



## Full wwPDB EM Validation Report ⓘ

Dec 26, 2024 – 10:00 AM EST

PDB ID : 6SCT  
EMDB ID : EMD-0126  
Title : Cryo-EM structure of the consensus triskelion hub of the clathrin coat complex  
Authors : Morris, K.L.; Cameron, A.D.; Sessions, R.; Smith, C.J.  
Deposited on : 2019-07-25  
Resolution : 4.69 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev113  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.40

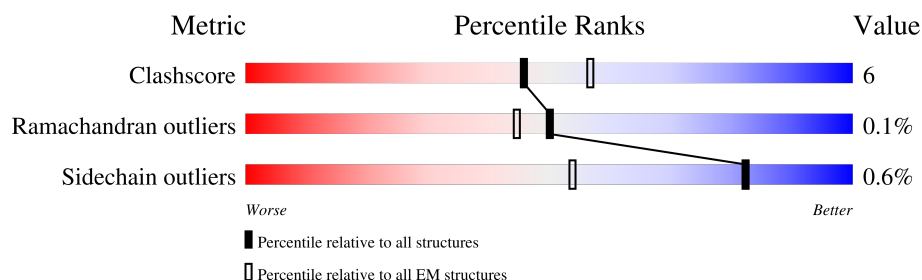
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 4.69 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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  $\geq 3$ , 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	1675	<div> <div>17%</div> <div>20%</div> <div>77%</div> </div>
1	B	1675	<div> <div>35%</div> <div>34%</div> <div>6%</div> <div>60%</div> </div>
1	C	1675	<div> <div>24%</div> <div>22%</div> <div>5%</div> <div>74%</div> </div>
1	F	1675	<div> <div>17%</div> <div>19%</div> <div>77%</div> </div>
1	G	1675	<div> <div>35%</div> <div>34%</div> <div>6%</div> <div>60%</div> </div>
1	H	1675	<div> <div>24%</div> <div>22%</div> <div>74%</div> </div>
1	K	1675	<div> <div>17%</div> <div>19%</div> <div>77%</div> </div>
1	L	1675	<div> <div>35%</div> <div>34%</div> <div>6%</div> <div>60%</div> </div>

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Mol	Chain	Length	Quality of chain
1	M	1675	<div><div><div></div><div></div><div></div></div><div>24% 22% 74%</div></div>
2	D	229	<div><div><div></div><div></div><div></div></div><div>44% 38% 7% 55%</div></div>
2	E	229	<div><div><div></div><div></div><div></div></div><div>26% 23% 74%</div></div>
2	I	229	<div><div><div></div><div></div><div></div></div><div>44% 37% 8% 55%</div></div>
2	J	229	<div><div><div></div><div></div><div></div></div><div>26% 22% 74%</div></div>
2	N	229	<div><div><div></div><div></div><div></div></div><div>44% 38% 7% 55%</div></div>
2	O	229	<div><div><div></div><div></div><div></div></div><div>26% 22% 74%</div></div>

