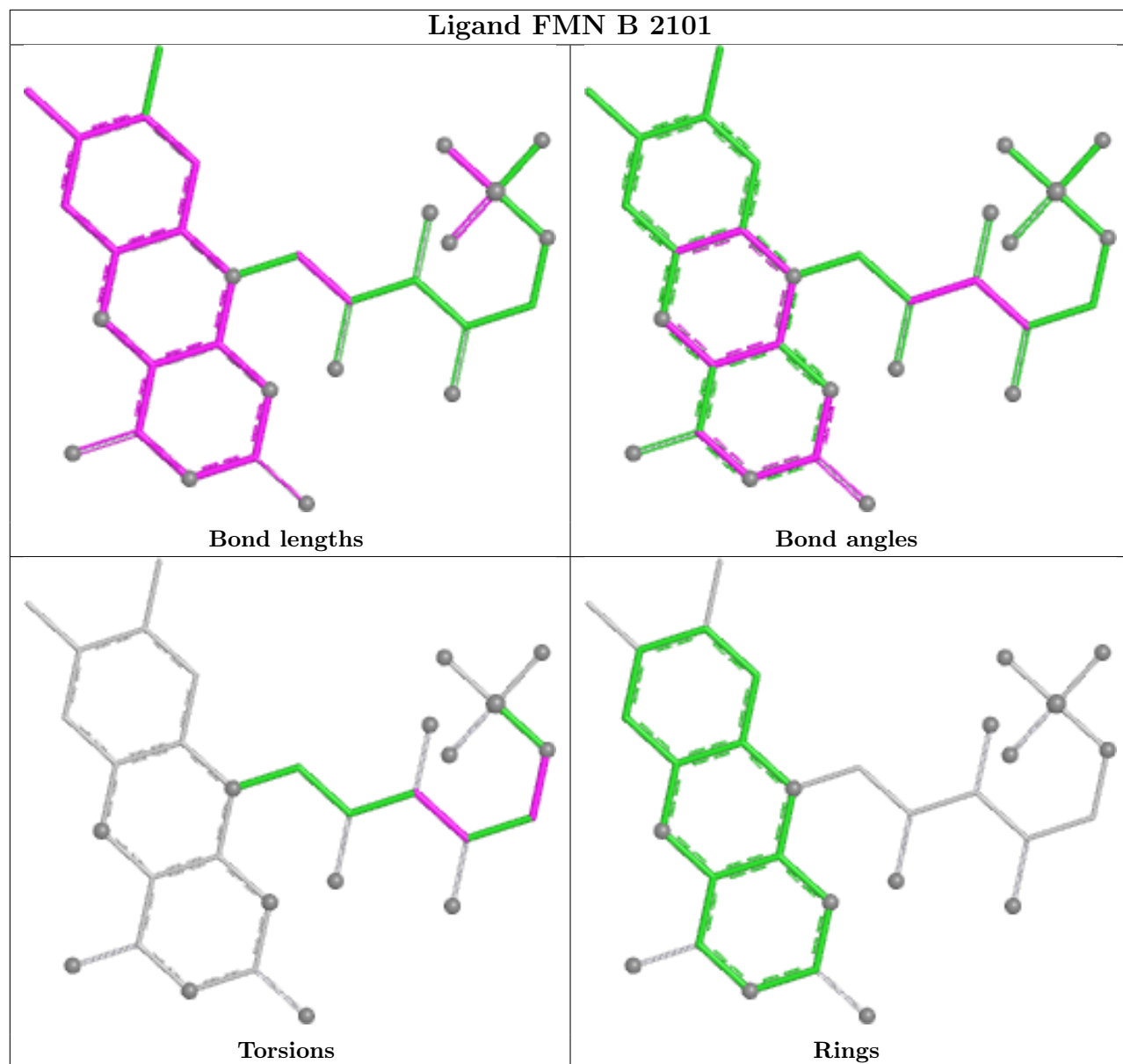
Mol	Chain	Res	Type	Atoms
3	A	1901	PNS	C29-C28-O27-P24
4	B	2101	FMN	C2'-C3'-C4'-C5'
4	B	2101	FMN	O3'-C3'-C4'-C5'
4	B	2101	FMN	C2'-C3'-C4'-O4'
4	B	2101	FMN	O3'-C3'-C4'-O4'

