



Full wwPDB EM Validation Report ⓘ

Mar 23, 2026 – 06:48 AM UTC

PDB ID : 6BF6 / pdb_00006bf6
EMDB ID : EMD-7090
Title : Cryo-EM structure of human insulin degrading enzyme
Authors : Liang, W.G.; Zhang, Z.; Bailey, L.J.; Kossiakoff, A.A.; Tan, Y.Z.; Wei, H.; Carragher, B.; Potter, S.C.; Tang, W.J.
Deposited on : 2017-10-26
Resolution : 6.50 Å(reported)

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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

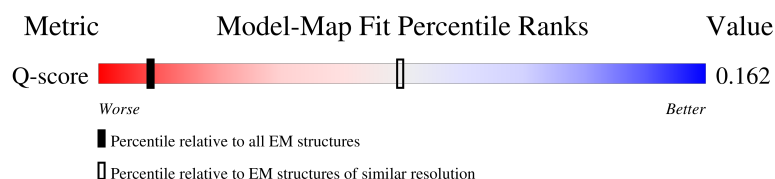
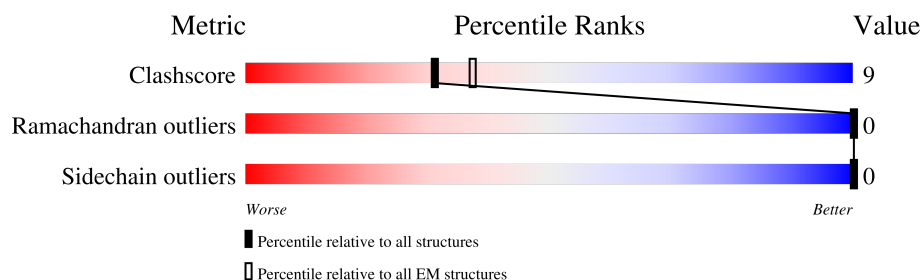
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.50 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	556 (6.00 - 7.00)

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	966	 76% 22% .
1	B	966	 75% 23% .

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 15407 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-degrading enzyme.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	949	Total	C	N	O	S	0	0
			7736	4983	1302	1429	22		
1	B	940	Total	C	N	O	S	0	0
			7671	4945	1288	1417	21		

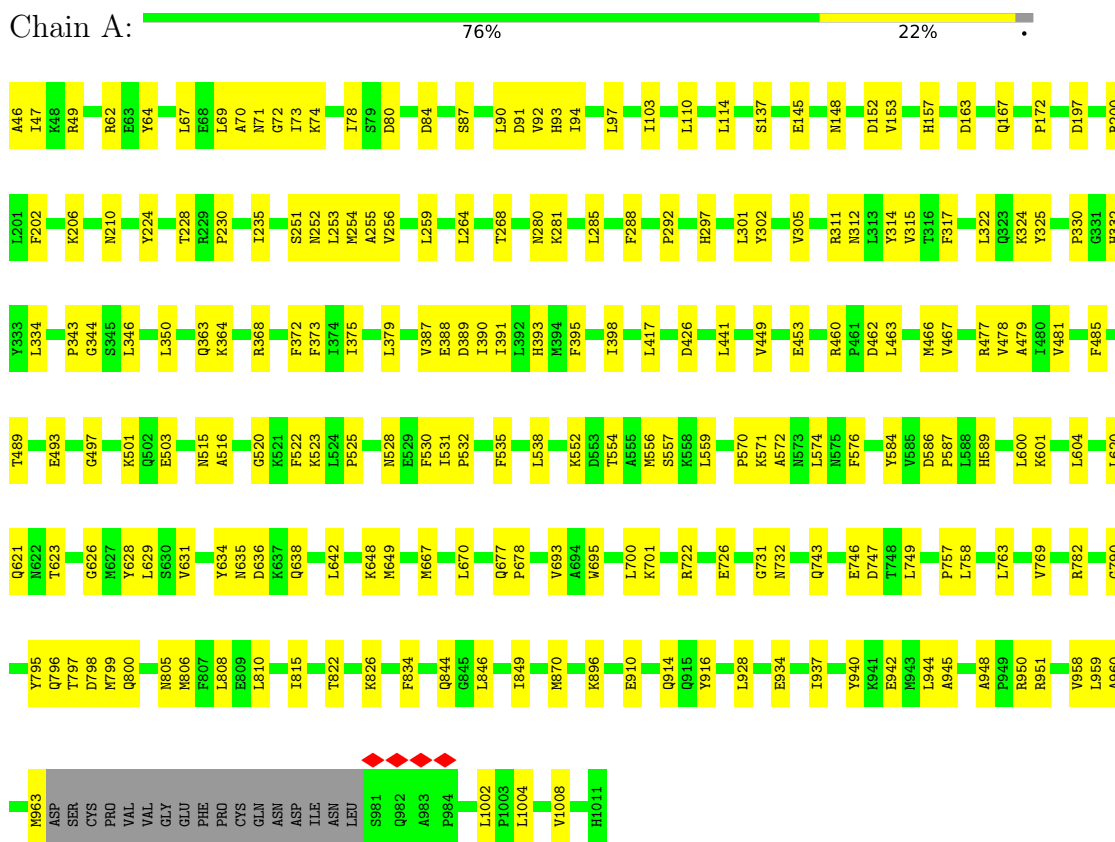
There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	110	LEU	CYS	engineered mutation	UNP P14735
A	171	SER	CYS	engineered mutation	UNP P14735
A	178	ALA	CYS	engineered mutation	UNP P14735
A	257	VAL	CYS	engineered mutation	UNP P14735
A	414	LEU	CYS	engineered mutation	UNP P14735
A	573	ASN	CYS	engineered mutation	UNP P14735
A	590	SER	CYS	engineered mutation	UNP P14735
A	789	SER	CYS	engineered mutation	UNP P14735
A	812	ALA	CYS	engineered mutation	UNP P14735
A	819	ALA	CYS	engineered mutation	UNP P14735
A	904	SER	CYS	engineered mutation	UNP P14735
B	110	LEU	CYS	engineered mutation	UNP P14735
B	171	SER	CYS	engineered mutation	UNP P14735
B	178	ALA	CYS	engineered mutation	UNP P14735
B	257	VAL	CYS	engineered mutation	UNP P14735
B	414	LEU	CYS	engineered mutation	UNP P14735
B	573	ASN	CYS	engineered mutation	UNP P14735
B	590	SER	CYS	engineered mutation	UNP P14735
B	789	SER	CYS	engineered mutation	UNP P14735
B	812	ALA	CYS	engineered mutation	UNP P14735
B	819	ALA	CYS	engineered mutation	UNP P14735
B	904	SER	CYS	engineered mutation	UNP P14735

