



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 12:26 PM UTC

PDB ID : 8EYY / pdb_00008eyy
EMDB ID : EMD-28724
Title : Cryo-EM structure of 4 insulins bound full-length mouse IR mutant with physically decoupled alpha CTs (C684S/C685S/C687S, denoted as IR-3CS) Asymmetric conformation 2
Authors : Li, J.; Wu, J.Y.; Hall, C.; Bai, X.C.; Choi, E.
Deposited on : 2022-10-29
Resolution : 4.90 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:

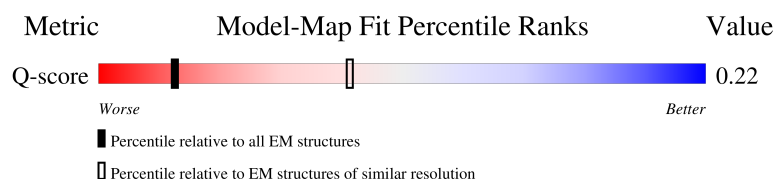
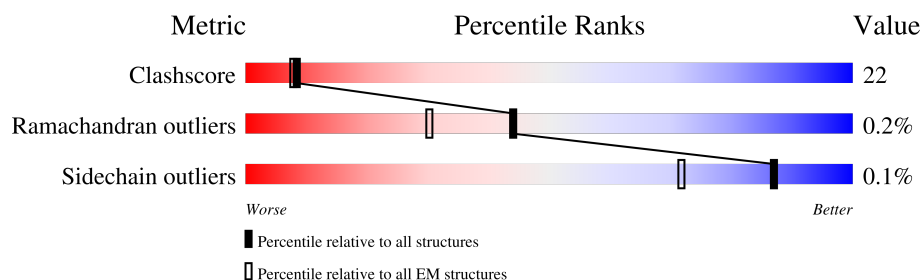
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 4.90 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	1274 (4.40 - 5.40)

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	1345	
1	B	1345	
2	C	110	
2	D	110	

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Mol	Chain	Length	Quality of chain
2	E	110	 35% 8% 56%
2	F	110	 25% 17% 57%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 14301 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 Insulin receptor.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	775	Total	C	N	O	S	0	0
			6284	3995	1080	1168	41		
1	B	810	Total	C	N	O	S	0	0
			6540	4151	1127	1213	49		

There are 6 discrepancies between the modelled and reference sequences:

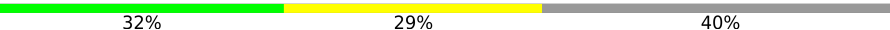
Chain	Residue	Modelled	Actual	Comment	Reference
A	684	SER	CYS	engineered mutation	UNP P15208
A	685	SER	CYS	engineered mutation	UNP P15208
A	687	SER	CYS	engineered mutation	UNP P15208
B	684	SER	CYS	engineered mutation	UNP P15208
B	685	SER	CYS	engineered mutation	UNP P15208
B	687	SER	CYS	engineered mutation	UNP P15208

- Molecule 2 is a protein called Insulin.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	47	Total	C	N	O	S	0	0
			370	235	60	69	6		
2	D	46	Total	C	N	O	S	0	0
			361	229	58	68	6		
2	E	48	Total	C	N	O	S	0	0
			376	238	61	71	6		
2	F	47	Total	C	N	O	S	0	0
			370	235	60	69	6		

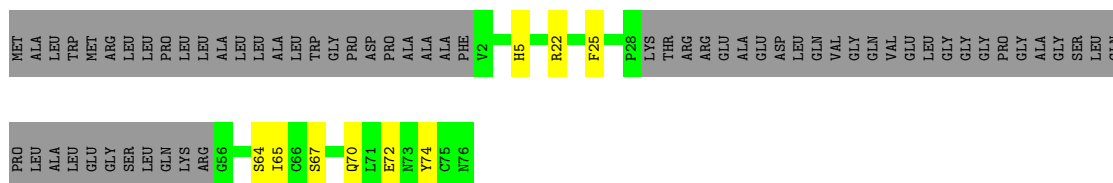
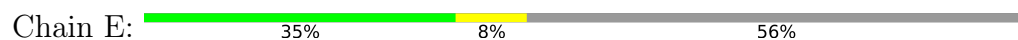
ARG	MET	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY	ASN	GLY
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• Molecule 1: Insulin receptor