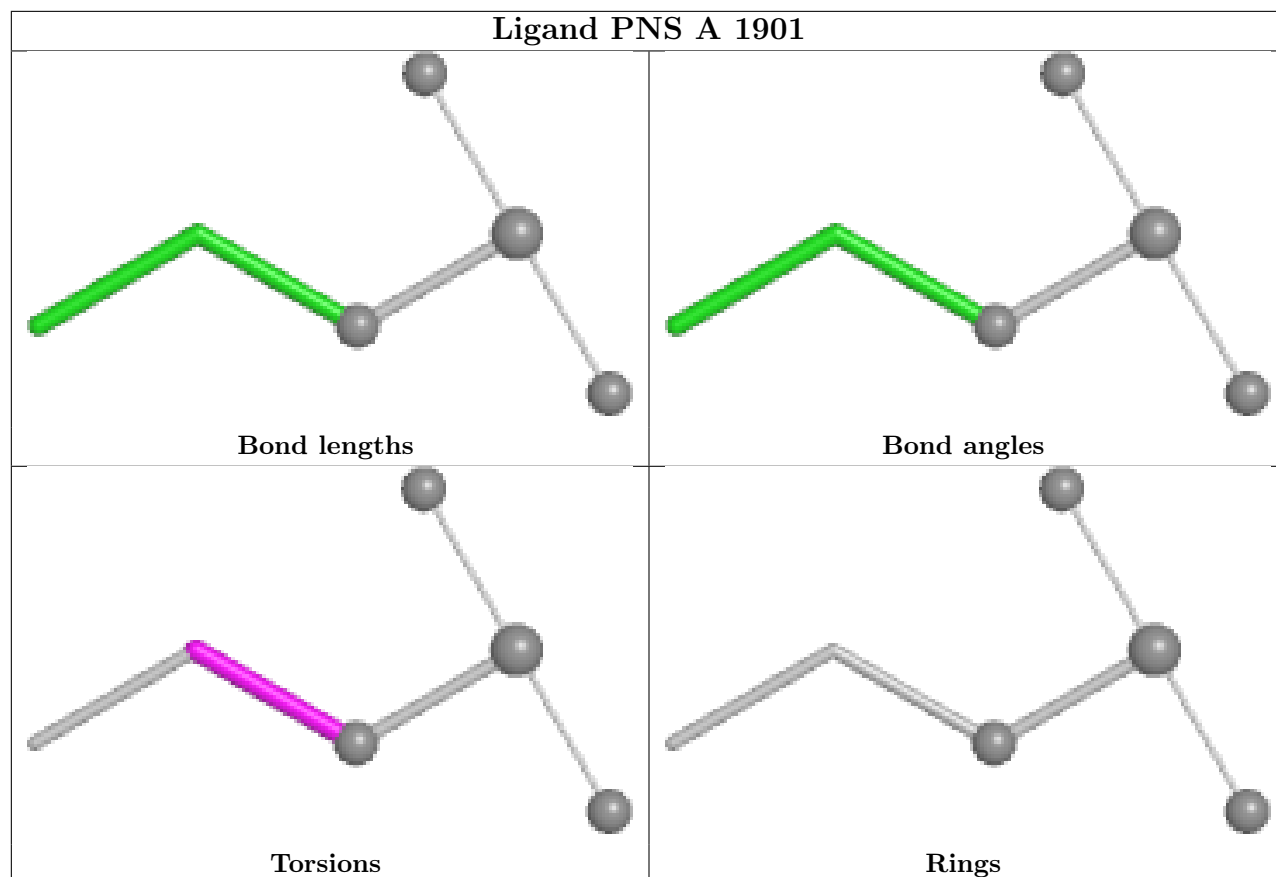
There are no ring outliers.

1 monomer is involved in 34 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	2101	FMN	34	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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

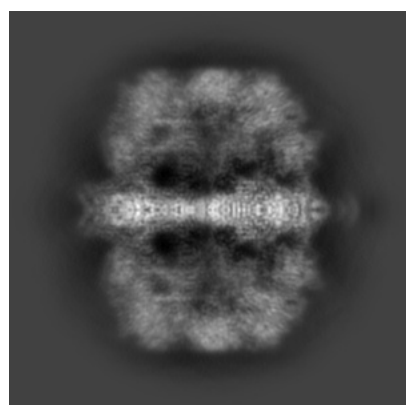
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20657. These allow visual inspection of the internal detail of the map and identification of artifacts.

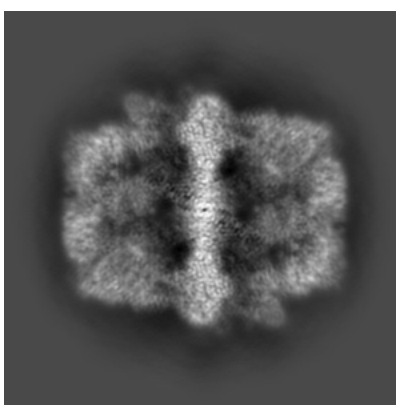
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