## 2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 40680 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 Clathrin heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	379	Total	C	N	O	S	0	0
			3168	2037	528	584	19		
1	B	666	Total	C	N	O	S	0	0
			5405	3438	927	1015	25		
1	C	441	Total	C	N	O	S	0	0
			3598	2293	615	675	15		
1	F	379	Total	C	N	O	S	0	0
			3168	2037	528	584	19		
1	K	379	Total	C	N	O	S	0	0
			3168	2037	528	584	19		
1	G	666	Total	C	N	O	S	0	0
			5405	3438	927	1015	25		
1	L	666	Total	C	N	O	S	0	0
			5405	3438	927	1015	25		
1	H	441	Total	C	N	O	S	0	0
			3598	2293	615	675	15		
1	M	441	Total	C	N	O	S	0	0
			3598	2293	615	675	15		

- Molecule 2 is a protein called Clathrin light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	104	Total	C	N	O	S	0	0
			875	539	165	168	3		
2	E	59	Total	C	N	O		0	0
			514	312	101	101			
2	J	59	Total	C	N	O		0	0
			514	312	101	101			
2	O	59	Total	C	N	O		0	0
			514	312	101	101			
2	I	104	Total	C	N	O	S	0	0
			875	539	165	168	3		
2	N	104	Total	C	N	O	S	0	0
			875	539	165	168	3		



SER	VAL	ALA	VAL	PRO	GLN	ALA	PRO	PHE	GLY	TYR	GLY	TYR	THR	ALA	PRO	PRO	TYR	GLY	GLN	PRO	GLN	PRO	GLY	PHE	GLY	TYR	SER	MET
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MET	ALA	ALA	GLN	LEU	LEU	PRO	ILE	ARG	PHE	GLN	GLY	HIS	LEU	GLN	LEU	GLN	ASN	ASN	GLY	ILE	GLY	PHE	SER	THR	LEU	THR	LEU	ASP	LYS	ILE	CYS	ILE	ARG	GLY	LYS	VAL	GLY	GLU	GLN	ALA	GLN	VAL	VAL	ASP	ILE	ASP	MET	ASN	ASP	PRO	SER	GLY	ASN
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[illegible]





CYS	THR	ASN	LEU	Q1025	P965	Y905	E944	F781	F721	E661	GLY	GLU	ARG	LEU	LEU	GLU	THR	GLU	THR
THR	ASP	SER	ILE	M1026	Y966	G906	L845	D782	S722	D662	ASN	PRO	ALA	ASP	ASP	PRO	ILE	ASP	THR
GLY	GLY	ASN	HIS	L1027	R967	K907	Y846	F783	Q723	S663	MET	LEU	ASN	GLN	GLN	VAL	PHE	LEU	ILE
ILE	MET	TRP	GLY	L1028	R968	Y908	A847	H785	D724	L664	THR	ILE	ASN	GLN	GLN	ASP	ARG	ALA	VAL
ASN	TRP	GLU	ASN	L1029	P969	C909	E948	D786	F725	E665	HIS	THR	LYS	LEU	ASN	THR	LYS	THR	ALA
LEU	GLU	GLU	LEU	L1030	L970	E910	Y849	D786	D726	C666	THR	GLN	VAL	ASN	ASN	PRO	PHE	PRO	ALA