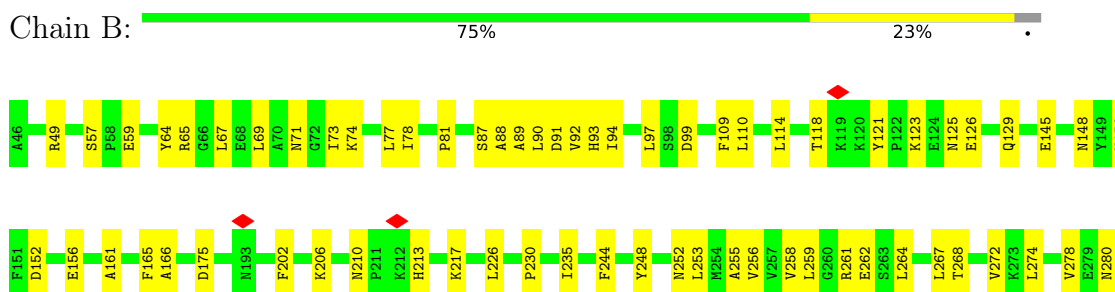
3 Residue-property plots

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: Insulin-degrading enzyme



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A948	E287	F578	Y779	H957	E290	F579	Q780	H958	V305	H291	I437	L600	A610	I310	E295	Q781	V958	L298	I311	E296	I440	A611	Y627	Q796	A960	L299	I312	V306	Q797	L301	I313	V307	Q798	L302	I314	V308	Q799	L303	I315	V309	Q800	L304	I316	V310	Q801	L305	I317	V311	Q802	L306	I318	V312	Q803	L307	I319	V313	Q804	L308	I320	V314	Q805	L309	I321	V315	Q806	L310	I322	V316	Q807	L311	I323	V317	Q808	L312	I324	V318	Q809	L313	I325	V319	Q810	L314	I326	V320	Q811	L315	I327	V321	Q812	L316	I328	V322	Q813	L317	I329	V323	Q814	L318	I330	V324	Q815	L319	I331	V325	Q816	L320	I332	V326	Q817	L321	I333	V327	Q818	L322	I334	V328	Q819	L323	I335	V329	Q820	L324	I336	V330	Q821	L325	I337	V331	Q822	L326	I338	V332	Q823	L327	I339	V333	Q824	L328	I340	V334	Q825	L329	I341	V335	Q826	L330	I342	V336	Q827	L331	I343	V337	Q828	L332	I344	V338	Q829	L333	I345	V339	Q830	L334	I346	V340	Q831	L335	I347	V341	Q832	L336	I348	V342	Q833	L337	I349	V343	Q834	L338	I350	V344	Q835	L339	I351	V345	Q836	L340	I352	V346	Q837	L341	I353	V347	Q838	L342	I354	V348	Q839	L343	I355	V349	Q840	L344	I356	V350	Q841	L345	I357	V351	Q842	L346	I358	V352	Q843	L347	I359	V353	Q844	L348	I360	V354	Q845	L349	I361	V355	Q846	L350	I362	V356	Q847	L351	I363	V357	Q848	L352	I364	V358	Q849	L353	I365	V359	Q850	L354	I366	V360	Q851	L355	I367	V361	Q852	L356	I368	V362	Q853	L357	I369	V363	Q854	L358	I370	V364	Q855	L359	I371	V365	Q856	L360	I372	V366	Q857	L361	I373	V367	Q858	L362	I374	V368	Q859	L363	I375	V369	Q860	L364	I376	V370	Q861	L365	I377	V371	Q862	L366	I378	V372	Q863	L367	I379	V373	Q864	L368	I380	V374	Q865	L369	I381	V375	Q866	L370	I382	V376	Q867	L371	I383	V377	Q868	L372	I384	V378	Q869	L373	I385	V379	Q870	L374	I386	V380	Q871	L375	I387	V381	Q872	L376	I388	V382	Q873	L377	I389	V383	Q874	L378	I390	V384	Q875	L379	I391	V385	Q876	L380	I392	V386	Q877	L381	I393	V387	Q878	L382	I394	V388	Q879	L383	I395	V389	Q880	L384	I396	V390	Q881	L385	I397	V391	Q882	L386	I398	V392	Q883	L387	I399	V393	Q884	L388	I400	V394	Q885	L389	I401	V395	Q886	L390	I402	V396	Q887	L391	I403	V397	Q888	L392	I404	V398	Q889	L393	I405	V399	Q890	L394	I406	V400	Q891	L395	I407	V401	Q892	L396	I408	V402	Q893	L397	I409	V403	Q894	L398	I410	V404	Q895	L399	I411	V405	Q896	L400	I412	V406	Q897	L401	I413	V407	Q898	L402	I414	V408	Q899	L403	I415	V409	Q900	L404	I416	V410	Q901	L405	I417	V411	Q902	L406	I418	V412	Q903	L407	I419	V413	Q904	L408	I420	V414	Q905	L409	I421	V415	Q906	L410	I422	V416	Q907	L411	I423	V417	Q908	L412	I424	V418	Q909	L413	I425	V419	Q910	L414	I426	V420	Q911	L415	I427	V421	Q912	L416	I428	V422	Q913	L417	I429	V423	Q914	L418	I430	V424	Q915	L419	I431	V425	Q916	L420	I432	V426	Q917	L421	I433	V427	Q918	L422	I434	V428	Q919	L423	I435	V429	Q920	L424	I436	V430	Q921	L425	I437	V431	Q922	L426	I438	V432	Q923	L427	I439	V433	Q924	L428	I440	V434	Q925	L429	I441	V435	Q926	L430	I442	V436	Q927	L431	I443	V437	Q928	L432	I444	V438	Q929	L433	I445	V439	Q930	L434	I446	V440	Q931	L435	I447	V441	Q932	L436	I448	V442	Q933	L437	I449	V443	Q934	L438	I450	V444	Q935	L439	I451	V445	Q936	L440	I452	V446	Q937	L441	I453	V447	Q938	L442	I454	V448	Q939	L443	I455	V449	Q940	L444	I456	V450	Q941	L445	I457	V451	Q942	L446	I458	V452	Q943	L447	I459	V453	Q944	L448	I460	V454	Q945	L449	I461	V455	Q946	L450	I462	V456	Q947	L451	I463	V457	Q948	L452	I464	V458	Q949	L453	I465	V459	Q950	L454	I466	V460	Q951	L455	I467	V461	Q952	L456	I468	V462	Q953	L457	I469	V463	Q954	L458	I470	V464	Q955	L459	I471	V465	Q956	L460	I472	V466	Q957	L461	I473	V467	Q958	L462	I474	V468	Q959	L463	I475	V469	Q960	L464	I476	V470	Q961	L465	I477	V471	Q962	L466	I478	V472	Q963	L467	I479	V473	Q964	L468	I480	V474	Q965	L469	I481	V475	Q966	L470	I482	V476	Q967	L471	I483	V477	Q968	L472	I484	V478	Q969	L473	I485	V479	Q970	L474	I486	V480	Q971	L475	I487	V481	Q972	L476	I488	V482	Q973	L477	I489	V483	Q974	L478	I490	V484	Q975	L479	I491	V485	Q976	L480	I492	V486	Q977	L481	I493	V487	Q978	L482	I494	V488	Q979	L483	I495	V489	Q980	L484	I496	V490	Q981	L485	I497	V491	Q982	L486	I498	V492	Q983	L487	I499	V493	Q984	L488	I500	V494	Q985	L489	I501	V495	Q986	L490	I502	V496	Q987	L491	I503	V497	Q988	L492	I504	V498	Q989	L493	I505	V499	Q990	L494	I506	V500	Q991	L495	I507	V501	Q992	L496	I508	V502	Q993	L497	I509	V503	Q994	L498	I510	V504	Q995	L499	I511	V505	Q996	L500	I512	V506	Q997	L501	I513	V507	Q998	L502	I514	V508	Q999	L503	I515	V509	Q1000	L504	I516	V510	Q1001	L505	I517	V511	Q1002	L506	I518	V512	Q1003	L507	I519	V513	Q1004	L508	I520	V514	Q1005	L509	I521	V515	Q1006	L510	I522	V516	Q1007	L511	I523	V517	Q1008	L512	I524	V518	Q1009	L513	I525	V519	Q1010	L514	I526	V520	Q1011	L515	I527	V521	Q1012	L516	I528	V522	Q1013	L517	I529	V523	Q1014	L518	I530	V524	Q1015	L519	I531	V525	Q1016	L520	I532	V526	Q1017	L521	I533	V527	Q1018	L522	I534	V528	Q1019	L523	I535	V529	Q1020	L524	I536	V530	Q1021	L525	I537	V531	Q1022	L526	I538	V532	Q1023	L527	I539	V533	Q1024	L528	I540	V534	Q1025	L529	I541	V535	Q1026	L530	I542	V536	Q1027	L531	I543	V537	Q1028	L532	I544	V538	Q1029	L533	I545	V539	Q1030	L534	I546	V540	Q1031	L535	I547	V541	Q1032	L536	I548	V542	Q1033	L537	I549	V543	Q1034	L538	I550	V544	Q1035	L539	I551	V545	Q1036	L540	I552	V546	Q1037	L541	I553	V547	Q1038	L542	I554	V548	Q1039	L543	I555	V549	Q1040	L544	I556	V550	Q1041	L545	I557	V551	Q1042	L546	I558	V552	Q1043	L547	I559	V553	Q1044	L548	I560	V554	Q1045	L549	I561	V555	Q1046	L550	I562	V556	Q1047	L551	I563	V557	Q1048	L552	I564	V558	Q1049	L553	I565	V559	Q1050	L554	I566	V560	Q1051	L555	I567	V561	Q1052	L556	I568	V562	Q1053	L557	I569	V563	Q1054	L558	I570	V564	Q1055	L559	I571	V565	Q1056	L560	I572	V566	Q1057	L561	I573	V567	Q1058	L562	I574	V568	Q1059	L563	I575	V569	Q1060	L564	I576	V570	Q1061	L565	I577	V571	Q1062	L566	I578	V572	Q1063	L567	I579	V573	Q1064	L568	I580	V574	Q1065	L569	I581	V575	Q1066	L570	I582	V576	Q1067	L571	I583	V577	Q1068	L572	I584	V578	Q1069	L573	I585	V579	Q1070	L574	I586	V580	Q1071	L575	I587	V581	Q1072	L576	I588	V582	Q1073	L577	I589	V583	Q1074	L578	I590	V584	Q1075	L579	I591	V585	Q1076	L580	I592	V586	Q1077	L581	I593	V587	Q1078	L582	I594	V588	Q1079	L583	I595	V589	Q1080	L584	I596	V590	Q1081	L585	I597	V591	Q1082	L586	I598	V592	Q1083	L587	I599	V593	Q1084	L588	I600	V594	Q1085	L589	I601	V595	Q1086	L590	I602	V596	Q1087	L591	I603	V597	Q1088	L592	I604	V598	Q1089	L593	I605	V599	Q1090	L594	I606	V600	Q1091	L595	I607	V601	Q1092	L596	I608	V602	Q1093	L597	I609	V603	Q1094	L598	I610	V604	Q1095	L599	I611	V605	Q1096	L600	I612	V606	Q1097	L601	I613	V607	Q1098	L602	I614	V608	Q1099	L603	I615	V609	Q1100	L604	I616	V610	Q1101	L605	I617	V611	Q1102	L606	I618	V612	Q1103	L607	I619	V613	Q1104	L608	I620	V614	Q1105	L609	I621	V615	Q1106	L610	I622	V616	Q1107	L611	I623	V617	Q1108	L612	I624	V618	Q1109	L613	I625	V619	Q1110	L614	I626	V620	Q1111	L615	I627	V621	Q1112	L616	I628	V622	Q1113	L617	I629	V623	Q1114	L618	I630	V624	Q1115	L619	I631	V625	Q1116	L620	I632	V626	Q1117	L621	I633	V627	Q1118	L622	I634	V628	Q1119	L623	I635	V629	Q1120	L624	I636	V630	Q1121	L625	I637	V631	Q1122	L626	I638	V632	Q1123	L627	I639	V633	Q1124	L628	I640	V634	Q1125	L629	I641	V635	Q1126	L630	I642	V636	Q1127	L631	I643	V637	Q1128	L632	I644	V638	Q1129	L633	I645	V639	Q1130	L634	I646	V640	Q1131	L635	I647	V641	Q1132	L636	I648	V642	Q1133	L637	I649	V643	Q1134	L638	I650	V644	Q1135	L639	I651	V645	Q1136	L640	I652	V646	Q1137	L641	I653	V647	Q1138	L642	I654	V648	Q1139	L643	I655	V649	Q1140	L644	I656	V650	Q1141	L645	I657	V651	Q1142	L646	I658	V652	Q1143	L647	I659	V653	Q1144	L648	I660	V654	Q1145	L649	I661	V655	Q1146	L650	I662	V656	Q1147	L651	I663	V657	Q1148	L652	I664	V658	Q1149	L653	I665	V659	Q1150	L654	I666	V660	Q1151	L655	I667	V661	Q1152	L656	I668	V662	Q1153	L657	I669	V663	Q1154	L658	I670	V664	Q1155	L659	I671	V665	Q1156	L660	I672	V666	Q1157	L661
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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	16944	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 ($e^-/\text{\AA}^2$)	7.9, 6.8	Depositor
Minimum defocus (nm)	940	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	46598	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k), GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.106	Depositor
Minimum map value	-0.148	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.017	Depositor
Map size ($\text{\AA}$)	343.36, 343.36, 343.36	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.073, 1.073, 1.073	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	0.33	0/7930	0.68	0/10728
1	B	0.31	0/7863	0.69	0/10635
All	All	0.32	0/15793	0.68	0/21363

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	7736	0	7650	134	0
1	B	7671	0	7588	138	0
All	All	15407	0	15238	268	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 9.