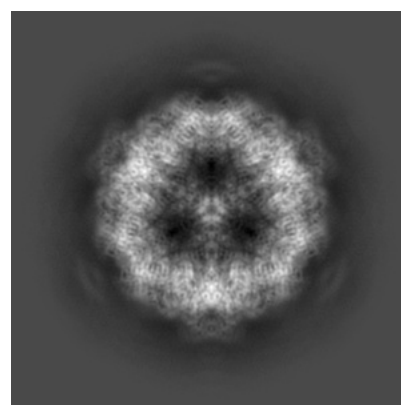
6.1.1 Primary map



X



Y

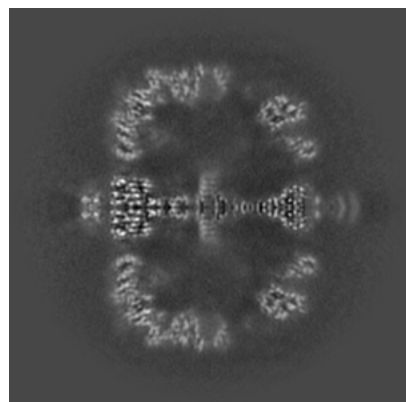


Z

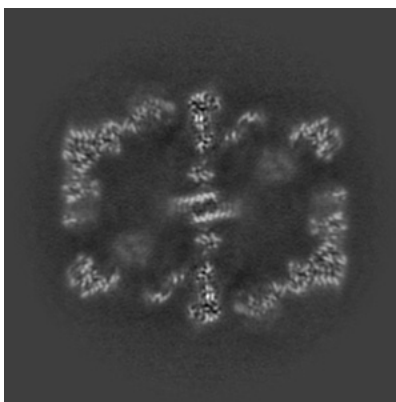
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

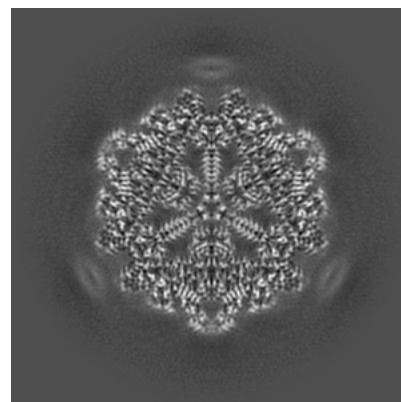
6.2.1 Primary map



X Index: 176



Y Index: 176

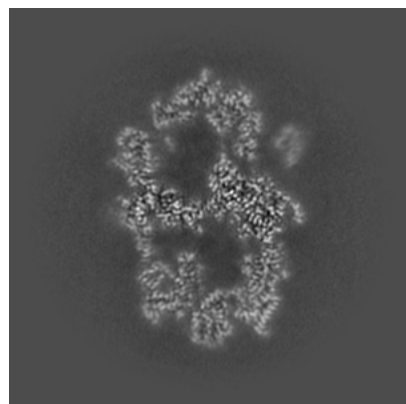


Z Index: 176

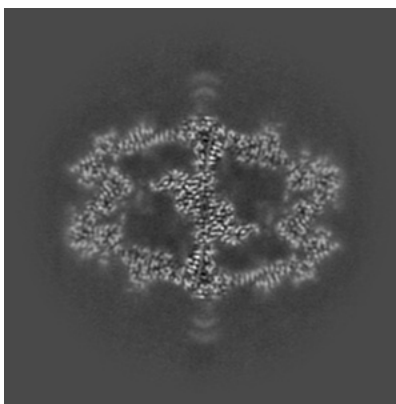
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

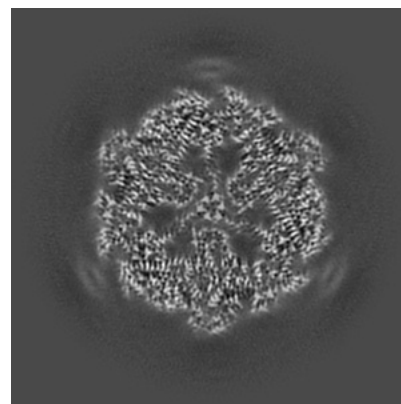
6.3.1 Primary map



X Index: 237



Y Index: 120

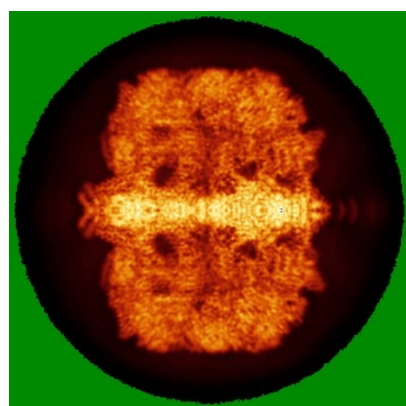


Z Index: 172

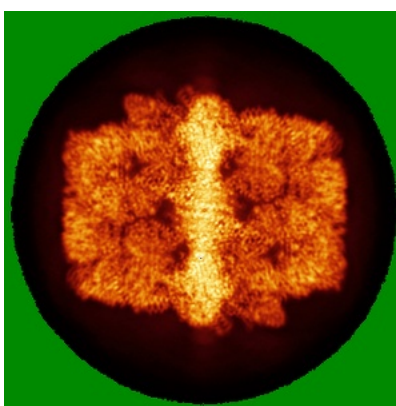
The images above show the largest variance slices of the map in three orthogonal directions.