ASP	ALA	ASP	ASP	T1031	D972	X911	E850		Y727	L667	ASP	ILE	VAL	ILE	ILE	ILE	ASN	HIS	HIS
ALA	ALA	VAL	ARG	A1032	Q973	R912	R851	L789	H728	R668	ARG	VAL	ALA	ASP	GLU	VAL	GLN	GLU	GLU
ALA	LYS	LYS	ALA	I1033	Y974	D913	R852	Y790	F729	R669	ALA	VAL	ASP	GLU	ASP	VAL	ASP	ALA	ALA
LEU	LEU	TRP	TYR	K1034	V975	P914	N853	L791	K730	M670	HIS	VAL	PHE	LEU	LEU	VAL	PHE	THR	THR
LEU	LEU	GLN	PHE	A1035	Q976	H915	R854	Y792	Y731	L671	ILE	ALA	ALA	GLU	GLU	ALA	ALA	ALA	GLY
THR	THR	ASN	MET	D1036	T977	L916	L855	R793	I732	S672	GLY	MET	GLU	LEU	LEU	GLY	GLY	ILE	ILE
ASN	ASN	ALA	GLU	R1037	A978	A917	R856	N794	I732	A673	ILE	THR	GLY	ASN	ASN	ASN	ASN	ASN	GLY
VAL	VAL	ARG	ARG	D1038	L979	C918	L857	N795	A734	N674	VAL	VAL	VAL	ARG	PRO	VAL	SER	VAL	VAL
VAL	LYS	LYS	CYS	T1038	S980	Y919	L858	L796	A735	I675	LYS	ILE	GLN	VAL	ASN	GLN	ASN	ASN	ASN
ASN	LYS	ASN	ASN	R1039	E981	A920	L859	Q797	C736	R676	ILE	GLN	LYS	VAL	ALA	ALA	ALA	ARG	ARG
PHE	ALA	ARG	ARG	E982	T982	Y921	P860	K798	K737	Q677	GLY	GLN	ILE	LEU	LEU	LYS	ALA	ALA	LYS
GLY	GLY	GLU	GLU	E1042	Q983	E922	W861	Y799	T738	N678	GLY	THR	VAL	GLN	GLN	VAL	VAL	GLY	GLY
ARG	ARG	GLU	GLU	Y1043	T984	R923	L862	I800	G739	L679	LEU	THR	ALA	VAL	VAL	ALA	ALA	VAL	VAL
ALA	ALA	ALA	TRP	I1044	P985	G924	E863	E801	G740	Q680	ALA	PHE	ALA	LYS	LYS	ALA	ALA	LEU	LEU
SER	SER	GLU	SER	I1044	E986	Q925	A864	I802	I741	I681	LEU	PRO	LYS	GLN	ASN	ASN	SER	SER	SER
THR	THR	THR	LEU			C926	R865	Q905	K742	C882	LEU	ASN	LYS	LEU	LEU	ALA	ALA	VAL	VAL
LEU	LEU	GLU	ALA	M1045	E987	D927	L866	K806	E743	Q684	GLU	LEU	VAL	LEU	LEU	VAL	VAL	ALA	ALA
VAL	VAL	GLU	LYS	R1046	V988	L928	H667	V807	E744	Q684	GLY	LEU	VAL	GLY	GLY	VAL	VAL	ALA	LYS
HIS	HIS	LEU	ALA	L1047	S989	E929	E868	V807	E745	V885	THR	THR	THR	LYS	ILE	LYS	THR	THR	GLY
LEU	LEU	ILE	ALA	M1048	M996	L930	T575		R746	A686	PHE	LEU	ALA	GLY	GLY	VAL	VAL	VAL	VAL
GLY	GLY	ALA	GLN	D1049	T997	E936	T576		I747	S687	THR	LEU	THR	THR	THR	THR	THR	GLU	GLU
GLU	GLU	ALA	ALA	Y1050	A998	N937	H876	G817	C753	S694	ARG	LEU	ARG	LEU	GLY	VAL	VAL	GLY	GLY
THR	THR	ALA	GLY	D1051	K993	Y933	N877	G818	Y754	T695	LEU	LEU	ILE	LEU	GLY	VAL	VAL	ASN	ASN