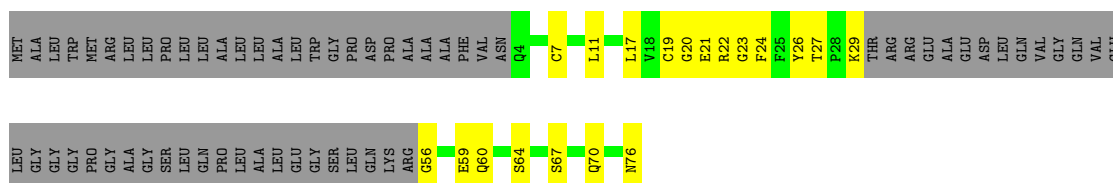
Chain B:  32% 29% 40%

H1	Y91	LYS	W251	R345	T448	P537	Q538	R539	J542	PRO	LYS	SER	GLN	T547	P548	S549	H550	P551	G552	N553	L554	M555	R556	G557	L558	W561	T562	Q563	Y564	A565	L566	F567	V568	K569	T570	L571	F574	E577	R578	R579	T580	Y581	G582	A583	K584	S585	L588	T592	D593	A594	P597	S598	V599	P600	L601	S609																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														
A92	A92	GLY	C253	E353	R451	Q538	Q538	R539	D542	LYS	LYS	SER	GLN	T547	P548	S549	H550	P551	G552	N553	L554	M555	R556	G557	L558	W561	T562	Q563	Y564	A565	L566	F567	V568	K569	T570	L571	F574	E577	R578	R579	T580	Y581	G582	A583	K584	S585	L588	T592	D593	A594	P597	S598	V599	P600	L601	S609																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														
R94	Y94	THR	C253	E353	R451	Q538	Q538	R539	D542	LYS	LYS	SER	GLN	T547	P548	S549	H550	P551	G552	N553	L554	M555	R556	G557	L558	W561	T562	Q563	Y564	A565	L566	F567	V568	K569	T570	L571	F574	E577	R578	R579	T580	Y581	G582	A583	K584	S585	L588	T592	D593	A594	P597	S598	V599	P600	L601	S609																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														
F96	F96	C169	F258	E362	R454	E453	E453	R454	J542	PRO	LYS	SER	GLN	T547	P548	S549	H550	P551	G552	N553	L554	M555	R556	G557	L558	W561	T562	Q563	Y564	A565	L566	F567	V568	K569	T570	L571	F574	E577	R578	R579	T580	Y581	G582	A583	K584	S585	L588	T592	D593	A594	P597	S598	V599	P600	L601	S609																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														
E97	E97	P170	L262	S365	N455	D456	L457	GLN	J542	PRO	LYS	SER	GLN	T547	P548	S549	H550	P551	G552	N553	L554	M555	R556	G557	L558	W561	T562	Q563	Y564	A565	L566	F567	V568	K569	T570	L571	F574	E577	R578	R579	T580	Y581	G582	A583	K584	S585	L588	T592	D593	A594	P597	S598	V599	P600	L601	S609																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														
M98	M98	A171	H263	S365	N455	D456	L457	GLN	J542	PRO	LYS	SER	GLN	T547	P548	S549	H550	P551	G552	N553	L554	M555	R556	G557	L558	W561	T562	Q563	Y564	A565	L566	F567	V568	K569	T570	L571	F574	E577	R578	R579	T580	Y581	G582	A583	K584	S585	L588	T592	D593	A594	P597	S598	V599	P600	L601	S609																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														
V99	V99	V172	R267	T370	R371	R372	S373	L379	S380	R383	K384	L385	H386	L387	L388	R389	E394	Y398	S399	F400	N405	R409	Q410	L411	N412	D413	W414	T420	I421	T422	L426	F427	F428	H429	K433	L436	L439	H440	C441	N442	E443	N444	V445	W446	T447	L448	P449	S450	H451	C452	D453	E454	F455	G456	H457	I458	J459	K460	L461	M462	N463	O464	P465	Q466	R467	S468	T469	U470	V471	W472	X473	Y474	Z475	AA476	AB477	AC478	AD479	AE480	AF481	AG482	AH483	AI484	AJ485	AK486	AL487	AM488	AN489	AO490	AP491	AQ492	AR493	AS494	AT495	AU496	AV497	AW498	AX499	AY500	AZ501	BA502	BB503	BC504	BD505	BE506	BF507	BG508	BH509	BI510	BJ511	BK512	BL513	BM514	BN515	BO516	BP517	BQ518	BR519	BS520	BT521	BU522	BV523	BW524	BX525	BY526	BZ527	CA528	CB529	CC530	CD531	CE532	CF533	CG534	CH535	CI536	CJ537	CK538	CL539	CM540	CN541	CO542	CP543	CQ544	CR545	CS546	CT547	CU548	CV549	CW550	CX551	CY552	CZ553	DA554	DB555	DC556	DD557	DE558	DF559	DG560	DH561	DI562	DJ563	DK564	DL565	DM566	DN567	DO568	DP569	DQ570	DR571	DS572	DT573	DU574	DV575	DW576	DX577	DY578	DZ579	EA580	EB581	EC582	ED583	EE584	EF585	EG586	EH587	EI588	EJ589	EK590	EL591	EM592	EN593	EO594	EP595	EQ596	ER597	ES598	ET599	EU600	EV601	EW602	EX603	EY604	EZ605	FA606	FB607	FC608	FD609	FE610	FF611	FG612	FH613	FI614	FJ615	FK616	FL617	FM618	FN619	FO620	FP621	FQ622	FR623	FS624	FT625	FU626	FV627	FW628	FX629	FY630	FZ631	GA632	GB633	GC634	GD635	GE636	GF637	GG638	GH639	GI640	GJ641	GK642	GL643	GM644	GN645	GO646	GP647	GQ648	GR649	GS650	GT651	GU652	GV653	GW654	GX655	GY656	GZ657	HA658	HB659	HC660	HD661	HE662	HF663	HG664	HH665	HI666	HJ667	HK668	HL669	HM670	HN671	HO672	HP673	HQ674	HR675	HS676	HT677	HU678	HV679	HW680	HX681	HY682	HZ683	IA684	IB685	IC686	ID687	IE688	IF689	IG690	IH691	II692	IJ693	IK694	IL695	IM696	IN697	IO698	IP699	IQ700	IR701	IS702	IT703	IU704	IV705	IW706	IX707	IY708	IZ709	JA710	JB711	JC712	JD713	JE714	JF715	JG716	JH717	JI718	JJ719	JK720	JL721	JM722	JN723	JO724	JP725	jq726	JR727	JS728	JT729	JU730	JV731	JW732	JX733	JY734	JZ735	KA736	KB737	KC738	KD739	KE740	KF741	KG742	KH743	KI744	KJ745	KK746	KL747	KM748	KN749	KO750	KP751	KQ752	KR753	KS754	KT755	KU756	KV757	KW758	KX759	KY760	KZ761	LA762	LB763	LC764	LD765	LE766	LF767	LG768	LH769	LI770	LJ771	LK772	LM773	LN774	LO775	LP776	LQ777	LR778	LS779	LT780	LU781	LV782	LV783	LV784	LV785	LV786	LV787	LV788	LV789	LV790	LV791	LV792	LV793	LV794	LV795	LV796	LV797	LV798	LV799	LV800	LV801	LV802	LV803	LV804	LV805	LV806	LV807	LV808	LV809	LV810	LV811	LV812	LV813	LV814	LV815	LV816	LV817	LV818	LV819	LV820	LV821	LV822	LV823	LV824	LV825	LV826	LV827	LV828	LV829	LV830	LV831	LV832	LV833	LV834	LV835	LV836	LV837	LV838	LV839	LV840	LV841	LV842	LV843	LV844	LV845	LV846	LV847	LV848	LV849	LV850	LV851	LV852	LV853	LV854	LV855	LV856	LV857	LV858	LV859	LV860	LV861	LV862	LV863	LV864	LV865	LV866	LV867	LV868	LV869	LV870	LV871	LV872	LV873	LV874	LV875	LV876	LV877	LV878	LV879	LV880	LV881	LV882	LV883	LV884	LV885	LV886	LV887	LV888	LV889	LV890	LV891	LV892	LV893	LV894	LV895	LV896	LV897	LV898	LV899	LV900	LV901	LV902	LV903	LV904	LV905	LV906	LV907	LV908	LV909	LV910	LV911	LV912	LV913	LV914	LV915	LV916	LV917	LV918	LV919	LV920	LV921	LV922	LV923	LV924	LV925	LV926	LV927	LV928	LV929	LV930	LV931	LV932	LV933	LV934	LV935	LV936	LV937	LV938	LV939	LV940	LV941	LV942	LV943	LV944	LV945	LV946	LV947	LV948	LV949	LV950	LV951	LV952	LV953	LV954	LV955	LV956	LV957	LV958	LV959	LV960	LV961	LV962	LV963	LV964	LV965	LV966	LV967	LV968	LV969	LV970	LV971	LV972	LV973	LV974	LV975	LV976	LV977	LV978	LV979	LV980	LV981	LV982	LV983	LV984	LV985	LV986	LV987	LV988	LV989	LV990	LV991	LV992	LV993	LV994	LV995	LV996	LV997	LV998	LV999	LV1000	LV1001	LV1002	LV1003	LV1004	LV1005	LV1006	LV1007	LV1008	LV1009	LV1010	LV1011	LV1012	LV1013	LV1014	LV1015	LV1016	LV1017	LV1018	LV1019	LV1020	LV1021	LV1022	LV1023	LV1024	LV1025	LV1026	LV1027	LV1028	LV1029	LV1030	LV1031	LV1032	LV1033	LV1034	LV1035	LV1036	LV1037	LV1038	LV1039	LV1040	LV1041	LV1042	LV1043	LV1044	LV1045	LV1046	LV1047	LV1048	LV1049	LV1050	LV1051	LV1052	LV1053	LV1054	LV1055	LV1056	LV1057	LV1058	LV1059	LV1060	LV1061	LV1062	LV1063	LV1064	LV1065	LV1066	LV1067	LV1068	LV1069	LV1070	LV1071	LV1072	LV1073	LV1074	LV1075	LV1076	LV1077	LV1078	LV1079	LV1080	LV1081	LV1082	LV1083	LV1084	LV1085	LV1086	LV1087	LV1088	LV1089	LV1090	LV1091	LV1092	LV1093	LV1094	LV1095	LV1096	LV1097	LV1098	LV1099	LV1100	LV1101	LV1102	LV1103	LV1104	LV1105	LV1106	LV1107	LV1108	LV1109	LV1110	LV1111	LV1112	LV1113	LV1114	LV1115	LV1116	LV1117	LV1118	LV1119	LV1120	LV1121	LV1122	LV1123	LV1124	LV1125	LV1126	LV1127	LV1128	LV1129	LV1130	LV1131	LV1132	LV1133	LV1134	LV1135	LV1136	LV1137	LV1138	LV1139	LV1140	LV1141	LV1142	LV1143	LV1144	LV1145	LV1146	LV1147	LV1148	LV1149	LV1150	LV1151	LV1152	LV1153	LV1154	LV1155	LV1156	LV1157	LV1158	LV1159	LV1160	LV1161	LV1162	LV1163	LV1164	LV1165	LV1166	LV1167	LV1168	LV1169	LV1170	LV1171	LV1172	LV1173	LV1174	LV1175	LV1176	LV1177	LV1178	LV1179	LV1180	LV1181	LV1182	LV1183	LV1184	LV1185	LV1186	LV1187	LV1188	LV1189	LV1190	LV1191	LV1192	LV1193	LV1194	LV1195	LV1196	LV1197	LV1198	LV1199	LV1200	LV1201	LV1202	LV1203	LV1204	LV1205	LV1206	LV1207	LV1208	LV1209	LV1210	LV1211	LV1212	LV1213	LV1214	LV1215	LV1216	LV1217	LV1218	LV1219	LV1220	LV1221	LV1222	LV1223	LV1224	LV1225	LV1226	LV1227	LV1228	LV1229	LV1230	LV1231	LV1232	LV1233	LV1234	LV1235	LV1236	LV1237	LV1238	LV1239	LV1240	LV1241	LV1242	LV1243	LV1244	LV1245	LV1246	LV1247	LV1248	LV1249	LV1250	LV1251	LV1252	LV1253	LV1254	LV1255	LV1256	LV1257	LV1258	LV1259	LV1260	LV1261	LV1262	LV1263	LV1264	LV1265	LV1266	LV1267	LV1268	LV1269	LV1270	LV1271	LV1272	LV1273	LV1274	LV1275	LV1276	LV1277	LV1278	LV1279	LV1280	LV1281	LV1282	LV1283	LV1284	LV1285	LV1286	LV1287	LV1288	LV1289	LV1290	LV1291	LV1292	LV1293	LV1294	LV1295	LV1296	LV1297	LV1298	LV1299	LV1300	LV1301	LV1302	LV1303	LV1304	LV1305	LV1306	LV1307	LV1308	LV1309	LV1310	LV1311	LV1312	LV1313	LV1314	LV1315	LV1316	LV1317	LV1318	LV1319	LV1320	LV1321	LV1322	LV1323	LV1324	LV1325	LV1326	LV1327	LV1328	LV1329	LV1330	LV1331	LV1332	LV1333	LV1334	LV1335	LV1336	LV1337	LV1338	LV1339	LV1340	LV1341	LV1342	LV1343	LV1344	LV1345	LV1346	LV1347	LV1348	LV1349	LV1350	LV1351	LV1352	LV1353	LV1354	LV1355	LV1356	LV1357	LV1358	LV1359	LV1360	LV1361	LV1362	LV1363	LV1364	LV1365	LV1366	LV1367	LV1368	LV1369	LV1370	LV1371	LV1372	LV1373	LV1374	LV1375	LV1376	LV1377	LV1378	LV1379	LV1380	LV1381	LV1382	LV1383	LV1384	LV1385	LV1386	LV1387	LV1388	LV1389	LV1390	LV1391	LV1392	LV1393	LV1394	LV1395	LV1396	LV1397	LV1398	LV1399	LV1400	LV1401	LV1402	LV1403	LV1404	LV1405	LV1406	LV1407	LV1408	LV1409	LV1410	LV1411	LV1412	LV1413	LV1414	LV1415	LV1416	LV1417	LV1418	LV1419	LV1420	LV1421	LV1422	LV1423	LV1424	LV1425	LV1426	LV1427	LV1428	LV1429	LV1430	LV1431	LV1432