All (268) 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:A:317:PHE:HB2	1:A:373:PHE:HB3	1.69	0.72
1:B:317:PHE:HB2	1:B:373:PHE:HB3	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:538:LEU:H	1:A:732:ASN:HD21	1.37	0.69
1:B:621:GLN:HB3	1:B:628:TYR:HB3	1.75	0.68
1:B:806:MET:HE3	1:B:924:GLU:HB3	1.76	0.68
1:A:346:LEU:HD11	1:A:393:HIS:HB3	1.77	0.67
1:B:638:GLN:O	1:B:642:LEU:HB3	1.94	0.66
1:A:576:PHE:HB2	1:A:629:LEU:HB3	1.78	0.66
1:B:834:PHE:HB3	1:B:849:ILE:HB	1.76	0.66
1:A:834:PHE:HB3	1:A:849:ILE:HB	1.78	0.66
1:A:1004:LEU:HB2	1:B:1004:LEU:HB2	1.82	0.62
1:B:532:PRO:HB3	1:B:636:ASP:HB2	1.82	0.62
1:A:782:ARG:HA	1:A:959:LEU:HB2	1.81	0.62
1:B:805:ASN:ND2	1:B:924:GLU:OE2	2.33	0.61
1:B:156:GLU:HB3	1:B:261:ARG:HH21	1.64	0.61
1:B:579:PHE:HB3	1:B:724:HIS:HB3	1.82	0.61
1:B:690:MET:HE1	1:B:796:GLN:HE21	1.64	0.61
1:A:332:HIS:HE1	1:A:453:GLU:HG3	1.67	0.60
1:A:667:MET:HE3	1:A:701:LYS:HZ2	1.66	0.60
1:A:695:TRP:HH2	1:B:762:GLN:HB3	1.65	0.60
1:A:489:THR:HA	1:A:501:LYS:HB2	1.83	0.60
1:A:389:ASP:O	1:A:393:HIS:ND1	2.34	0.60
1:B:832:ILE:HB	1:B:851:GLN:HG2	1.84	0.60
1:A:635:ASN:ND2	1:A:732:ASN:O	2.36	0.59
1:B:301:LEU:HA	1:B:478:VAL:HB	1.85	0.59
1:A:769:VAL:O	1:A:796:GLN:NE2	2.35	0.59
1:B:576:PHE:HB2	1:B:629:LEU:HB3	1.84	0.59
1:B:769:VAL:O	1:B:796:GLN:NE2	2.35	0.59
1:B:69:LEU:HD21	1:B:272:VAL:HG13	1.84	0.58
1:B:790:GLY:N	1:B:958:VAL:O	2.32	0.58
1:A:800:GLN:HA	1:A:844:GLN:HE21	1.67	0.58
1:A:93:HIS:HB3	1:A:253:LEU:HB3	1.84	0.58
1:A:815:ILE:HG22	1:A:870:MET:HG3	1.85	0.58
1:A:251:SER:HA	1:A:281:LYS:H	1.69	0.58
1:A:92:VAL:HG12	1:A:94:ILE:H	1.69	0.58
1:A:670:LEU:HD13	1:A:701:LYS:HA	1.85	0.57
1:B:508:GLU:HG3	1:B:509:VAL:HG23	1.87	0.57
1:A:71:ASN:HA	1:A:280:ASN:HB3	1.87	0.57
1:A:795:TYR:HB2	1:A:846:LEU:HB3	1.87	0.57
1:B:575:ASN:ND2	1:B:904:SER:OG	2.38	0.56
1:B:577:GLU:HB3	1:B:726:GLU:HB3	1.86	0.56
1:B:822:THR:O	1:B:826:LYS:HB3	2.05	0.56
1:A:72:GLY:HA3	1:A:252:ASN:HA	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:759:LEU:HB2	1:B:762:GLN:HG2	1.87	0.56
1:B:600:LEU:HD11	1:B:649:MET:HA	1.88	0.56
1:A:74:LYS:O	1:A:256:VAL:N	2.37	0.56
1:B:638:GLN:O	1:B:642:LEU:CB	2.54	0.56
1:A:301:LEU:HD22	1:A:503:GLU:HB3	1.87	0.55
1:A:210:ASN:N	1:A:292:PRO:O	2.40	0.55
1:B:69:LEU:HB2	1:B:73:ILE:HB	1.89	0.55
1:B:834:PHE:N	1:B:849:ILE:O	2.40	0.55
1:A:315:VAL:HB	1:A:375:ILE:HB	1.89	0.54
1:B:99:ASP:O	1:B:217:LYS:NZ	2.41	0.54
1:A:532:PRO:HB3	1:A:636:ASP:HB2	1.90	0.54
1:A:571:LYS:HA	1:A:634:TYR:HA	1.88	0.54
1:A:574:LEU:HB2	1:A:631:VAL:HB	1.90	0.54
1:B:262:GLU:HB2	1:B:267:LEU:HD23	1.90	0.54
1:B:574:LEU:HB2	1:B:631:VAL:HB	1.89	0.54
1:A:163:ASP:O	1:A:167:GLN:NE2	2.41	0.54
1:B:800:GLN:HA	1:B:844:GLN:HE21	1.73	0.53
1:B:528:ASN:ND2	1:B:610:ALA:O	2.42	0.53
1:B:305:VAL:HG22	1:B:485:PHE:HB2	1.91	0.53
1:A:934:GLU:HA	1:A:937:ILE:HD12	1.90	0.53
1:A:806:MET:HE2	1:A:928:LEU:HB2	1.90	0.53
1:A:264:LEU:O	1:A:268:THR:OG1	2.19	0.53
1:A:552:LYS:HB3	1:A:559:LEU:HB3	1.91	0.53
1:A:330:PRO:HG3	1:A:463:LEU:HD23	1.90	0.53
1:A:1004:LEU:HD12	1:B:1004:LEU:HD12	1.90	0.53
1:A:638:GLN:O	1:A:642:LEU:HB3	2.09	0.52
1:B:552:LYS:HB3	1:B:559:LEU:HB3	1.91	0.52
1:B:619:ASP:HB3	1:B:630:SER:HB3	1.90	0.52
1:A:554:THR:HB	1:A:557:SER:H	1.74	0.52
1:B:781:GLN:O	1:B:959:LEU:N	2.41	0.52
1:A:137:SER:N	1:A:152:ASP:OD1	2.42	0.52
1:B:389:ASP:O	1:B:393:HIS:ND1	2.39	0.52
1:B:81:PRO:HA	1:B:261:ARG:HG3	1.91	0.52
1:B:92:VAL:HG12	1:B:94:ILE:H	1.75	0.52
1:A:153:VAL:HB	1:A:157:HIS:HB2	1.93	0.51
1:B:470:LYS:O	1:B:475:ASN:ND2	2.39	0.51
1:B:596:TYR:O	1:B:600:LEU:HB2	2.11	0.51
1:B:798:ASP:HB3	1:B:804:GLU:HG3	1.93	0.50
1:A:726:GLU:OE2	1:A:916:TYR:OH	2.28	0.50
1:A:301:LEU:HA	1:A:478:VAL:HB	1.93	0.50
1:A:388:GLU:HA	1:A:391:ILE:HD12	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:125:ASN:O	1:B:129:GLN:N	2.42	0.49
1:A:746:GLU:HA	1:A:749:LEU:HD12	1.94	0.49
1:B:264:LEU:O	1:B:268:THR:OG1	2.19	0.49
1:A:84:ASP:OD2	1:A:896:LYS:NZ	2.44	0.49
1:A:224:TYR:O	1:A:228:THR:HB	2.12	0.49
1:A:110:LEU:O	1:A:114:LEU:N	2.45	0.49
1:B:93:HIS:HB3	1:B:253:LEU:HB3	1.95	0.49
1:B:252:ASN:ND2	1:B:280:ASN:OD1	2.43	0.49
1:A:297:HIS:ND1	1:A:302:TYR:OH	2.43	0.49
1:B:65:ARG:HB3	1:B:77:LEU:HD12	1.94	0.49
1:B:295:GLU:HA	1:B:298:LEU:HB2	1.94	0.49
1:A:74:LYS:HB3	1:A:441:LEU:HG	1.95	0.49
1:A:334:LEU:HD11	1:A:467:VAL:HG21	1.93	0.49
1:B:315:VAL:HB	1:B:375:ILE:HB	1.93	0.49
1:A:49:ARG:HB2	1:A:67:LEU:HD22	1.95	0.48
1:A:253:LEU:HD21	1:A:285:LEU:HG	1.95	0.48
1:A:572:ALA:HA	1:A:731:GLY:HA3	1.95	0.48
1:B:563:GLN:NE2	1:B:733:ILE:O	2.45	0.48
1:B:805:ASN:OD1	1:B:844:GLN:NE2	2.46	0.48
1:B:801:SER:O	1:B:805:ASN:ND2	2.46	0.48
1:A:722:ARG:HG2	1:A:758:LEU:HD23	1.95	0.48
1:B:88:ALA:HA	1:B:258:VAL:HA	1.96	0.48
1:A:87:SER:HA	1:A:152:ASP:HA	1.95	0.48
1:B:554:THR:OG1	1:B:557:SER:N	2.39	0.48
1:B:780:GLN:HA	1:B:957:HIS:HB2	1.96	0.48
1:B:833:VAL:HG13	1:B:850:ILE:HG12	1.96	0.48
1:B:213:HIS:NE2	1:B:290:GLU:O	2.47	0.48
1:A:47:ILE:HA	1:A:69:LEU:HD22	1.95	0.48
1:B:575:ASN:HB2	1:B:728:LEU:HB3	1.96	0.48
1:A:311:ARG:HB3	1:A:379:LEU:HB2	1.95	0.47
1:A:940:TYR:O	1:A:945:ALA:N	2.46	0.47
1:B:779:TYR:HB3	1:B:992:ILE:HB	1.95	0.47
1:A:493:GLU:HB3	1:A:497:GLY:H	1.79	0.47
1:B:600:LEU:HD21	1:B:649:MET:HB2	1.96	0.47
1:A:395:PHE:HD1	1:A:398:ILE:HD12	1.80	0.47
1:B:123:LYS:HB2	1:B:126:GLU:HB2	1.95	0.47
1:A:798:ASP:O	1:A:844:GLN:N	2.42	0.47
1:B:311:ARG:HB3	1:B:379:LEU:HB2	1.97	0.47
1:B:350:LEU:O	1:B:354:GLY:N	2.48	0.47
1:B:948:ALA:HB3	1:B:951:ARG:HB2	1.96	0.47
1:A:297:HIS:HB2	1:A:477:ARG:HH12	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:822:THR:O	1:A:826:LYS:HB3	2.14	0.47
1:A:312:ASN:HB2	1:A:481:VAL:HB	1.96	0.47
1:A:515:ASN:OD1	1:A:516:ALA:N	2.48	0.47
1:A:556:MET:HB2	1:A:757:PRO:HG3	1.97	0.47
1:B:535:PHE:HA	1:B:570:PRO:HB3	1.97	0.47
1:A:74:LYS:HB2	1:A:255:ALA:HA	1.96	0.46
1:A:790:GLY:N	1:A:958:VAL:O	2.39	0.46
1:B:57:SER:O	1:B:59:GLU:N	2.44	0.46
1:B:552:LYS:O	1:B:559:LEU:N	2.43	0.46
1:A:78:ILE:HB	1:A:259:LEU:HA	1.96	0.46
1:B:759:LEU:H	1:B:762:GLN:HE21	1.63	0.46
1:A:46:ALA:HB1	1:A:70:ALA:HB3	1.97	0.46
1:A:600:LEU:HD11	1:A:649:MET:HA	1.97	0.46
1:B:210:ASN:HB3	1:B:213:HIS:HB2	1.97	0.46
1:B:637:LYS:HG2	1:B:640:ILE:HD12	1.97	0.46
1:B:877:MET:O	1:B:933:LYS:NZ	2.38	0.46