ALA	ALA	THR	MET	A1052	A994	E933	E872	P813	E749	H690	THR	LEU	THR	THR	GLY	VAL	VAL	ASN	ASN
ALA	ALA	ALA	VAL	P1053	F995	C934	P873	V814	E750	E591	GLY	LEU	LEU	ILE	GLY	VAL	VAL	ASN	ASN
VAL	VAL	ASN	VAL	D1054	M996	N935	A874	V815	S751	Q692	ARG	LEU	ASN	THR	CYS	ARG	ARG	THR	THR
ASP	ASP	ARG	GLY	I1055	T997	E936	T575	V815	S751	Q692	PRO	GLY	LEU	THR	GLY	VAL	VAL	ASN	ASN
LYS	LYS	GLY	ILE	A1056	A998	N937	H876	I816	N752	L693	THR	THR	VAL	GLY	GLY	GLY	GLY	VAL	VAL
ALA	ALA	GLY	ASP	M1057	D999	S938	N877	G817	C753	S694	LEU	LEU	ARG	LEU	GLY	VAL	VAL	GLN	GLN
ASN	ASN	GLU	TYR	I1058	D999	S938	N877	G818	Y754	T695	LEU	LEU	ILE	GLY	GLY	VAL	VAL	ASN	ASN
SER	SER	PHE	ILE	A1059	P1000	L939	A878	L819	D755	Q696	LEU	LEU	ILE	GLY	ASP	PRO	PRO	PRO	PRO
THR	THR	ILE	LYS	I1060	L1001	F940	K881	L820	D756	Q696	LEU	LEU	SER	ASP	ALA	ALA	ALA	ASP	ASP
ARG	ARG	ASN	ALA	K941	N1002	X941	L882	V822	E757	S697	LEU	LEU	VAL	GLN	LYS	PRO	PRO	GLY	GLY
THR	THR	PRO	ASP	S1061	E1003	S942	Y883	D823	R758	L698	LEU	LEU	GLY	GLY	ASN	ASN	ASN	ASN	ASN
TRP	TRP	ASP	ASP	M1062	L1004	L943	I884	E924	K760	E700	LEU	LEU	GLY	GLY	VAL	VAL	VAL	VAL	VAL
LYS	LYS	ASN	PRO	E1063	I1005	R945	D885	C924	N761	L701	LEU	LEU	GLN	GLN	GLN	GLN	GLN	THR	THR
GLY	GLY	ASN	SER	L1064	E1006	R945	S886	E926	F762	S704	LEU	LEU	GLN	GLN	GLN	GLN	GLN	THR	THR
VAL	VAL	ALA	SER	F1065	L1007	Y946	N887	E926	K764	F705	LEU	LEU	GLN	GLN	GLN	GLN	GLN	THR	THR
CYS	CYS	HIS	TYR	E1066	L1008	L947	N888	D927	L763	E703	LEU	LEU	GLN	GLN	GLN	GLN	GLN	THR	THR
ALA	ALA	ILE	MET	E1067	L1009	Y946	N889	E929	K764	F705	LEU	LEU	GLN	GLN	GLN	GLN	GLN	THR	THR
VAL	VAL	GLN	GLY	A1068	E1009	R949	N889	K830	A766	S706	LEU	LEU	GLN	GLN	GLN	GLN	GLN	THR	THR
VAL	VAL	VAL	VAL	F1069	K1010	R950	E990	E991	A766	S706	LEU	LEU	GLN	GLN	GLN	GLN	GLN	THR	THR
ASP	ASP	GLY	GLN	A1070	I1011	R950	E991	K830	A766	S706	LEU	LEU	GLN	GLN	GLN	GLN	GLN	THR	THR
GLY	GLY	ALA	ALA	V1012	V1012	K951	R892	N831	K767	S707	LEU	LEU	GLN	GLN	GLN	GLN	GLN	THR	THR
LYS	LYS	ALA	ALA	I1071	L1013	D952	F893	L832	L768	E709	LEU	LEU	GLN	GLN	GLN	GLN	GLN	THR	THR