- Molecule 2: Insulin



- Molecule 2: Insulin



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	104347	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1600	Depositor
Maximum defocus (nm)	2600	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.110	Depositor
Minimum map value	-0.040	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.018	Depositor
Map size (Å)	324.0, 324.0, 324.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08, 1.08, 1.08	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.12	0/6437	0.32	0/8722
1	B	0.12	0/6703	0.33	0/9091
2	C	0.12	0/377	0.39	0/508
2	D	0.15	0/368	0.39	0/497
2	E	0.10	0/383	0.30	0/518
2	F	0.10	0/377	0.31	0/508
All	All	0.12	0/14645	0.33	0/19844

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	6284	0	6118	273	0
1	B	6540	0	6344	292	0
2	C	370	0	344	23	0
2	D	361	0	331	18	0
2	E	376	0	346	7	0
2	F	370	0	344	14	0
All	All	14301	0	13827	605	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 22.

The worst 5 of 605 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)
1:B:886:VAL:O	1:B:902:PRO:HA	1.72	0.88
1:A:354:LEU:O	1:A:358:LEU:HB2	1.83	0.78
1:B:853:ARG:NH1	1:B:881:PRO:O	2.18	0.77
1:A:245:TYR:HB3	1:A:253:CYS:HB3	1.68	0.76
1:B:547:THR:O	1:B:549:SER:N	2.19	0.75

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	761/1345 (57%)	710 (93%)	49 (6%)	2 (0%)	36	71
1	B	798/1345 (59%)	731 (92%)	66 (8%)	1 (0%)	48	83
2	C	43/110 (39%)	37 (86%)	6 (14%)	0	100	100
2	D	42/110 (38%)	42 (100%)	0	0	100	100
2	E	44/110 (40%)	44 (100%)	0	0	100	100
2	F	43/110 (39%)	39 (91%)	3 (7%)	1 (2%)	5	28
All	All	1731/3130 (55%)	1603 (93%)	124 (7%)	4 (0%)	44	77

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	548	PRO
1	A	532	VAL
1	A	794	ASP
2	F	26	TYR

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	708/1211 (58%)	708 (100%)	0	100	100
1	B	737/1211 (61%)	736 (100%)	1 (0%)	88	88
2	C	42/88 (48%)	42 (100%)	0	100	100
2	D	41/88 (47%)	41 (100%)	0	100	100
2	E	43/88 (49%)	43 (100%)	0	100	100
2	F	42/88 (48%)	42 (100%)	0	100	100
All	All	1613/2774 (58%)	1612 (100%)	1 (0%)	87	88

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	470	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	418	ASN
1	B	513	GLN
2	C	73	ASN
1	B	766	ASN
1	B	786	GLN

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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.

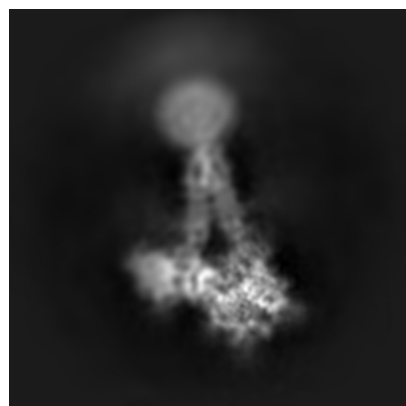
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-28724. These allow visual inspection of the internal detail of the map and identification of artifacts.

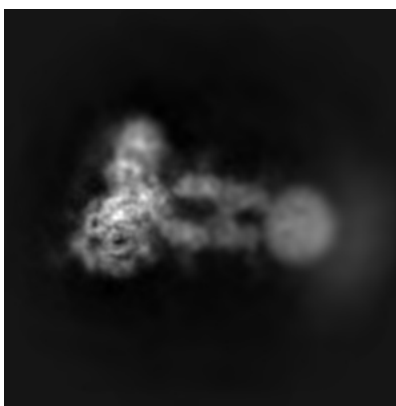
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