1:A:64:TYR:HE1	1:A:78:ILE:HG23	1.81	0.46
1:A:460:ARG:HE	1:A:463:LEU:HD13	1.80	0.46
1:A:324:LYS:HE2	1:A:324:LYS:HB3	1.82	0.46
1:A:103:ILE:HG12	1:A:230:PRO:HG3	1.98	0.45
1:A:799:MET:HE3	1:A:1008:VAL:HG22	1.98	0.45
1:B:255:ALA:HB1	1:B:441:LEU:HD23	1.99	0.45
1:B:334:LEU:HD11	1:B:467:VAL:HG21	1.97	0.45
1:B:337:LEU:HD21	1:B:410:VAL:HG11	1.98	0.45
1:A:535:PHE:HA	1:A:570:PRO:HB3	1.98	0.45
1:A:621:GLN:O	1:A:628:TYR:N	2.43	0.45
1:A:387:VAL:HA	1:A:390:ILE:HD12	1.98	0.45
1:A:97:LEU:HD13	1:A:288:PHE:HE2	1.82	0.45
1:A:314:TYR:HB2	1:A:479:ALA:HB3	1.99	0.45
1:B:49:ARG:HA	1:B:67:LEU:HB2	1.98	0.45
1:B:74:LYS:O	1:B:256:VAL:N	2.46	0.45
1:A:305:VAL:HG22	1:A:485:PHE:HB2	1.99	0.45
1:B:803:SER:HA	1:B:927:TYR:CE2	2.52	0.44
1:A:230:PRO:O	1:A:235:ILE:N	2.47	0.44
1:B:87:SER:HA	1:B:152:ASP:HA	1.99	0.44
1:B:145:GLU:OE2	1:B:368:ARG:N	2.50	0.44
1:A:960:ALA:H	1:A:963:MET:HB2	1.83	0.44
1:B:406:PRO:HB2	1:B:459:PHE:HZ	1.82	0.44
1:B:395:PHE:HD1	1:B:398:ILE:HD12	1.81	0.44
1:B:578:PHE:HB2	1:B:627:MET:HB2	2.00	0.44
1:A:426:ASP:OD1	1:A:426:ASP:N	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:332:HIS:HE1	1:B:453:GLU:HG3	1.82	0.44
1:A:62:ARG:HG2	1:A:80:ASP:HB2	2.00	0.44
1:A:797:THR:HG21	1:A:808:LEU:HD12	1.99	0.44
1:B:571:LYS:HA	1:B:634:TYR:HA	1.99	0.44
1:B:317:PHE:O	1:B:373:PHE:N	2.50	0.44
1:B:118:THR:HG1	1:B:121:TYR:H	1.59	0.44
1:B:175:ASP:OD1	1:B:175:ASP:N	2.51	0.44
1:B:349:GLU:O	1:B:353:LYS:N	2.47	0.44
1:B:579:PHE:N	1:B:724:HIS:O	2.46	0.44
1:A:601:LYS:HD2	1:A:620:LEU:HB2	2.00	0.43
1:A:91:ASP:HA	1:A:148:ASN:HA	2.00	0.43
1:B:71:ASN:HB2	1:B:278:VAL:HG12	2.00	0.43
1:A:364:LYS:HB3	1:A:372:PHE:HB2	1.99	0.43
1:A:441:LEU:HD12	1:A:449:VAL:HG11	2.00	0.43
1:B:558:LYS:HB3	1:B:726:GLU:HG3	1.99	0.43
1:A:520:GLY:H	1:A:522:PHE:HD2	1.65	0.43
1:A:584:TYR:HE2	1:A:693:VAL:HG13	1.83	0.43
1:B:670:LEU:HD23	1:B:670:LEU:HA	1.84	0.43
1:A:587:PRO:HB3	1:A:700:LEU:HD23	2.00	0.43
1:A:763:LEU:O	1:B:1000:ARG:NH2	2.51	0.43
1:B:677:GLN:HA	1:B:678:PRO:HD3	1.91	0.43
1:A:87:SER:O	1:A:259:LEU:N	2.49	0.43
1:A:638:GLN:O	1:A:642:LEU:CB	2.67	0.43
1:A:942:GLU:O	1:A:948:ALA:HB1	2.18	0.43
1:B:230:PRO:O	1:B:235:ILE:N	2.46	0.43
1:B:244:PHE:O	1:B:248:TYR:HB2	2.18	0.43
1:A:114:LEU:HD12	1:A:172:PRO:HB3	2.01	0.43
1:A:528:ASN:HD21	1:A:530:PHE:HB2	1.84	0.43
1:B:363:GLN:NE2	1:B:371:MET:SD	2.92	0.43
1:B:575:ASN:OD1	1:B:628:TYR:OH	2.36	0.43
1:B:785:VAL:O	1:B:961:ARG:NH1	2.52	0.43
1:A:417:LEU:HD21	1:A:531:ILE:HG22	2.01	0.42
1:B:596:TYR:O	1:B:600:LEU:CB	2.67	0.42
1:B:822:THR:O	1:B:827:GLU:N	2.45	0.42
1:A:322:LEU:HA	1:A:325:TYR:HD2	1.84	0.42
1:B:109:PHE:HB2	1:B:226:LEU:HD11	2.01	0.42
1:A:462:ASP:O	1:A:466:MET:HB2	2.19	0.42
1:B:287:GLU:HB3	1:B:368:ARG:HD3	2.01	0.42
1:B:350:LEU:HD23	1:B:350:LEU:HA	1.84	0.42
1:B:145:GLU:OE1	1:B:443:TYR:OH	2.29	0.42
1:B:515:ASN:OD1	1:B:516:ALA:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:910:GLU:O	1:B:914:GLN:N	2.52	0.42
1:B:310:ILE:HD12	1:B:312:ASN:HD22	1.85	0.42
1:B:995:MET:HA	1:B:998:PHE:HB3	2.02	0.42
1:A:363:GLN:HA	1:A:373:PHE:HA	2.01	0.42
1:A:202:PHE:O	1:A:206:LYS:HG2	2.20	0.42
1:A:620:LEU:HD13	1:A:620:LEU:HA	1.90	0.42
1:A:797:THR:OG1	1:A:798:ASP:N	2.53	0.42
1:B:540:LEU:HD21	1:B:544:ALA:HA	2.01	0.42
1:A:343:PRO:HG2	1:A:525:PRO:HA	2.02	0.42
1:A:90:LEU:HG	1:A:256:VAL:HG12	2.01	0.41
1:A:145:GLU:OE2	1:A:368:ARG:N	2.52	0.41
1:A:805:ASN:N	1:A:844:GLN:HE22	2.18	0.41
1:A:1002:LEU:HD23	1:A:1002:LEU:HA	1.91	0.41
1:B:97:LEU:C	1:B:217:LYS:HZ1	2.28	0.41
1:B:823:LEU:HD21	1:B:866:PHE:HB2	2.02	0.41
1:A:197:ASP:HA	1:A:200:ARG:HD3	2.02	0.41
1:A:317:PHE:N	1:A:373:PHE:O	2.44	0.41
1:A:623:THR:N	1:A:626:GLY:O	2.41	0.41
1:B:883:GLN:HA	1:B:886:ILE:HG12	2.02	0.41
1:A:460:ARG:HB3	1:A:463:LEU:HD13	2.03	0.41
1:B:89:ALA:HA	1:B:150:TYR:HA	2.02	0.41
1:B:437:ILE:HA	1:B:440:ILE:HG13	2.01	0.41
1:B:805:ASN:N	1:B:844:GLN:HE22	2.17	0.41
1:A:800:GLN:HA	1:A:844:GLN:NE2	2.34	0.41
1:B:202:PHE:O	1:B:206:LYS:HG2	2.20	0.41
1:B:49:ARG:HB2	1:B:67:LEU:HD22	2.03	0.41
1:B:773:ASP:HA	1:B:952:HIS:CD2	2.56	0.41
1:A:74:LYS:HD2	1:A:74:LYS:HA	1.83	0.41
1:A:604:LEU:HD22	1:A:648:LYS:HG2	2.02	0.41
1:A:940:TYR:HA	1:A:944:LEU:HB2	2.02	0.41
1:B:90:LEU:HD13	1:B:165:PHE:HZ	1.86	0.41
1:B:91:ASP:HA	1:B:148:ASN:HA	2.02	0.41
1:B:166:ALA:HB2	1:B:274:LEU:HD11	2.03	0.41
1:B:161:ALA:O	1:B:165:PHE:HB2	2.21	0.41
1:A:73:ILE:HA	1:A:254:MET:HB2	2.02	0.41
1:A:315:VAL:O	1:A:375:ILE:N	2.46	0.41
1:A:743:GLN:O	1:A:747:ASP:HB2	2.20	0.41
1:B:87:SER:O	1:B:259:LEU:N	2.53	0.41
1:B:311:ARG:HH11	1:B:380:THR:HA	1.84	0.41
1:B:313:LEU:HD11	1:B:478:VAL:HG13	2.02	0.41
1:B:681:HIS:CE1	1:B:685:TYR:HE2	2.39	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:810:LEU:HD11	1:B:886:ILE:HG22	2.02	0.41
1:B:110:LEU:O	1:B:114:LEU:N	2.52	0.41
1:B:299:LYS:HD3	1:B:474:GLU:HA	2.03	0.41
1:A:344:GLY:HA3	1:A:523:LYS:HB2	2.04	0.40
1:A:677:GLN:HA	1:A:678:PRO:HD3	1.93	0.40
1:A:810:LEU:HA	1:A:810:LEU:HD12	1.88	0.40
1:A:910:GLU:O	1:A:914:GLN:N	2.54	0.40
1:A:948:ALA:H	1:A:951:ARG:NH1	2.19	0.40
1:B:291:HIS:HA	1:B:292:PRO:HD3	1.93	0.40
1:B:773:ASP:OD1	1:B:952:HIS:NE2	2.55	0.40
1:B:942:GLU:O	1:B:948:ALA:HB1	2.21	0.40
1:A:942:GLU:O	1:A:950:ARG:HB2	2.20	0.40
1:B:64:TYR:HE1	1:B:78:ILE:HG23	1.85	0.40
1:B:530:PHE:HD2	1:B:611:ALA:HA	1.86	0.40
1:A:325:TYR:CD1	1:A:463:LEU:HD21	2.57	0.40
1:A:350:LEU:HD23	1:A:350:LEU:HA	1.89	0.40
1:A:535:PHE:HD1	1:A:570:PRO:HG3	1.87	0.40
1:A:586:ASP:CG	1:A:589:HIS:HD1	2.29	0.40
1:B:346:LEU:HD11	1:B:393:HIS:HB3	2.04	0.40
1:B:559:LEU:HD11	1:B:729:LEU:HG	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	945/966 (98%)	912 (96%)	33 (4%)	0	100	100
1	B	936/966 (97%)	902 (96%)	34 (4%)	0	100	100
All	All	1881/1932 (97%)	1814 (96%)	67 (4%)	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	A	836/861 (97%)	836 (100%)	0	100	100
1	B	829/861 (96%)	829 (100%)	0	100	100
All	All	1665/1722 (97%)	1665 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	102	ASN
1	A	157	HIS
1	A	329	ASN
1	A	332	HIS
1	A	376	ASN
1	A	591	ASN
1	A	805	ASN
1	A	844	GLN
1	A	857	HIS
1	B	190	HIS
1	B	245	HIS
1	B	312	ASN
1	B	332	HIS
1	B	340	HIS
1	B	681	HIS
1	B	743	GLN
1	B	762	GLN
1	B	796	GLN
1	B	841	ASN
1	B	844	GLN
1	B	993	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