				F1072	D1014	P953	L894	L833	L769	G710	LEU	LEU	GLN	GLN	GLN	GLN	GLN	THR	THR
				K1073	N1015	E964	R895	L834	D770	L711	LEU	LEU	GLN	GLN	GLN	GLN	GLN	THR	THR
				K1074	S1016	L955	E896	V835	Q771	F712	LEU	LEU	GLN	GLN	GLN	GLN	GLN	THR	THR
				F1075	V1017	K956	N897	V836	L772	S659	LEU	LEU	GLN	GLN	GLN	GLN	GLN	THR	THR
				ASP	V1018	G957	R898	R837	L774	F713	LEU	LEU	GLN	GLN	GLN	GLN	GLN	THR	THR
				VAL	S1019	S958	Y899	G838	I775	G716	LEU	LEU	GLN	GLN	GLN	GLN	GLN	THR	THR
				THR	E1020	Y959	Y899	G838	I775	G716	LEU	LEU	GLN	GLN	GLN	GLN	GLN	THR	THR
				SER	H1021	L960	D901	Q839	I776	G717	LEU	LEU	GLN	GLN	GLN	GLN	GLN	THR	THR
				ALA	R1022	L961	S902	F840	V777	I718	LEU	LEU	GLN	GLN	GLN	GLN	GLN	THR	THR
				VAL	N1023	E962	R903	T842	C778	V719	LEU	LEU	GLN	GLN	GLN	GLN	GLN	THR	THR
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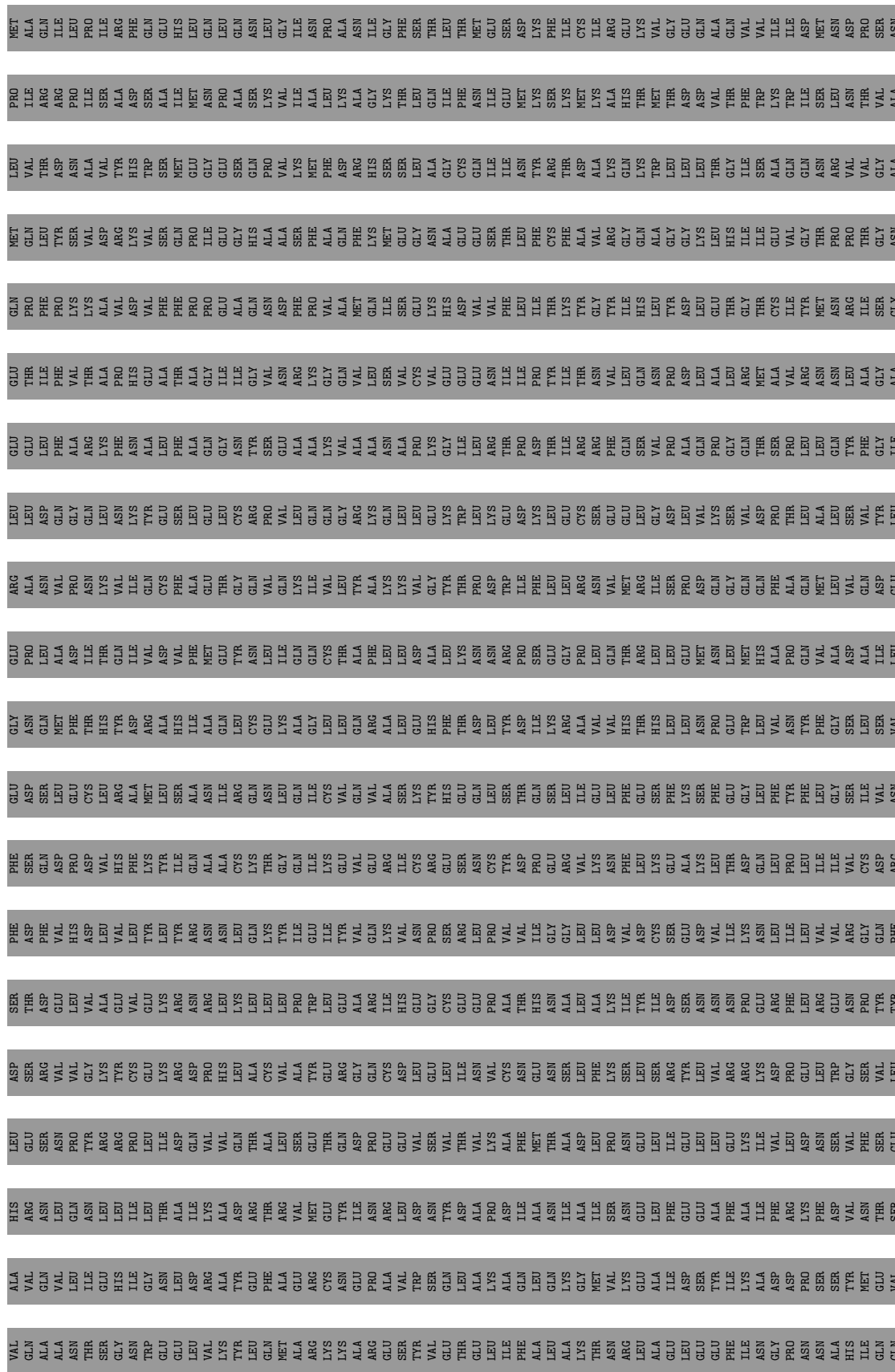
[illegible]

- Molecule 1: Clathrin heavy chain



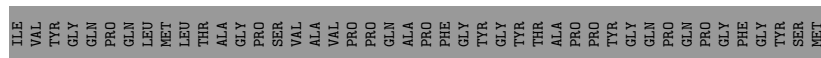
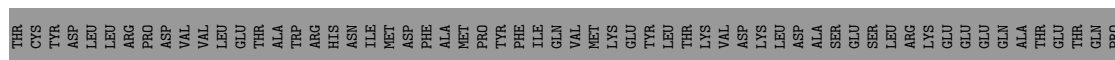
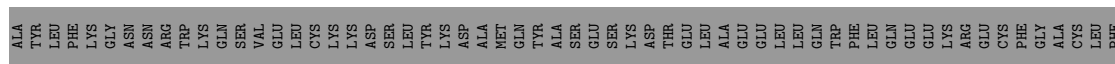
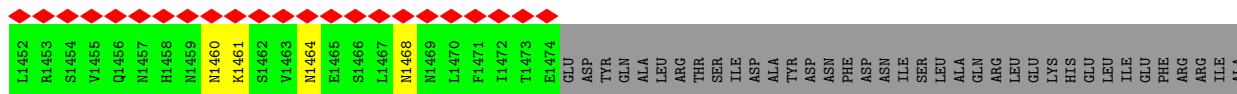
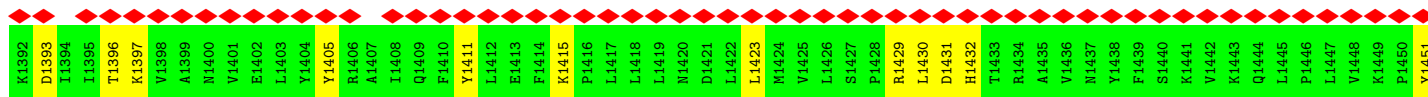
GLU	GLY	GLU	ARG	LEU	GLU	GLU	GLU	GLU	THR	GLN	GLN	PRO	GLN	LEU	MET	LEU	VAL	LEU	PRO	MET
ASP	ASN	PRO	ALA	LEU	GLU	GLU	GLN	THR	THR	PRO	PHE	THR	LEU	VAL	GLN	THR	THR	GLN	ILE	ALA
SER	ASN	LEU	ASN	ASP	GLN	GLN	LEU	ILE	VAL	ASN	GLN	GLN	TYR	ASP	SER	ASP	ASP	ARG	ARG	ILE
LEU	MET	ALA	VAL	GLY	PHE	ALA	PHE	VAL	VAL	VAL	LYS	LYS	SER	ASN	VAL	ALA	ALA	PRO	PRO	ILE
GLU	THR	ILE	ASN	GLN	ARG	ARG	GLN	THR	ALA	ALA	LYS	LYS	VAL	VAL	VAL	VAL	VAL	SER	SER	PRO
CYS	HIS	THR	LYS	GLN	GLN	GLN	GLN	THR	THR	PHE	PHE	PHE	SER	SER	GLN	MET	MET	ILE	ILE	ARG
LEU	HIS	GLN	VAL	LEU	LEU	PHE	LEU	ALA	ALA	PRO	PRO	PRO	PRO	GLU	PRO	GLU	GLN	GLN	GLN	ILE
ARG	THR	THR	VAL	SER	GLY	ALA	GLU	GLY	GLY	ALA	ALA	ALA	GLY	GLY	ILE	GLY	VAL	VAL	VAL	HIS
GLN	ILE	PHE	ALA	LEU	GLN	GLN	GLN	THR	THR	PRO	PRO	PRO	ILE	GLY	GLN	MET	MET	ILE	ILE	LEU
ASN	ALA	MET	GLU	GLU	GLU	GLN	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLU	GLY	GLN	GLN	GLN	GLN	ASN
ALA	GLN	GLY	THR	LEU	CYS	ASN	TYR	ILE	ALA	ALA	ALA	ALA	GLY	ASN	GLN	ALA	VAL	VAL	VAL	ASN