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

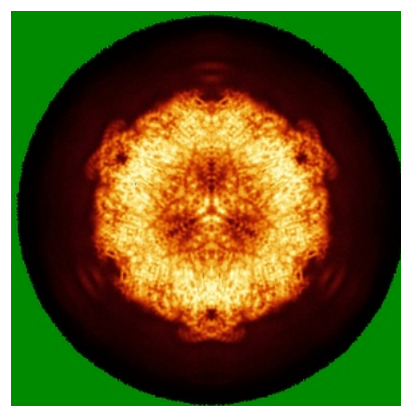
6.4.1 Primary map



X



Y

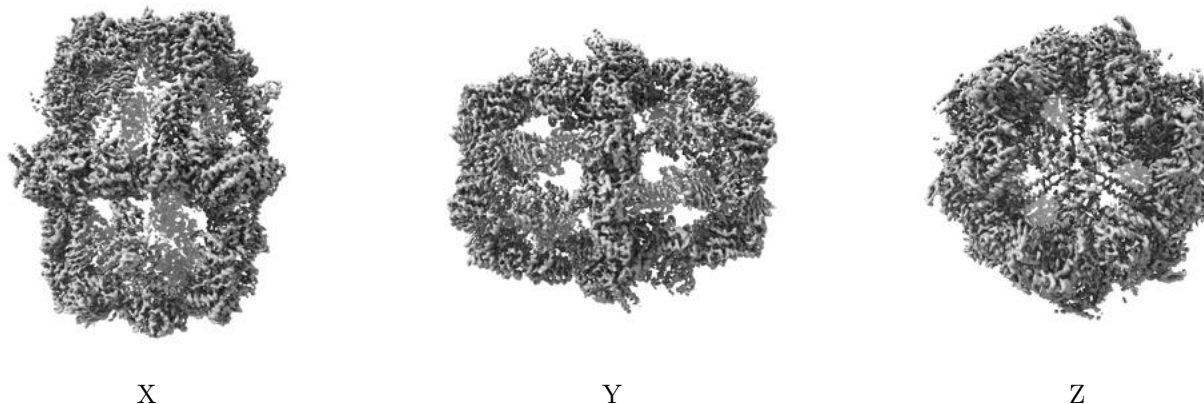


Z

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

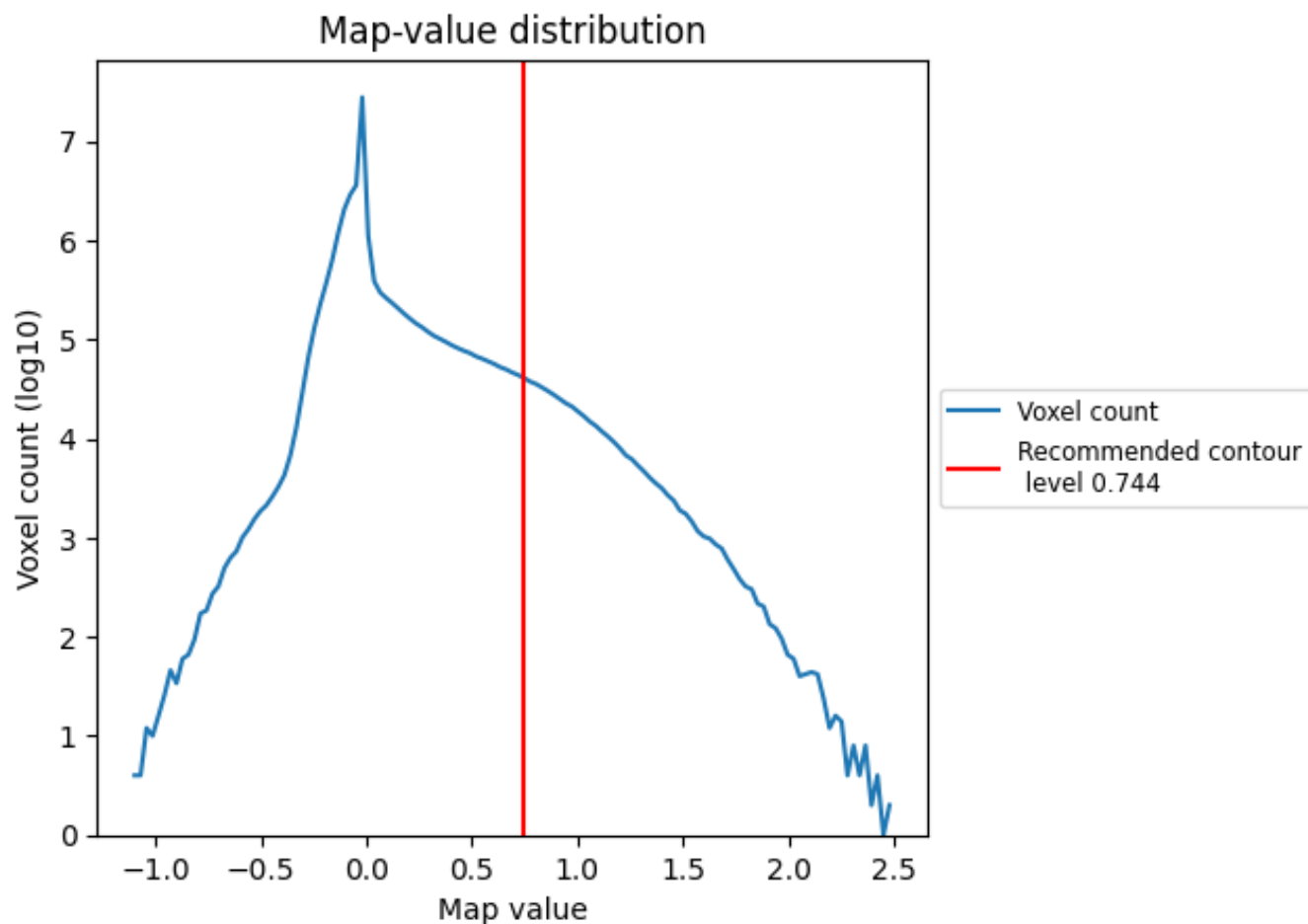
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