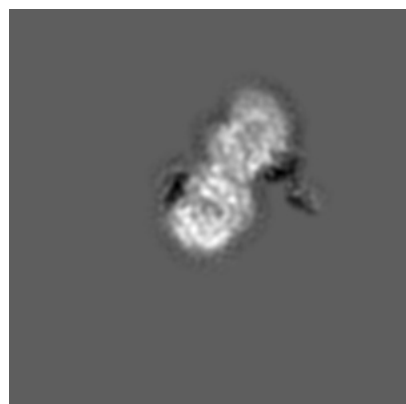
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-7090. These allow visual inspection of the internal detail of the map and identification of artifacts.

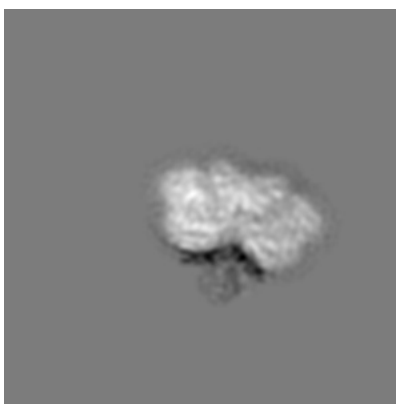
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

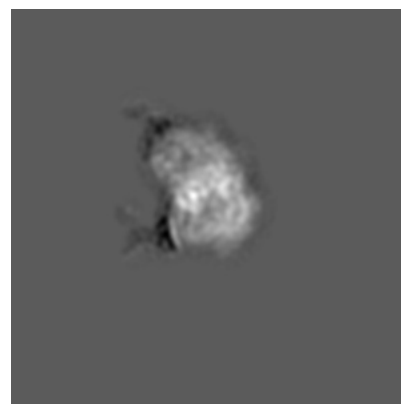
6.1.1 Primary map



X

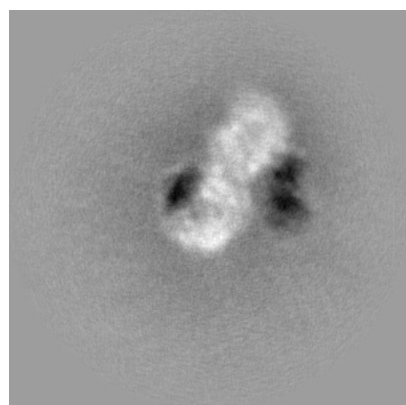


Y

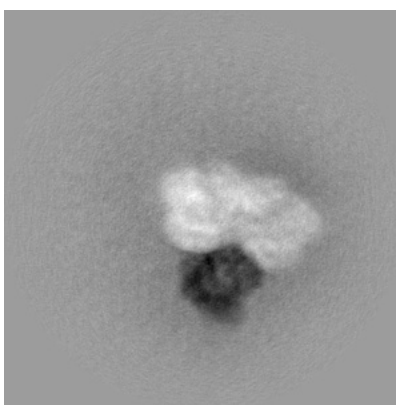


Z

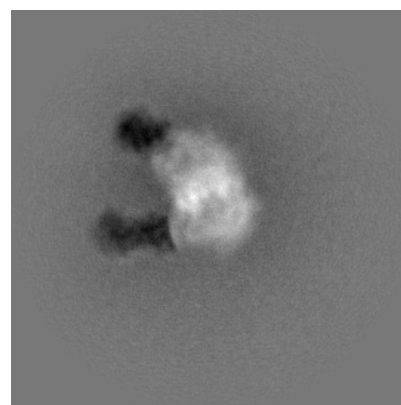
6.1.2 Raw map



X



Y

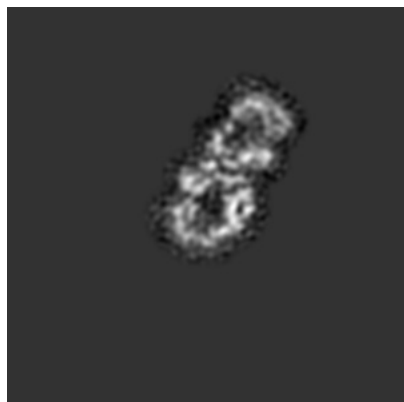


Z

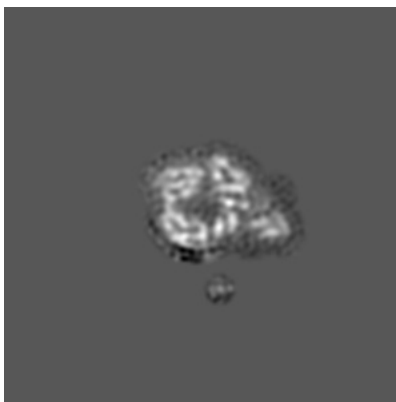
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 160

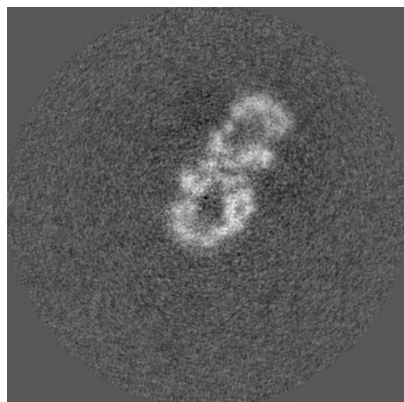


Y Index: 160

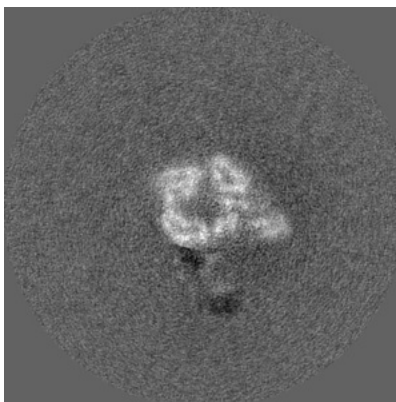


Z Index: 160

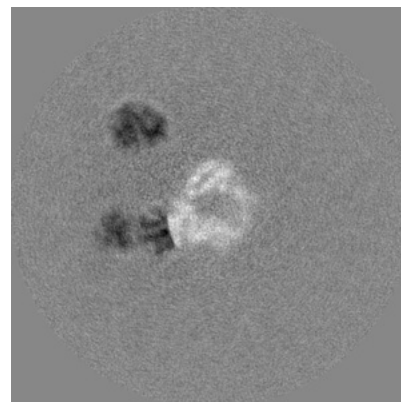
6.2.2 Raw map



X Index: 160



Y Index: 160

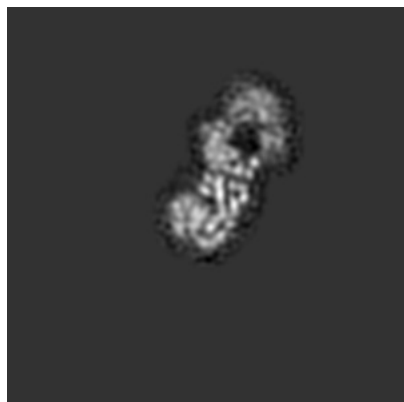


Z Index: 160

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

6.3 Largest variance slices [i](#)

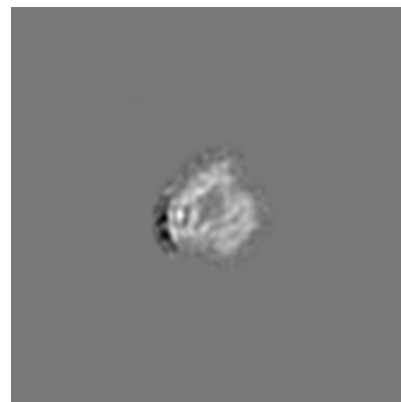
6.3.1 Primary map



X Index: 146

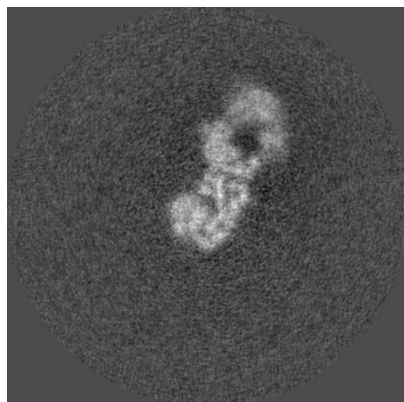


Y Index: 171

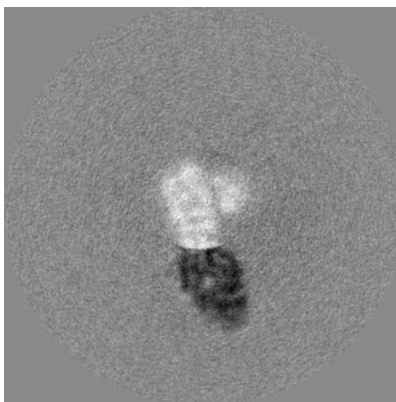


Z Index: 151

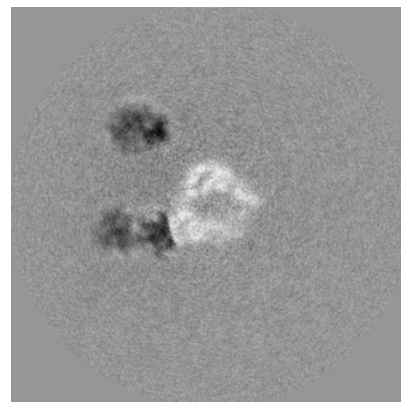
6.3.2 Raw map



X Index: 146



Y Index: 143



Z Index: 163

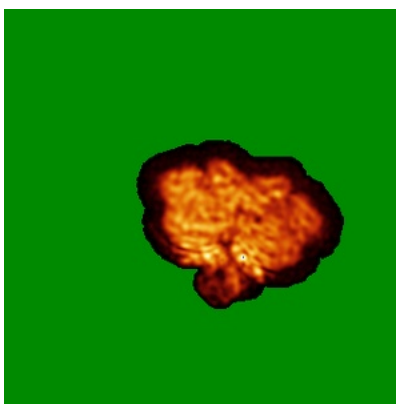
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X