ILE	GLN	TYR	GLN	ARG	GLY	PRO	GLY	VAL	VAL	ASN	ASN	ASN	ALA	PRO	SER	LYS	VAL	VAL	VAL	LEU
ARG	LEU	GLY	ILE	VAL	VAL	VAL	VAL	ARG	ARG	GLN	GLN	GLN	ASN	GLN	ALA	PRO	VAL	VAL	VAL	GLY
GLN	CYS	ASN	GLN	PRO	GLY	GLU	GLY	VAL	VAL	VAL	VAL	VAL	GLN	GLN	ALA	GLY	GLY	GLY	GLY	ALA
ASN	LYS	ILE	GLN	VAL	GLU	GLU	GLU	ASN	ASN	ASN	ASN	ASN	ALA	ALA	ALA	ALA	VAL	VAL	VAL	ASN
LEU	GLY	GLN	LYS	GLN	ALA	ALA	ALA	GLN	GLN	GLN	GLN	GLN	SER	GLN	PRO	PRO	GLY	GLY	GLY	GLY
GLN	ALA	GLN	ILE	LEU	GLN	ALA	ALA	ARG	ARG	ARG	PHE	PHE	SER	GLN	GLN	GLY	GLY	GLY	GLY	GLY
ILE	GLY	GLN	ILE	GLN	ILE	ALA	ALA	LYS	LYS	LYS	ILE	ILE	GLY	GLY	PHE	GLY	GLY	GLY	GLY	GLY
CYS	LEU	CYS	VAL	GLN	VAL	VAL	VAL	GLY	GLY	GLY	GLY	VAL	GLY	PHE	GLY	GLY	PHE	GLY	GLY	GLY
VAL	LEU	THR	ALA	GLY	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
GLN	GLN	ALA	THR	ARG	ALA	ALA	ALA	VAL	VAL	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
VAL	ARG	PHE	ALA	LYS	ALA	ALA	ALA	VAL	VAL	VAL	VAL	VAL	GLN	GLN	PHE	GLY	GLY	GLY	GLY	GLY
ALA	ALA	LEU	LYS	VAL	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
VAL	ARG	LEU	LEU	PRO	GLU	GLU	GLU	VAL	VAL	ASN	ASN	ASN	ALA	ALA	ALA	ALA	VAL	VAL	VAL	VAL
GLN	LYS	ILE	GLN	VAL	GLU	GLU	GLU	ASN	ASN	ASN	ASN	ASN	ALA	ALA	ALA	ALA	VAL	VAL	VAL	VAL
LEU	GLY	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	SER	GLY	GLY	GLY	GLY	GLY	GLY	GLY
ALA	ALA	LEU	ILE	GLN	GLU	GLU	GLU	VAL	VAL	VAL	PHE	PHE	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
SER	LEU	LEU	GLN	VAL	GLY	GLY	GLY	VAL	VAL	VAL	VAL	VAL	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
LEU	GLY	GLN	LYS	PRO	TYR	GLY	GLY	CYS	CYS	GLN	GLN	GLN	HIS	GLN	HIS	GLY	GLY	GLY	GLY	GLY
ALA	ALA	GLN	ILE	VAL	VAL	ALA	ALA	VAL	VAL	VAL	VAL	VAL	GLN	GLN	GLY	GLY	GLY	GLY	GLY	GLY
VAL	ARG	PHE	ALA	GLY	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	GLN	GLN	GLY	GLY	GLY	GLY	GLY	GLY
GLN	GLN	ALA	THR	ARG	ALA	ALA	ALA	VAL	VAL	VAL	VAL	VAL	GLN	GLN	GLY	GLY	GLY	GLY	GLY	GLY
VAL	ARG	LEU	LYS	VAL	GLY	GLY	GLY	VAL	VAL	VAL	VAL	VAL	GLN	GLN	GLY	GLY	GLY	GLY	GLY	GLY
ALA	ALA	LEU	GLN	PRO	GLU	GLU	GLU	ASN	ASN	ASN	ASN	ASN	ALA	ALA	ALA	ALA	VAL	VAL	VAL	VAL