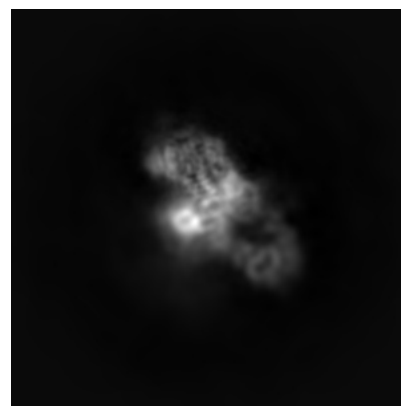
6.1.1 Primary map



X

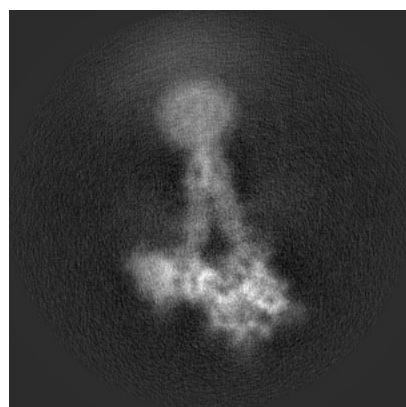


Y

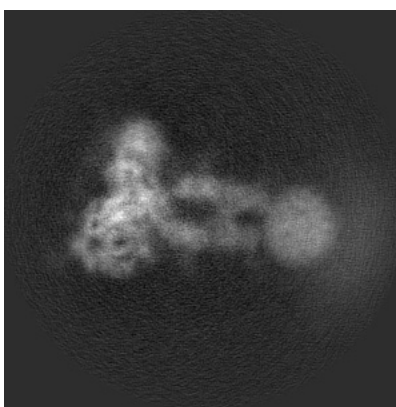


Z

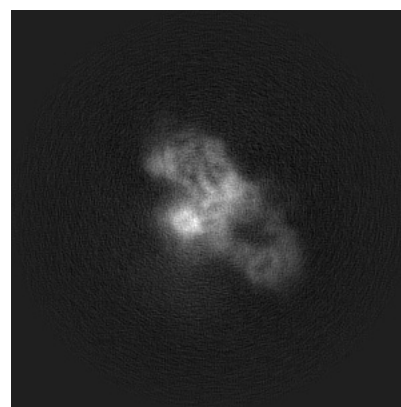
6.1.2 Raw map



X



Y

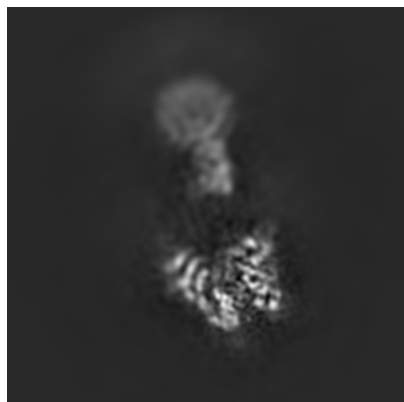


Z

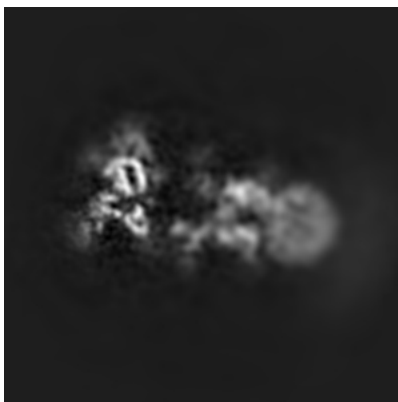
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

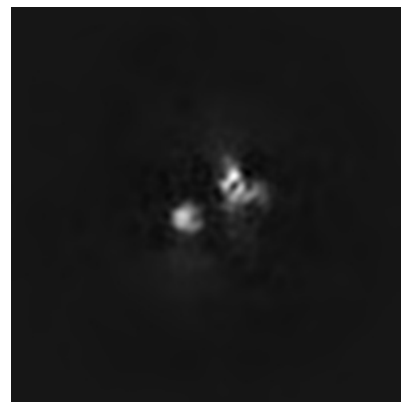
6.2.1 Primary map



X Index: 150

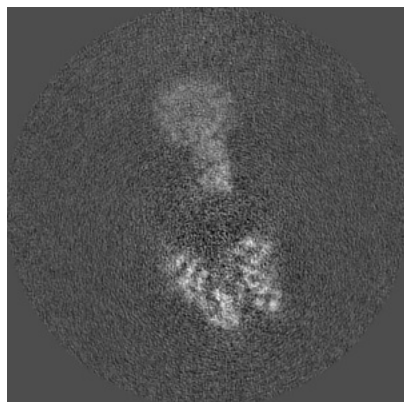


Y Index: 150

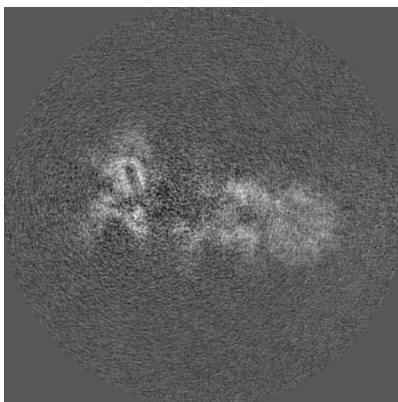


Z Index: 150

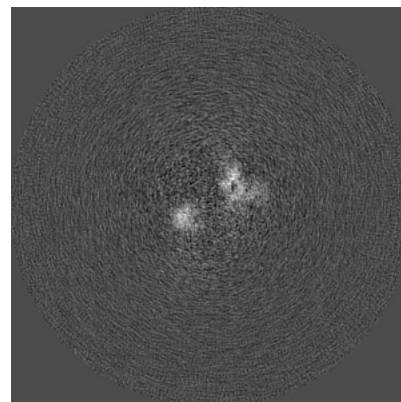
6.2.2 Raw map



X Index: 150



Y Index: 150

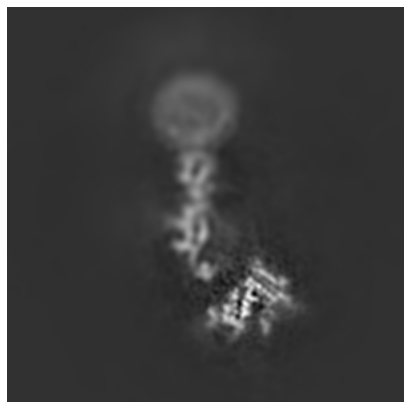


Z Index: 150

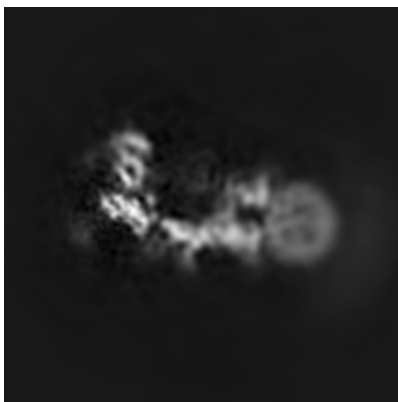
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

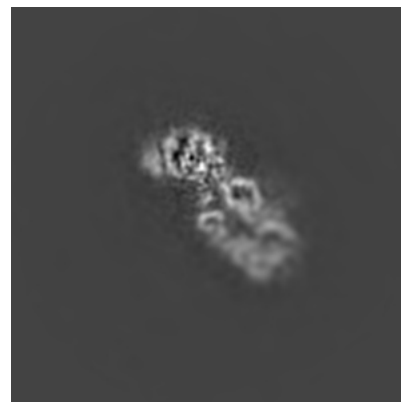
6.3.1 Primary map



X Index: 133

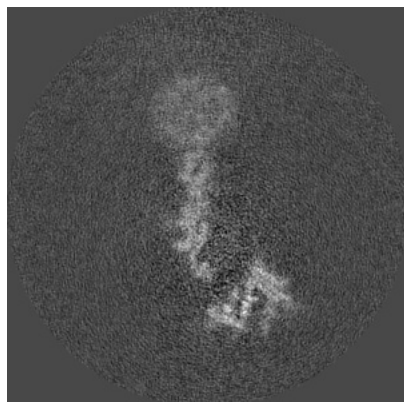


Y Index: 145

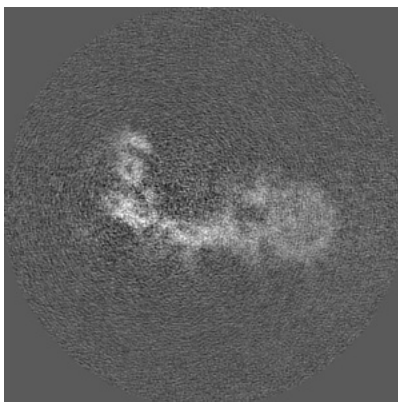


Z Index: 88

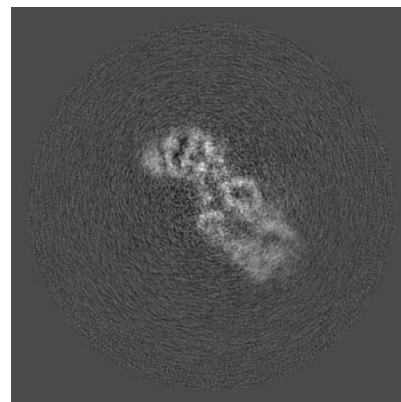
6.3.2 Raw map



X Index: 134



Y Index: 143



Z Index: 88

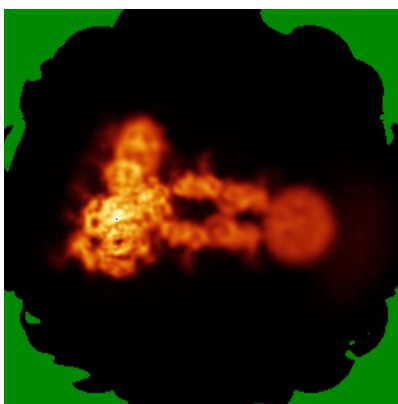
The images above show the largest variance slices of the map in three orthogonal directions.