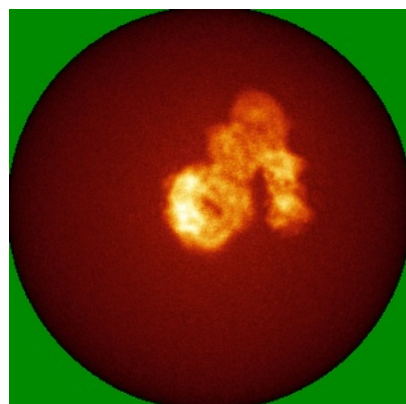


Y

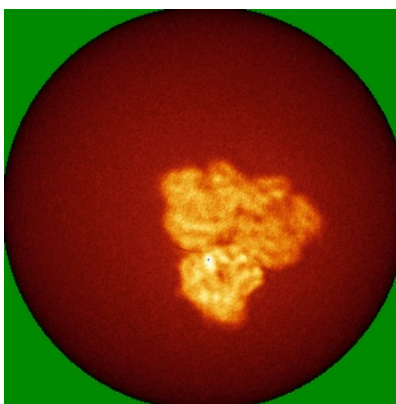


Z

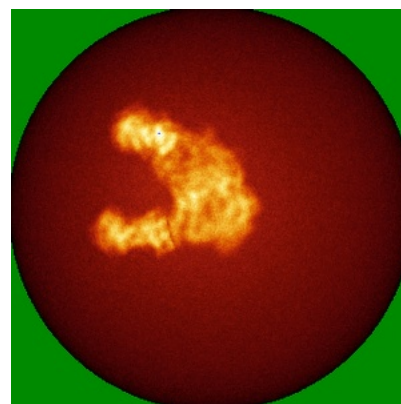
6.4.2 Raw map



X



Y

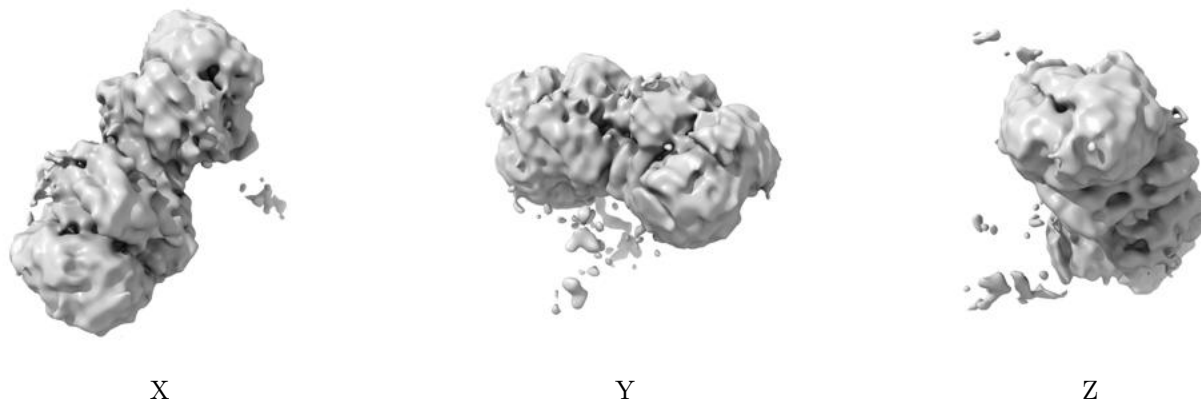


Z

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.

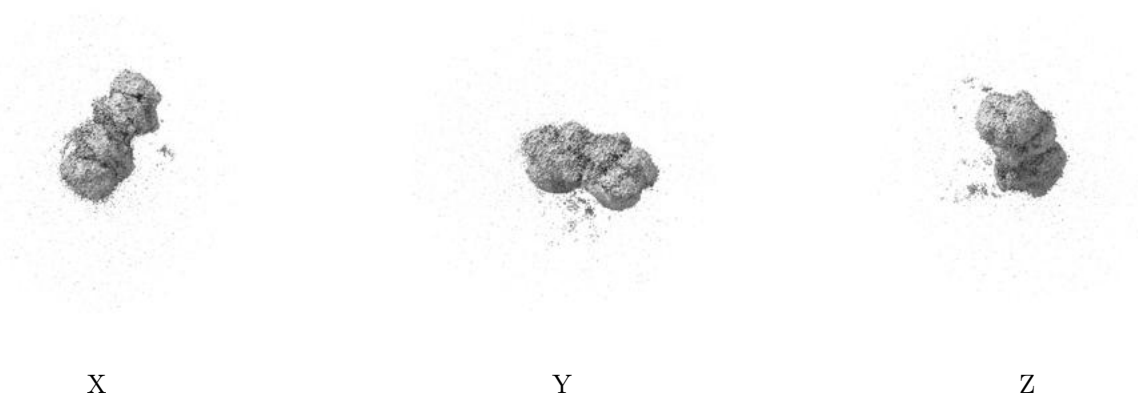
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.017. 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.

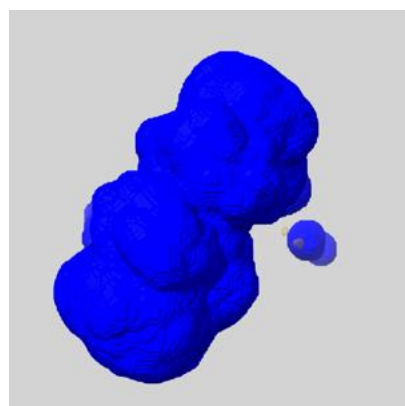
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

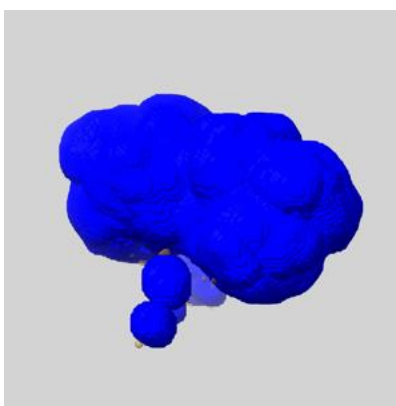
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

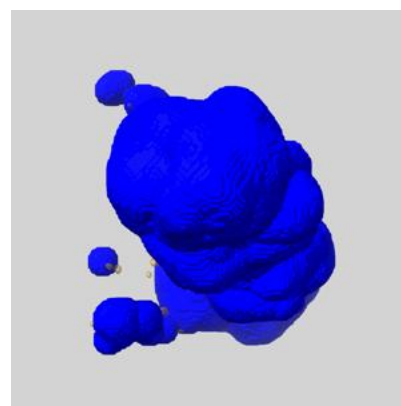
6.6.1 emd_7090_msk_1.map [i](#)