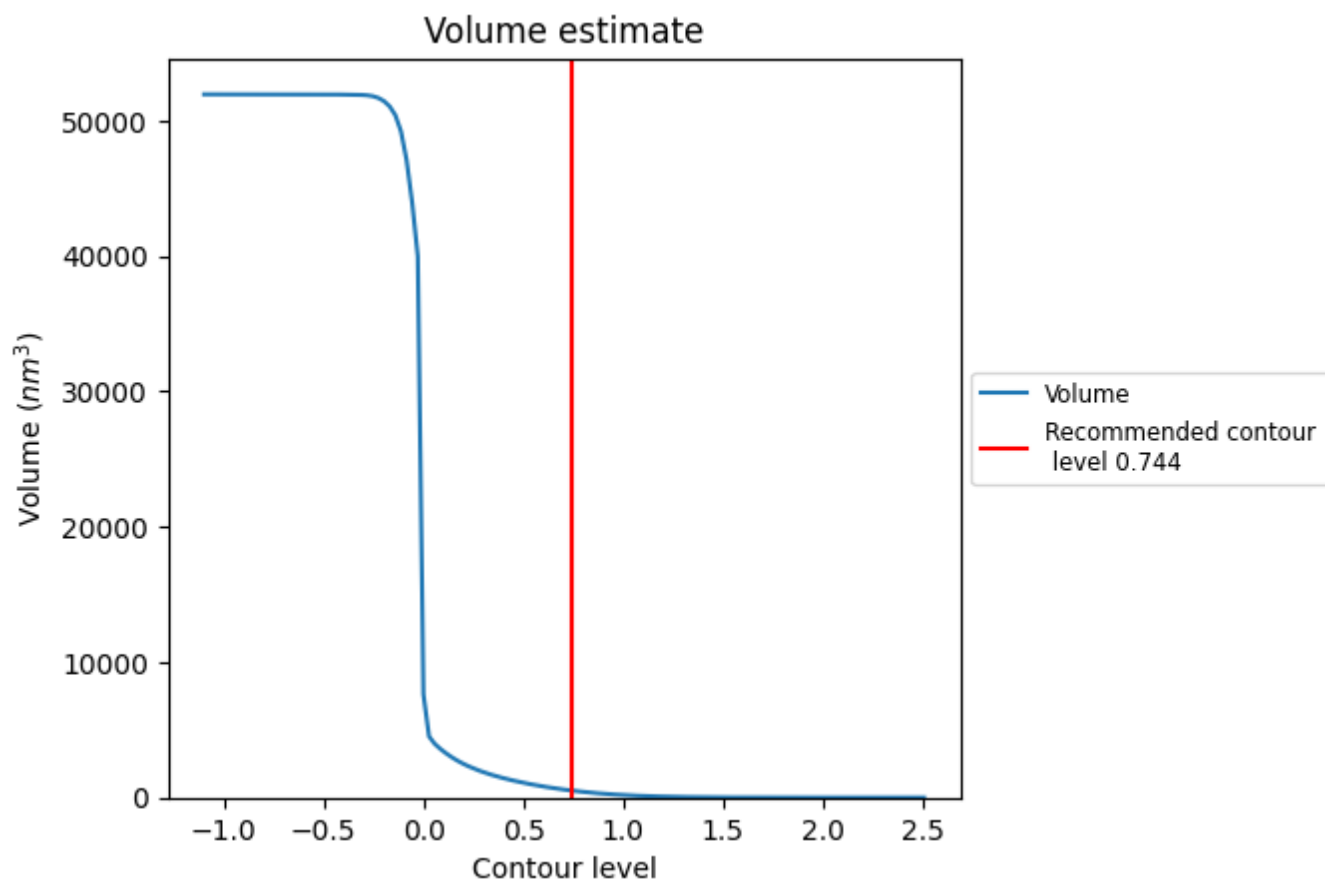
This section contains the results of statistical analysis of the map.

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.