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

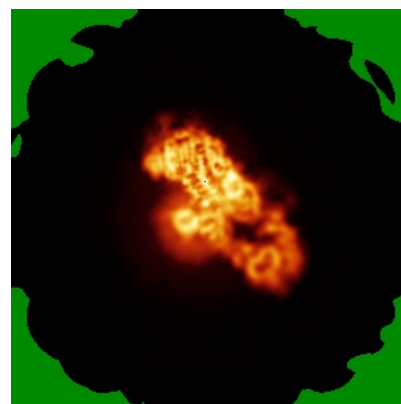
6.4.1 Primary map



X

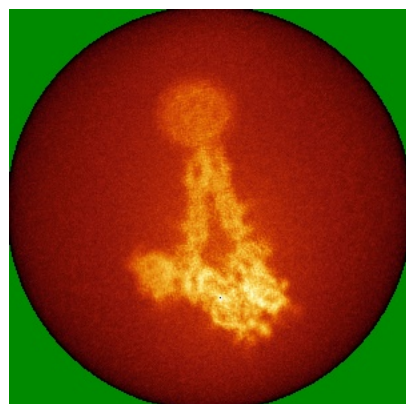


Y

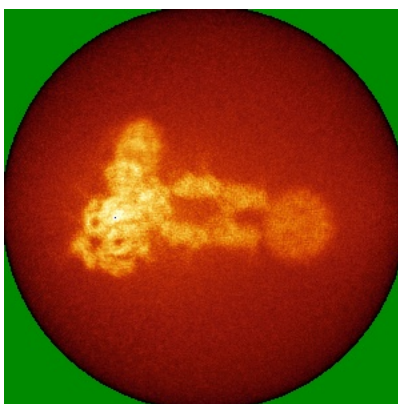


Z

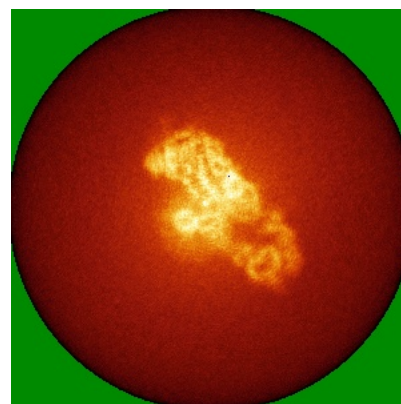
6.4.2 Raw map



X



Y

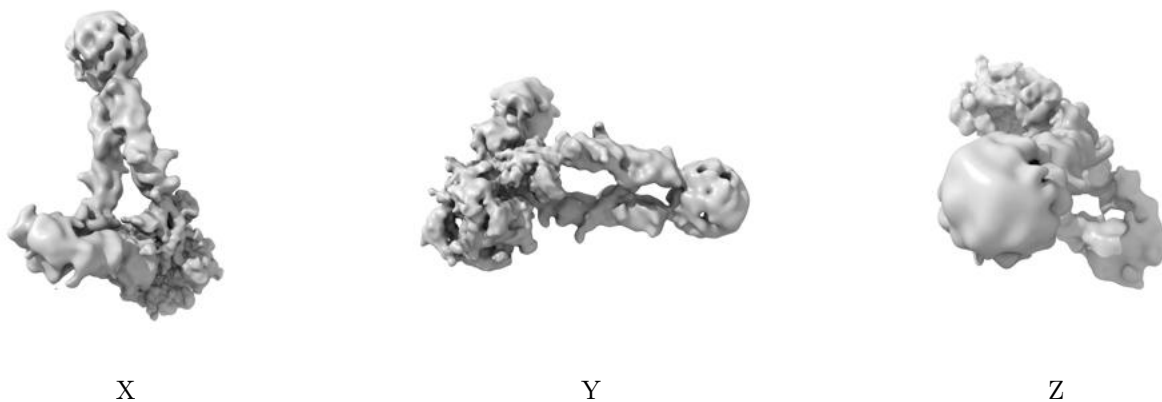


Z

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

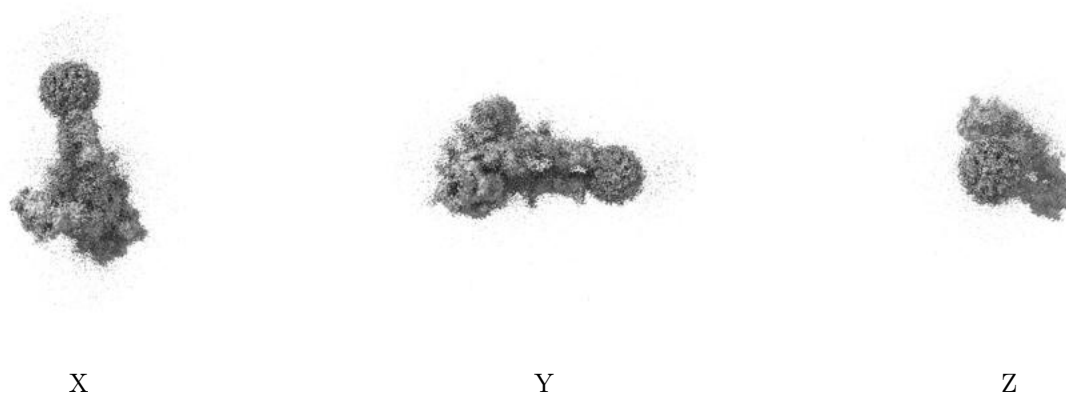
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.018. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