X



Y

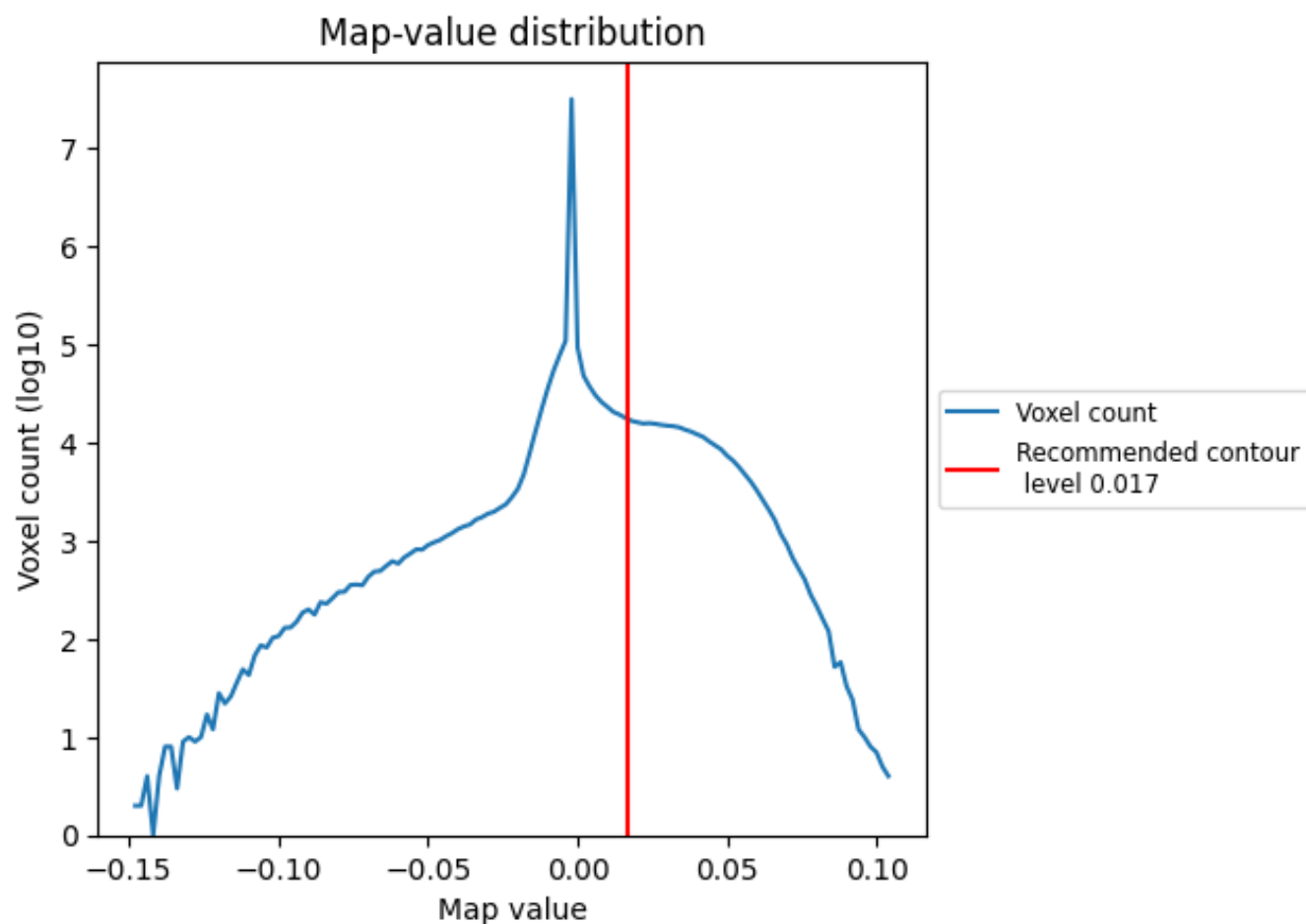


Z

7 Map analysis [i](#)

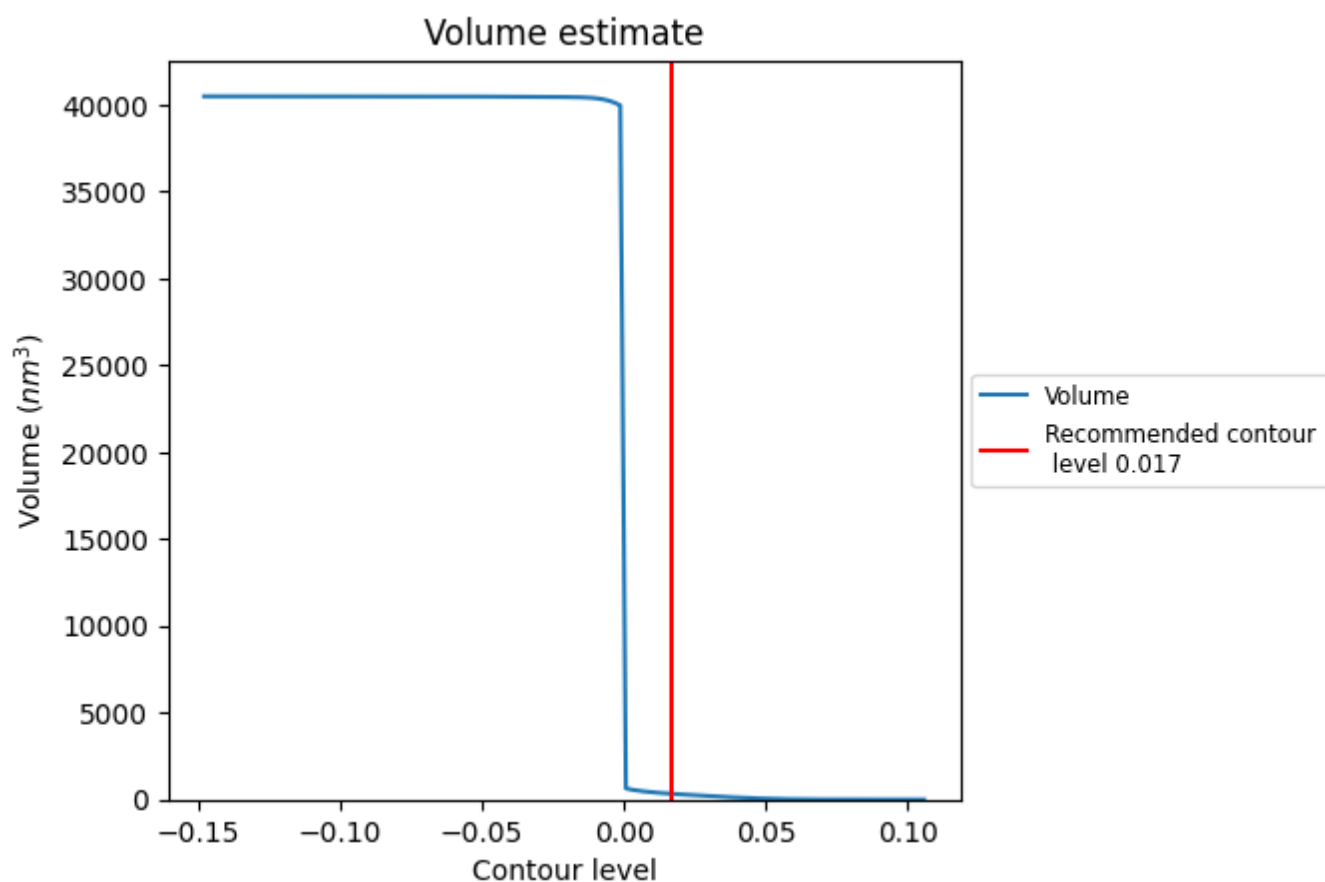
This section contains the results of statistical analysis of the map.

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.

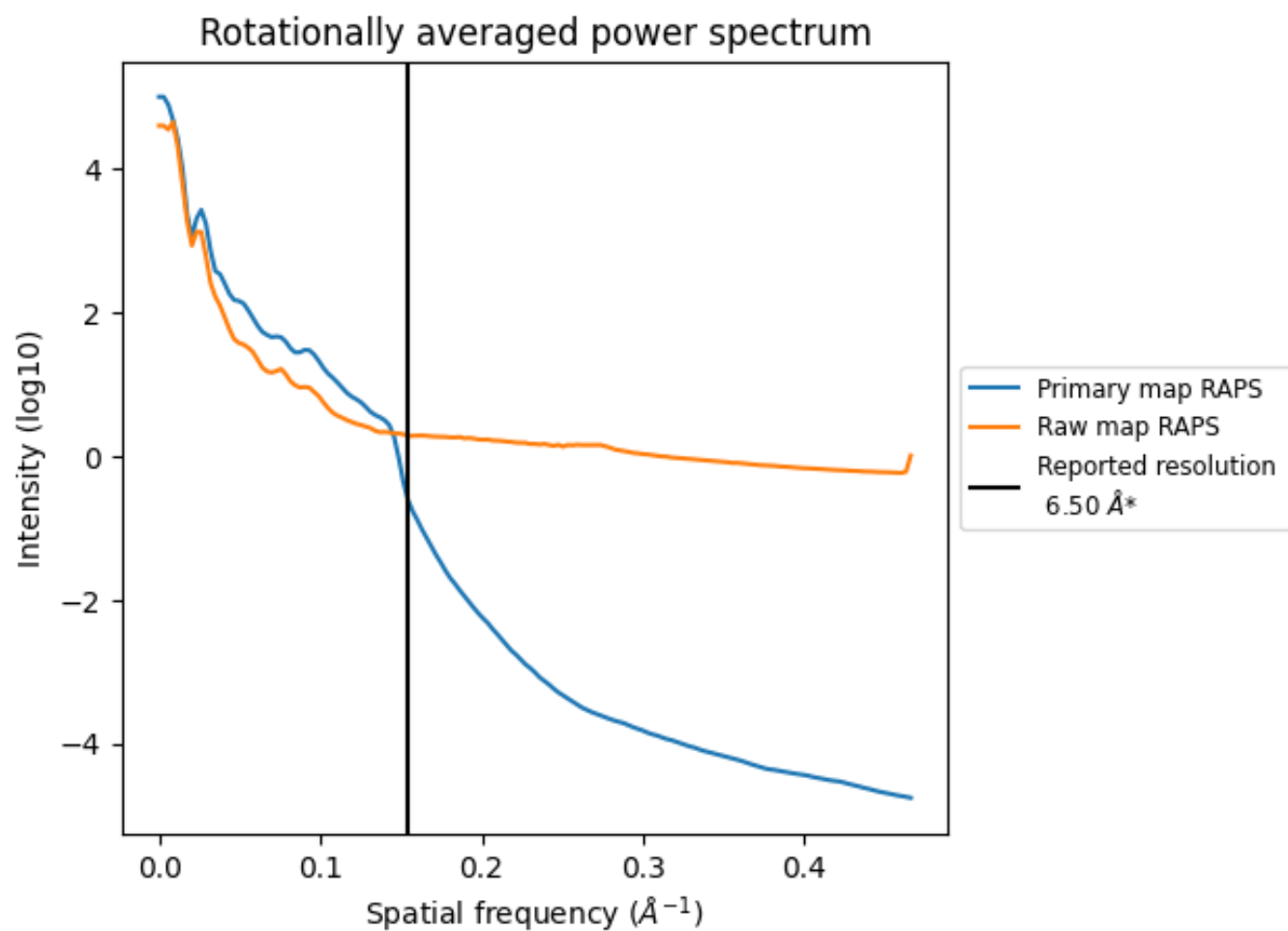
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 333 nm³; this corresponds to an approximate mass of 300 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 ⓘ