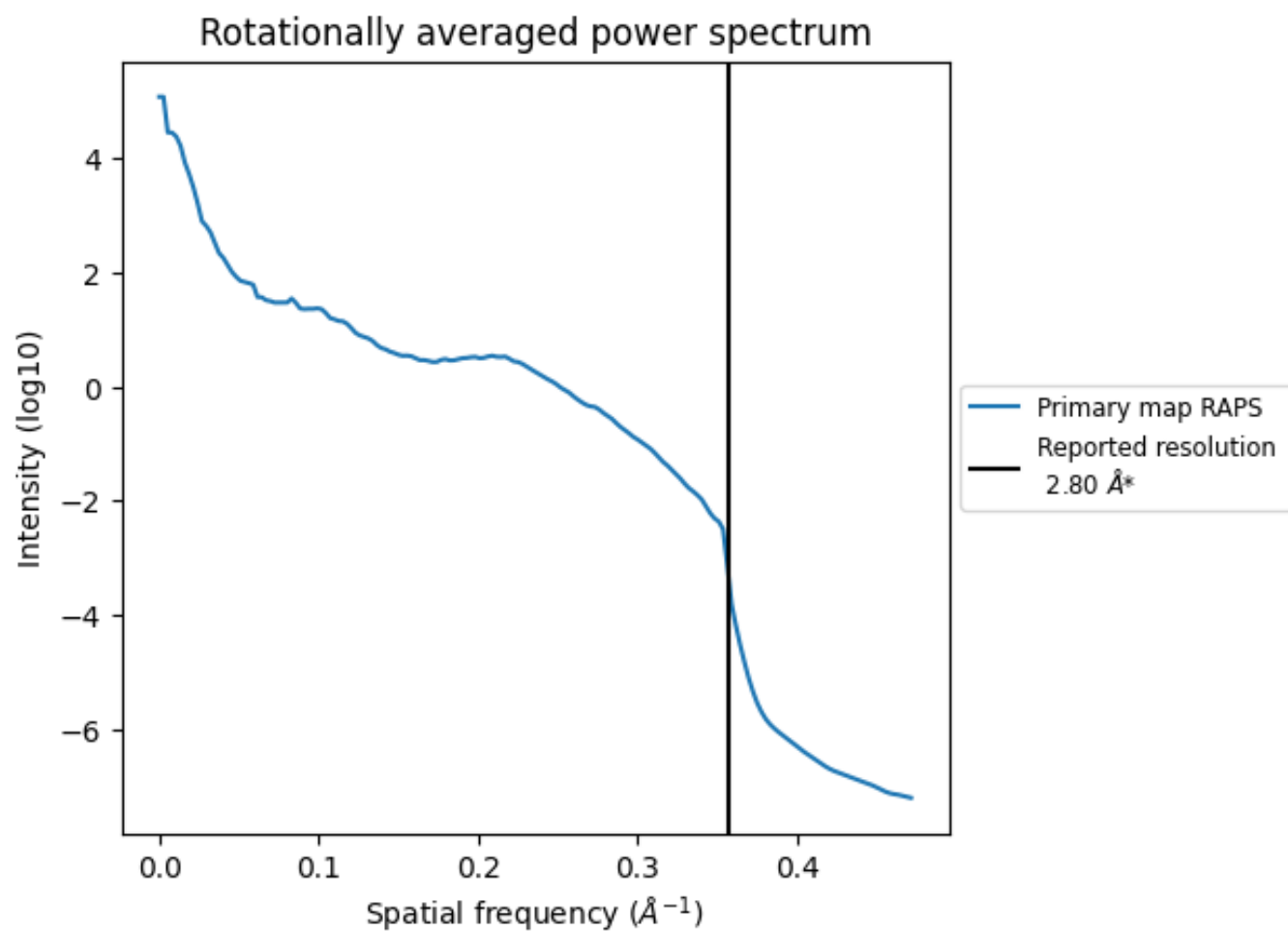
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 515 nm³; this corresponds to an approximate mass of 465 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 0.357 Å⁻¹

8 Fourier-Shell correlation

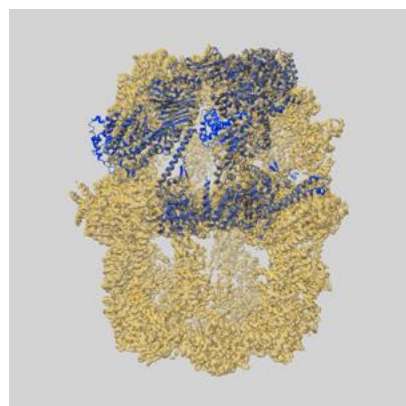
This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

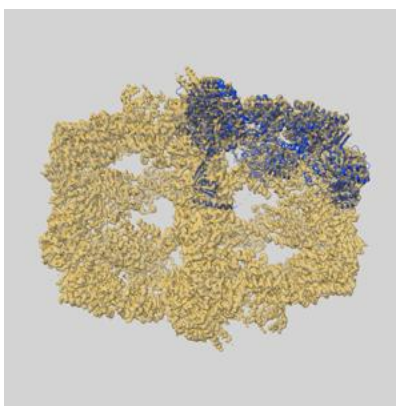
This section contains information regarding the fit between EMDB map EMD-20657 and PDB model 6U5V. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlays