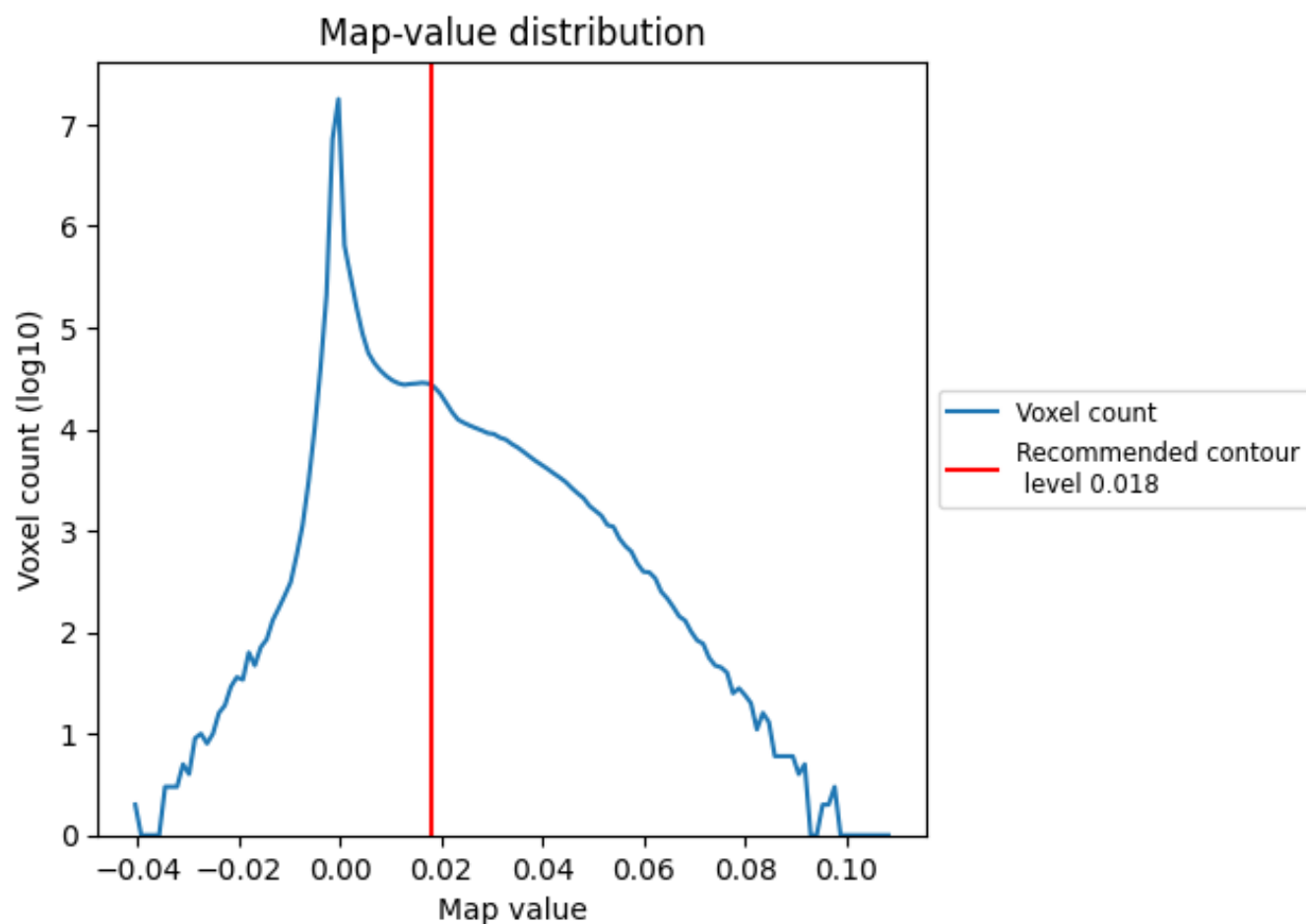
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

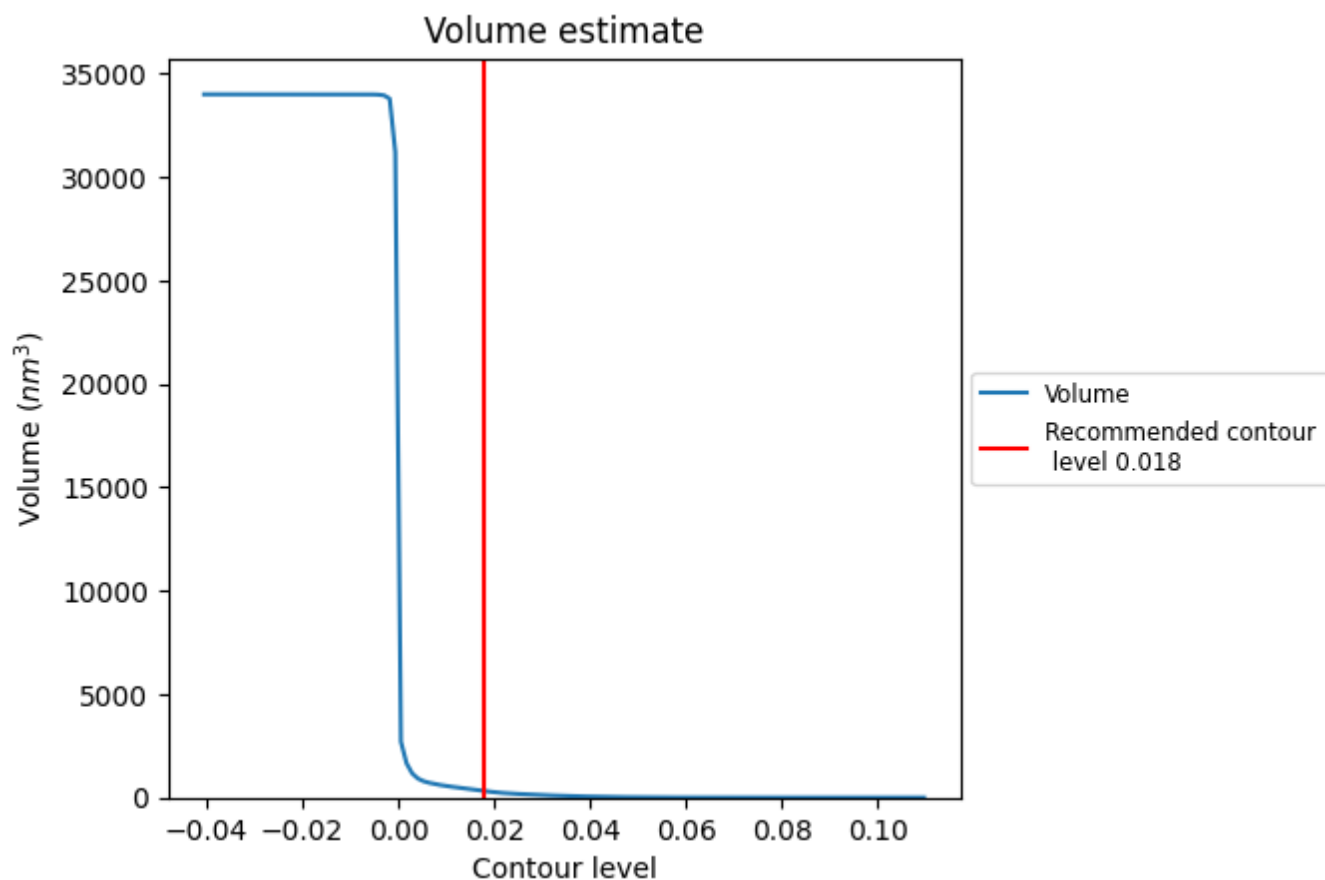
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