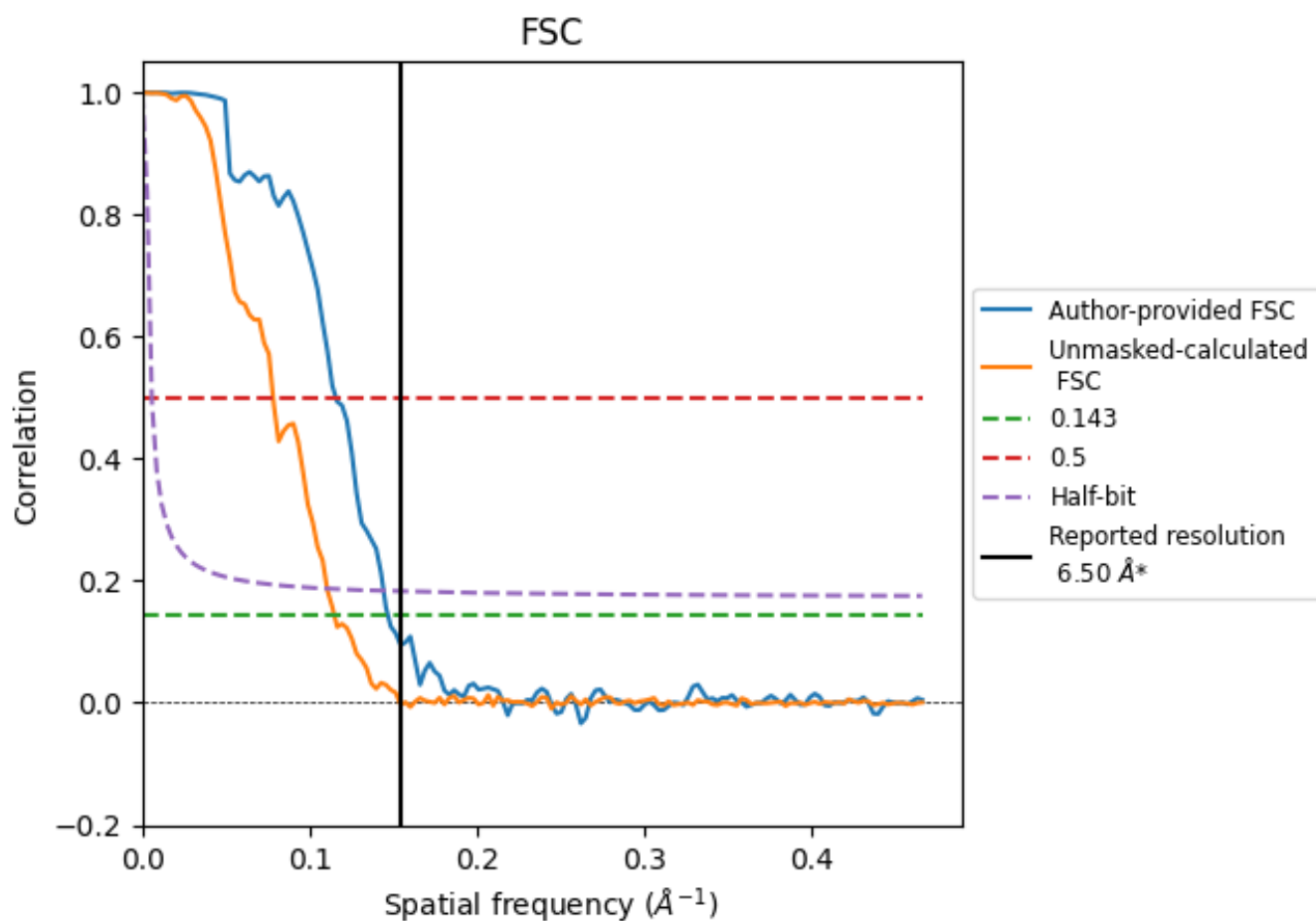


*Reported resolution corresponds to spatial frequency of 0.154 Å⁻¹

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 0.154 Å⁻¹

8.2 Resolution estimates [i](#)

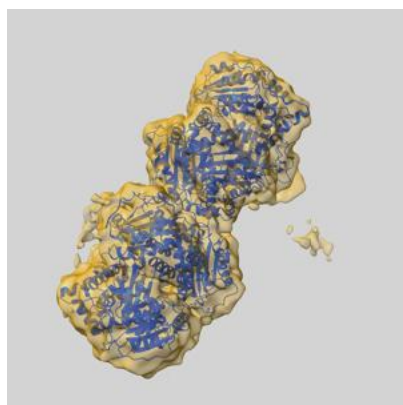
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.50	-	-
Author-provided FSC curve	6.81	8.64	6.93
Unmasked-calculated*	8.71	12.79	9.05

*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 8.71 differs from the reported value 6.5 by more than 10 %

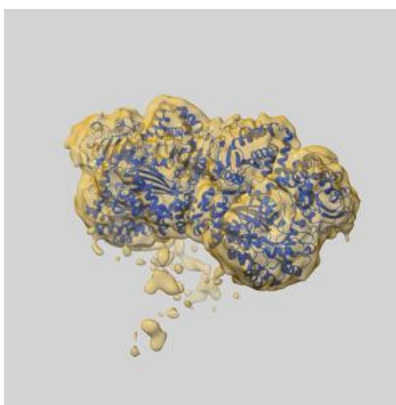
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-7090 and PDB model 6BF6. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

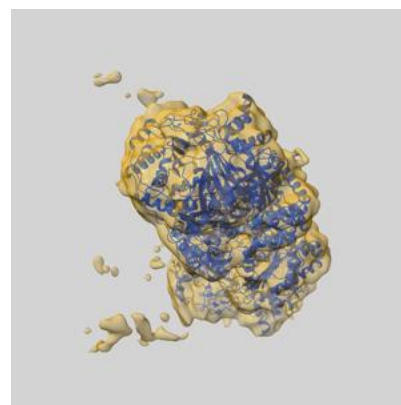
9.1 Map-model overlay [i](#)



X



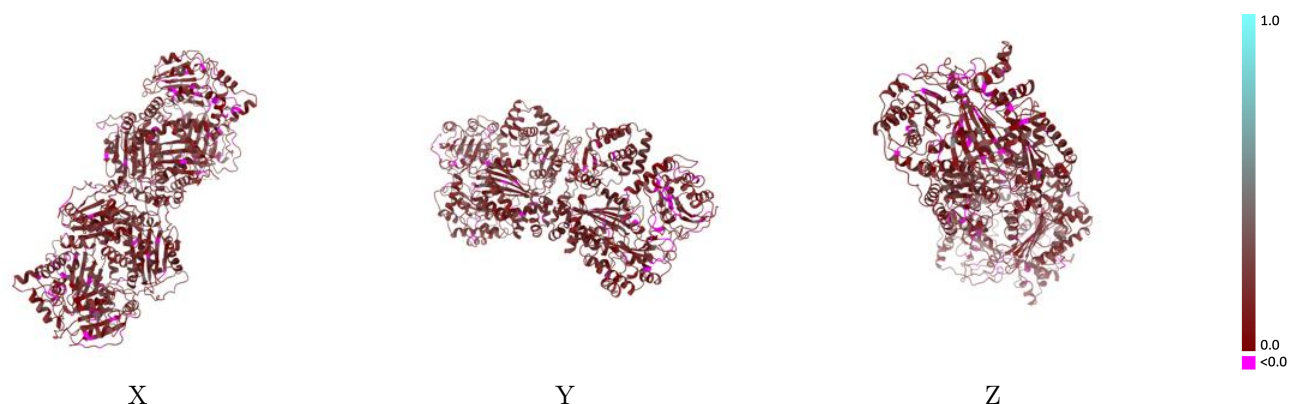
Y



Z

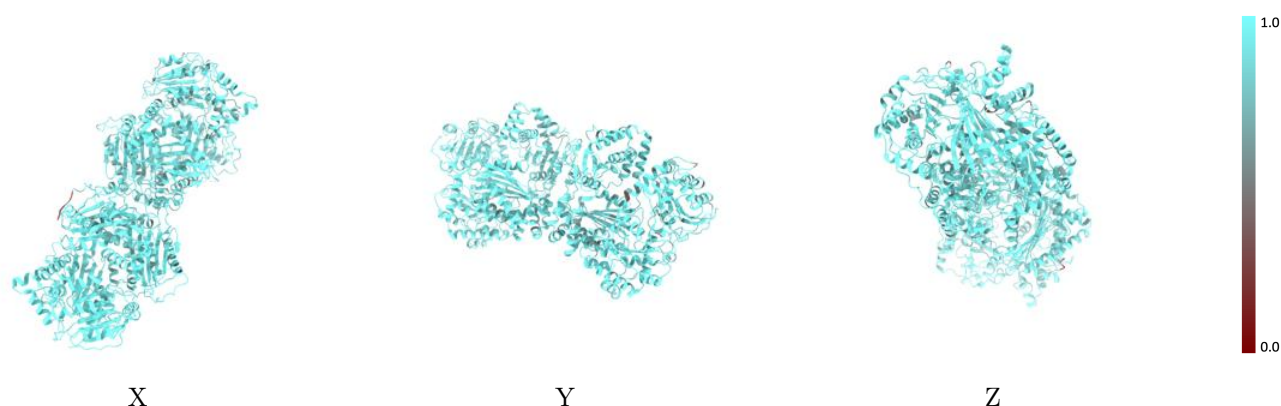
The images above show the 3D surface view of the map at the recommended contour level 0.017 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



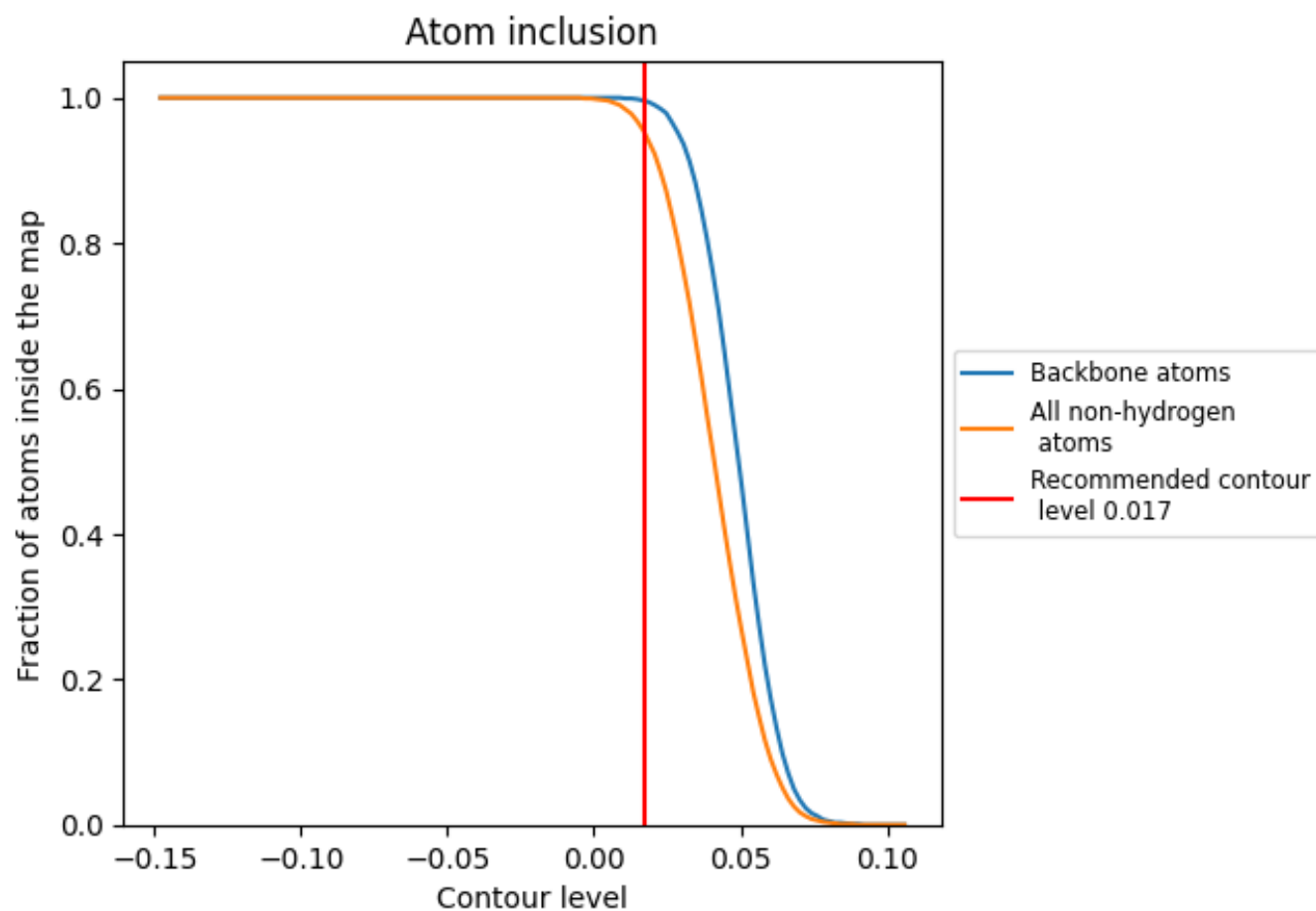
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.017).

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 (0.017) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9540	0.1620
A	0.9720	0.1660
B	0.9360	0.1580