VAL	ARG	LEU	LEU	VAL	GLU	GLU	GLU	VAL	VAL	VAL	VAL	VAL	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
GLN	LYS	ILE	GLN	VAL	GLU	GLU	GLU	ASN	ASN	ASN	ASN	ASN	ALA	ALA	ALA	ALA	VAL	VAL	VAL	VAL
LEU	GLY	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	SER	GLY	GLY	GLY	GLY	GLY	GLY	GLY
ALA	ALA	LEU	ILE	GLN	GLU	GLU	GLU	VAL	VAL	VAL	VAL	VAL	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
SER	LEU	LEU	GLN	VAL	GLY	GLY	GLY	VAL	VAL	VAL	VAL	VAL	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
LEU	GLY	GLN	LYS	PRO	TYR	GLY	GLY	CYS	CYS	GLN	GLN	GLN	HIS	GLN	HIS	GLY	GLY	GLY	GLY	GLY
ALA	ALA	GLN	ILE	VAL	VAL	ALA	ALA	VAL	VAL	VAL	VAL	VAL	GLN	GLN	GLY	GLY	GLY	GLY	GLY	GLY
VAL	ARG	PHE	ALA	GLY	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	GLN	GLN	GLY	GLY	GLY	GLY	GLY	GLY
GLN	GLN	ALA	THR	ARG	ALA	ALA	ALA	VAL	VAL	VAL	VAL	VAL	GLN	GLN	GLY	GLY	GLY	GLY	GLY	GLY
VAL	ARG	LEU	LYS	VAL	GLY	GLY	GLY	VAL	VAL	VAL	VAL	VAL	GLN	GLN	GLY	GLY	GLY	GLY	GLY	GLY
ALA	ALA	LEU	GLN	PRO	GLU	GLU	GLU	ASN	ASN	ASN	ASN	ASN	ALA	ALA	ALA	ALA	VAL	VAL	VAL	VAL
VAL	ARG	LEU	LEU	VAL	GLU	GLU	GLU	VAL	VAL	VAL	VAL	VAL	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
GLN	LYS	ILE	GLN	VAL	GLU	GLU	GLU	ASN	ASN	ASN	ASN	ASN	ALA	ALA	ALA	ALA	VAL	VAL	VAL	VAL
LEU	GLY	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	SER	GLY	GLY	GLY	GLY	GLY	GLY	GLY
ALA	ALA	LEU	ILE	GLN	GLU	GLU	GLU	VAL	VAL	VAL	VAL	VAL	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
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LEU	GLY	GLN	LYS	PRO	TYR	GLY	GLY	CYS	CYS	GLN	GLN	GLN	HIS	GLN	HIS	GLY	GLY	GLY	GLY	GLY
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VAL	ARG	LEU	LEU	VAL	GLU	GLU	GLU	VAL	VAL	VAL	VAL	VAL	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
GLN	LYS	ILE	GLN	VAL	GLU	GLU	GLU	ASN	ASN	ASN	ASN	ASN	ALA	ALA	ALA	ALA	VAL	VAL	VAL	VAL
LEU	GLY	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	SER	GLY	GLY	GLY	GLY	GLY	GLY	GLY
ALA	ALA	LEU	ILE	GLN	GLU	GLU	GLU	VAL	VAL	VAL	VAL	VAL	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