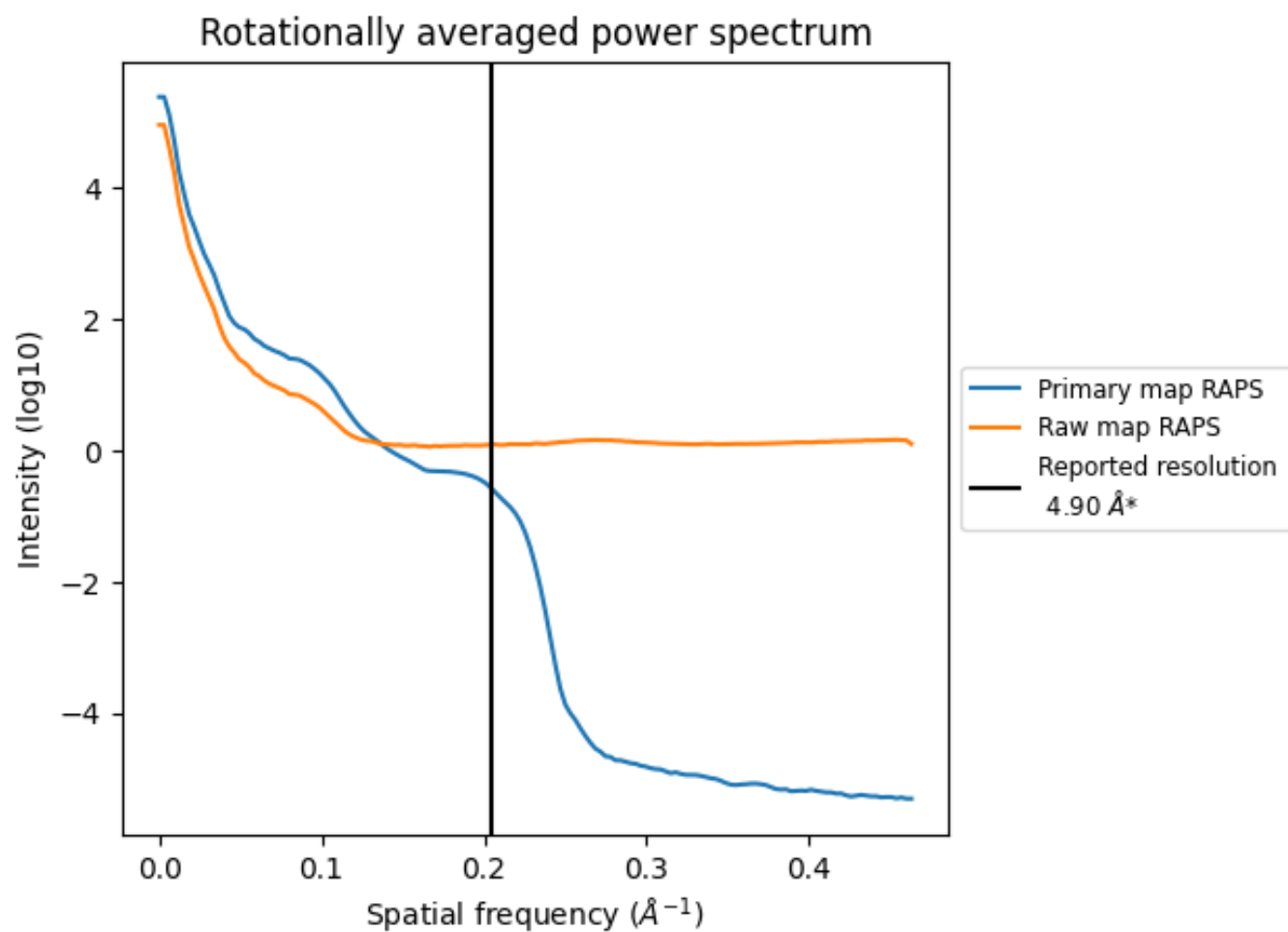
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 317 nm³; this corresponds to an approximate mass of 287 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 ⓘ

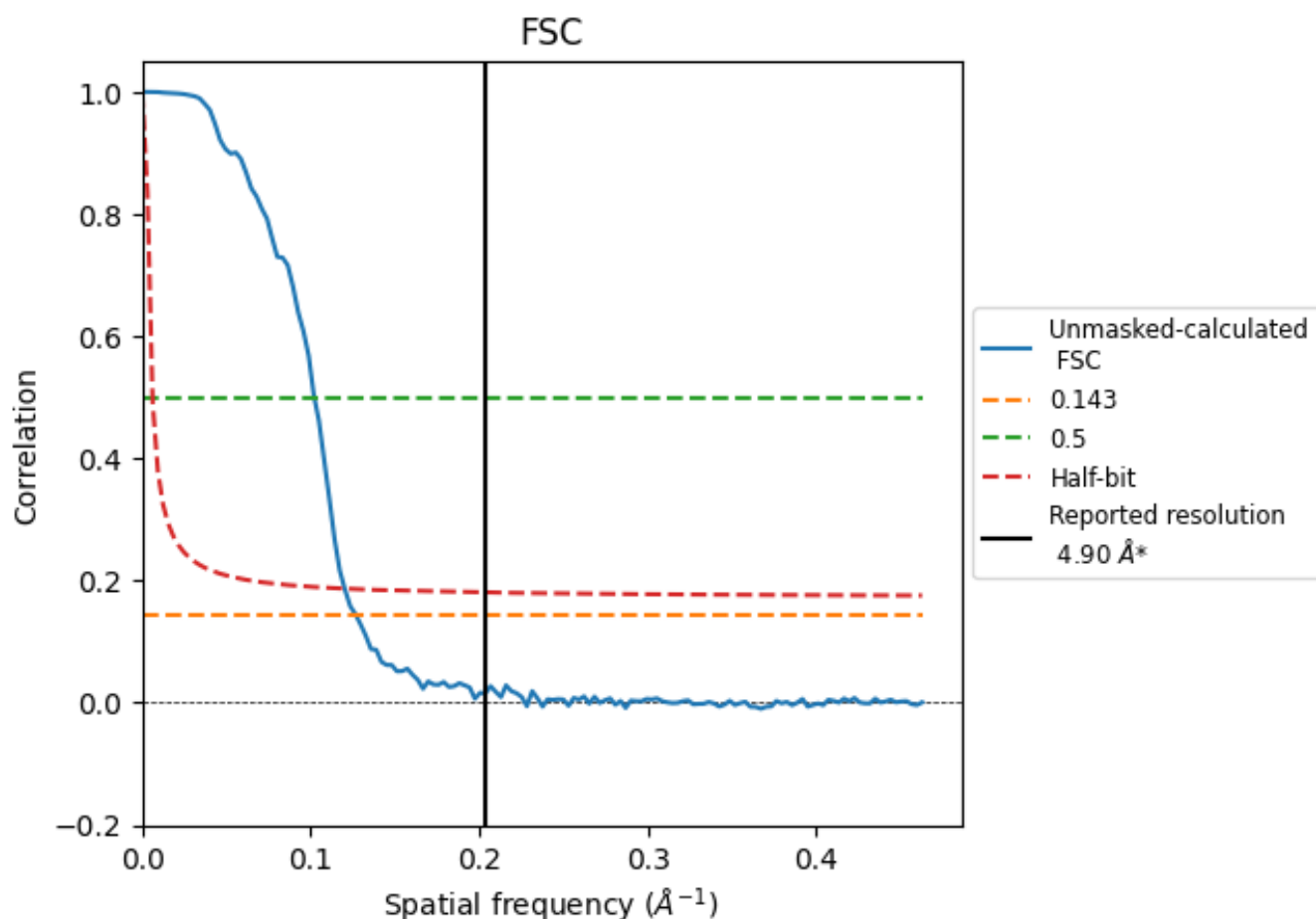


*Reported resolution corresponds to spatial frequency of 0.204 Å⁻¹

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 0.204 Å⁻¹

8.2 Resolution estimates [i](#)

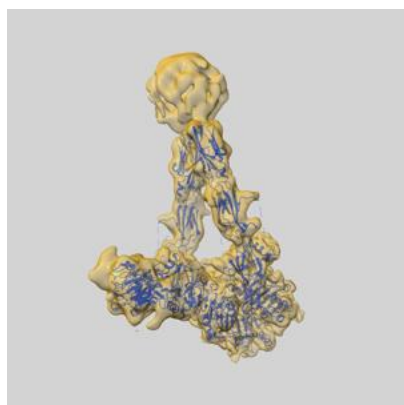
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.90	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	7.87	9.79	8.32

*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 7.87 differs from the reported value 4.9 by more than 10 %

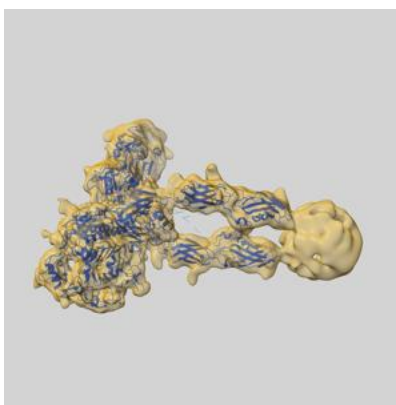
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-28724 and PDB model 8EYY. Per-residue inclusion information can be found in section [3](#) on page [5](#).