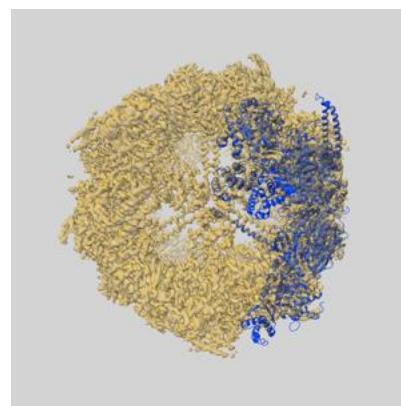
9.1.1 Map-model overlay [i](#)



X

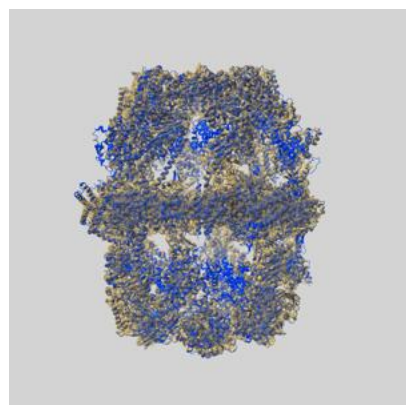


Y

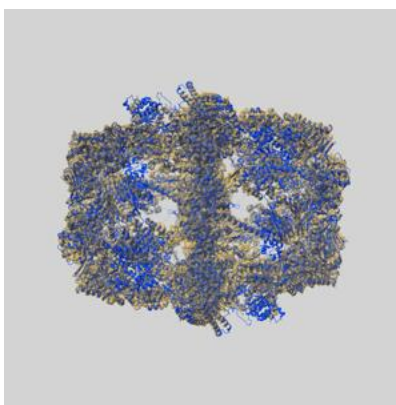


Z

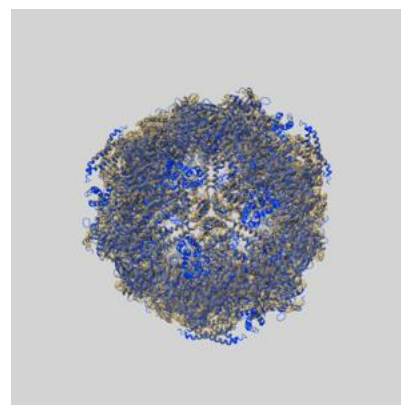
9.1.2 Map-model assembly overlay [i](#)



X



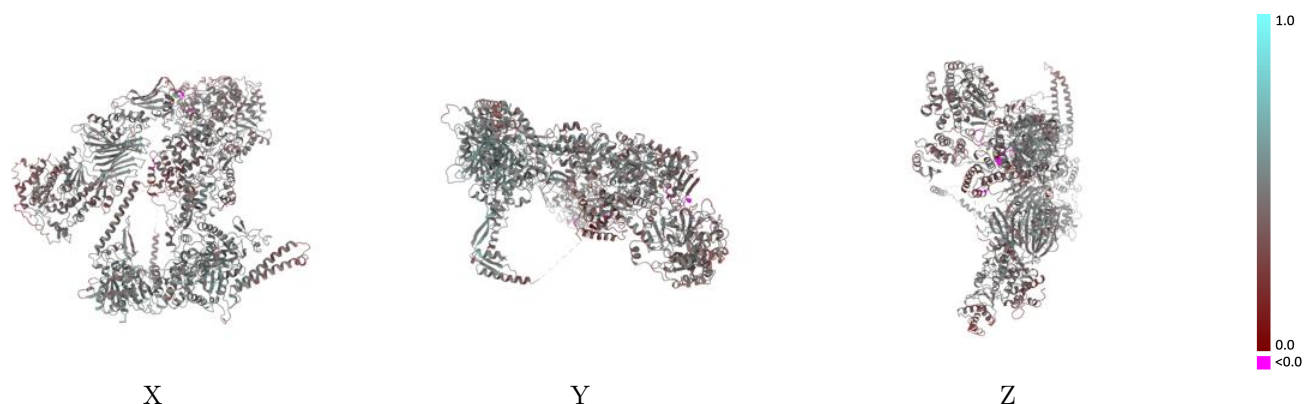
Y



Z

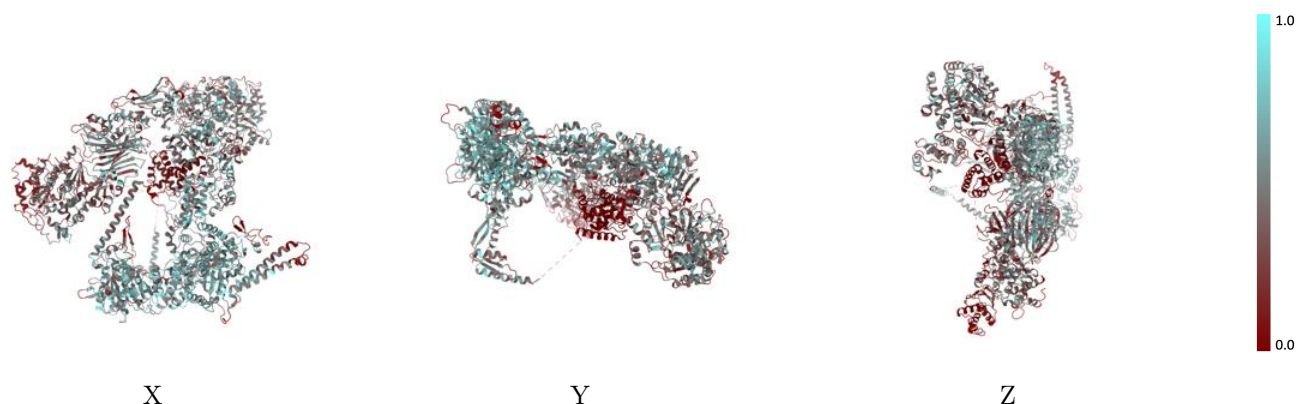
The images above show the 3D surface view of the map at the recommended contour level 0.744 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



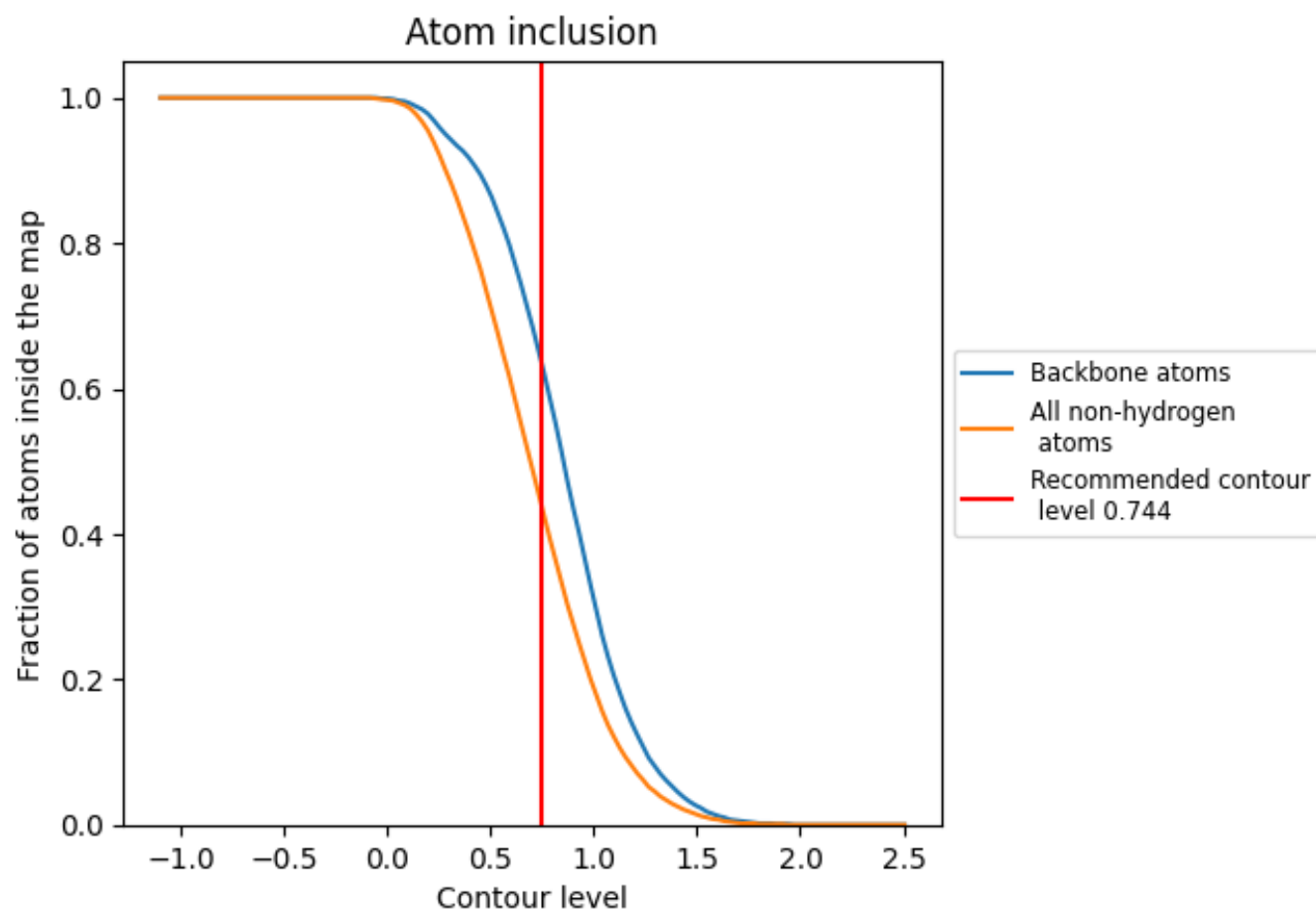
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.744).

9.4 Atom inclusion [i](#)



At the recommended contour level, 64% of all backbone atoms, 44% 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 (0.744) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4420	0.4530
A	0.4990	0.4750
B	0.4000	0.4360