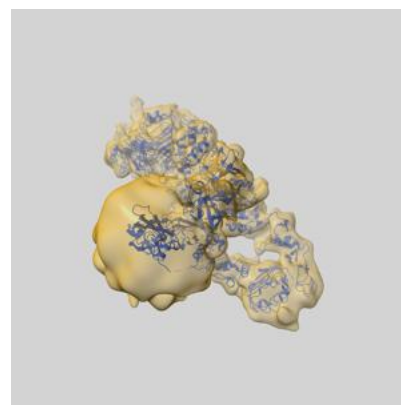
9.1 Map-model overlay [i](#)



X



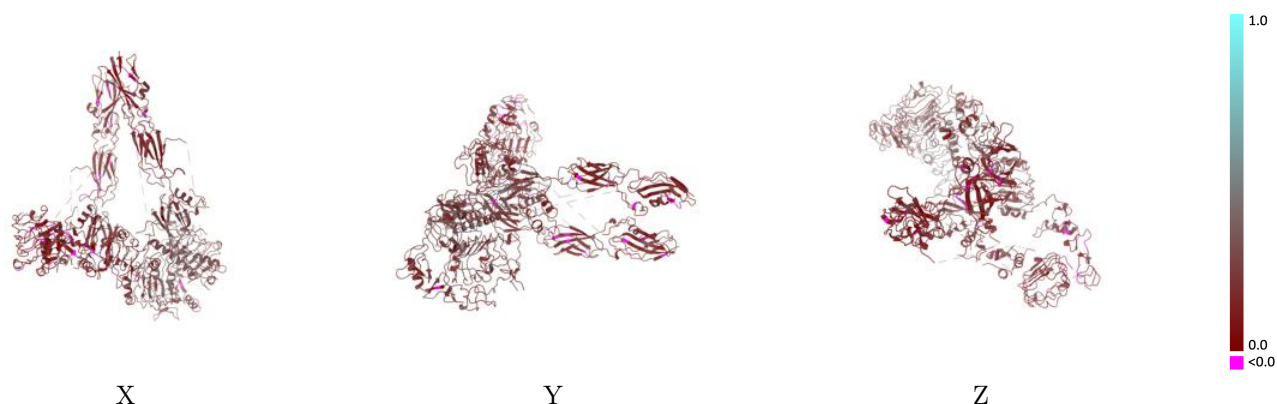
Y



Z

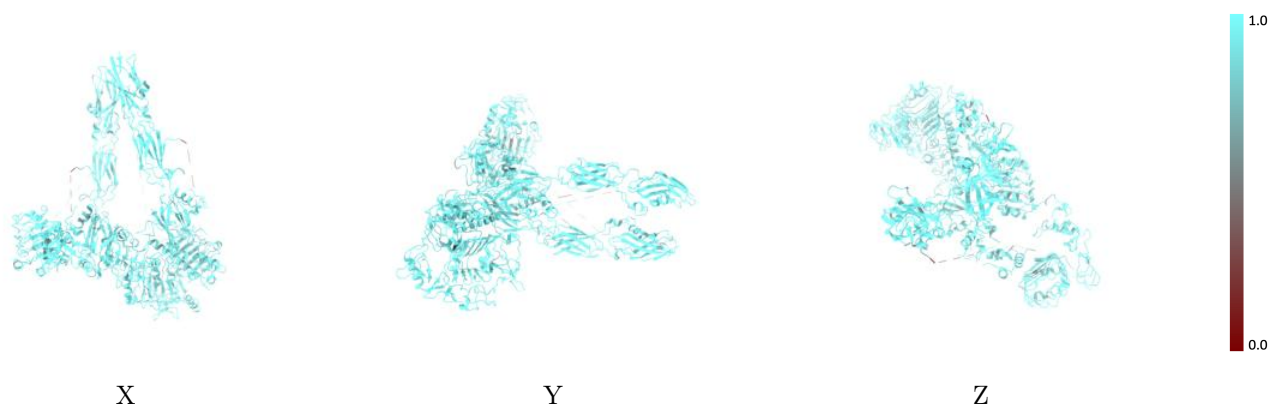
The images above show the 3D surface view of the map at the recommended contour level 0.018 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



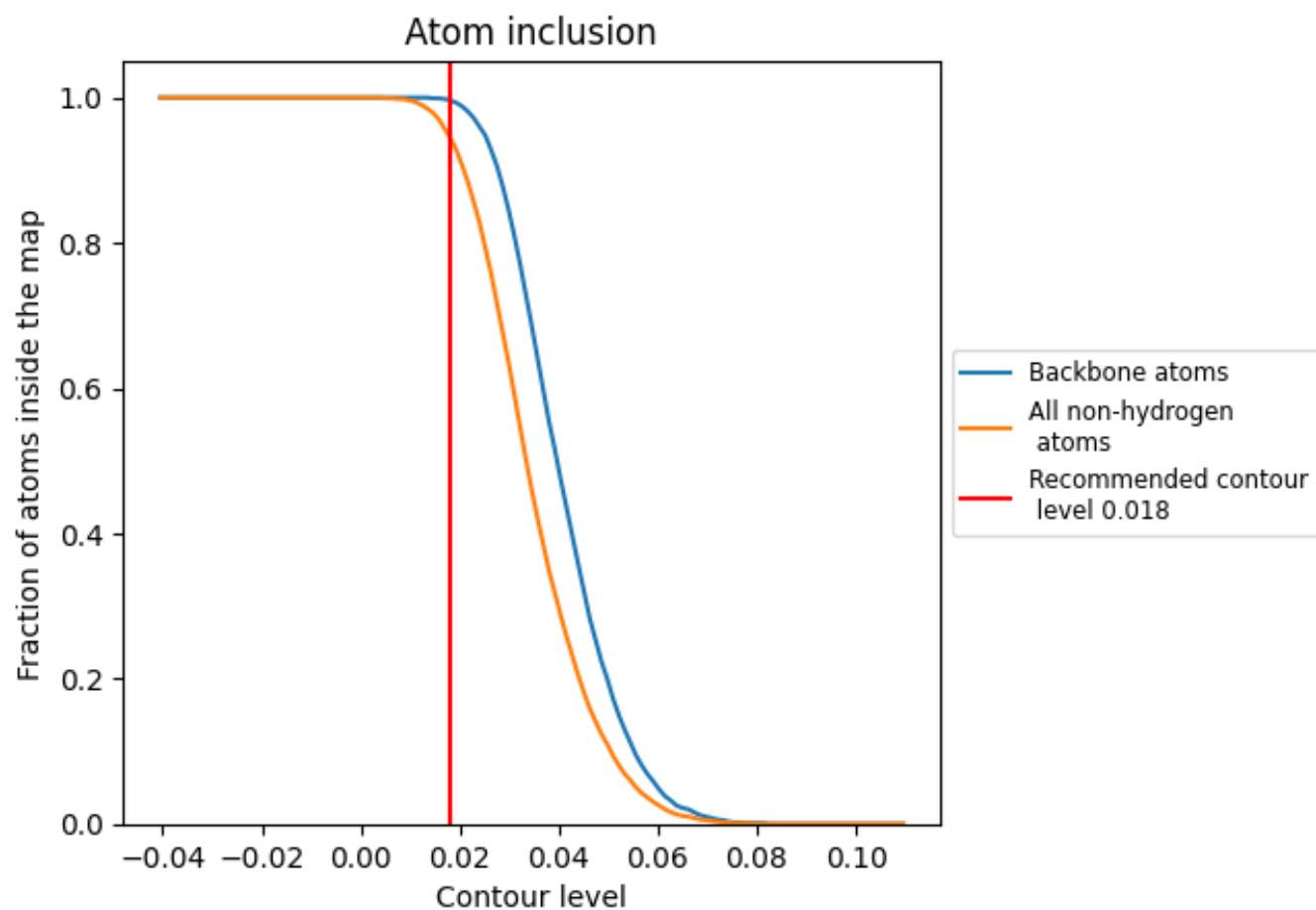
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



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 (0.018).

9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 95% 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 (0.018) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9460	0.2200
A	0.9460	0.1990
B	0.9450	0.2390
C	0.9370	0.2060
D	0.9470	0.1800
E	0.9650	0.2850
F	0.9560	0.2300

1.0

0.0

<0.0