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LEU	GLY	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	SER	GLY	GLY	GLY	GLY	GLY	GLY	GLY
ALA	ALA	LEU	ILE	GLN	GLU	GLU	GLU	VAL	VAL	VAL	VAL	VAL	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
SER	LEU	LEU	GLN	VAL	GLY	GLY	GLY	VAL	VAL	VAL	VAL	VAL	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
LEU	GLY	GLN	LYS	PRO	TYR	GLY	GLY	CYS	CYS	GLN	GLN	GLN	HIS	GLN	HIS	GLY	GLY	GLY	GLY	GLY
ALA	ALA	GLN	ILE	VAL	VAL	ALA	ALA	VAL	VAL	VAL	VAL	VAL	GLN	GLN	GLY	GLY	GLY	GLY	GLY	GLY
VAL	ARG	PHE	ALA	GLY	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	GLN	GLN	GLY	GLY	GLY	GLY	GLY	GLY
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GLN	LYS	ILE	GLN	VAL	GLU	GLU	GLU	ASN	ASN	ASN	ASN	ASN	ALA	ALA	ALA	ALA	VAL	VAL	VAL	VAL
LEU	GLY	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	SER	GLY	GLY	GLY	GLY	GLY	GLY	GLY
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LEU	GLY	GLN	LYS	PRO	TYR	GLY	GLY	CYS	CYS	GLN	GLN	GLN	HIS	GLN	HIS	GLY	GLY	GLY	GLY	GLY
ALA	ALA	GLN	ILE	VAL	VAL	ALA	ALA	VAL	VAL	VAL	VAL	VAL	GLN	GLN	GLY	GLY	GLY	GLY	GLY	GLY
VAL	ARG	PHE	ALA	GLY	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	GLN	GLN	GLY	GLY	GLY	GLY	GLY	GLY
GLN	GLN	ALA	THR	ARG	ALA	ALA	ALA	VAL	VAL	VAL	VAL	VAL	GLN	GLN	GLY	GLY	GLY	GLY	GLY	GLY
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- Molecule 1: Clathrin heavy chain

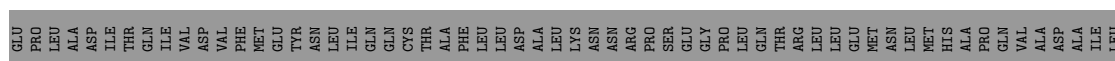
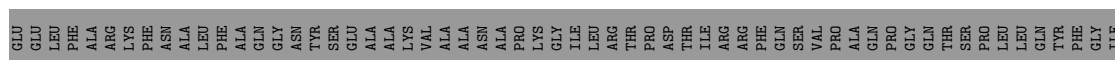
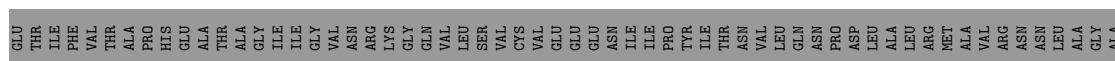
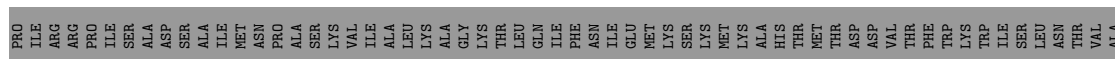
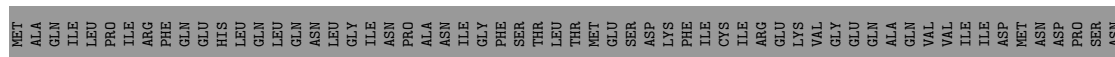








- Molecule 1: Clathrin heavy chain



Y1451	F1391	K1331	Q1270	M1210	W1149	L1085	R1022	E962	D901	S841	PHE
L1452	K1392	M1332	M1271	Y1211	W1150	I1086	N1023	S963	S902	T842	ASP
R1453	D1393	R1333	C1272	D1212	E1151	E1087		R964	R903	D843	GLN
S1454	I1394	E1334	G1273	A1213	E1152	H1088	N1026	P965	P904	E344	PRO
V1455	I1395	H1335	L1274	A1214	L1153	I1089	L1027	R966	V905	V845	ASP
Q1456	T1396	L1336	H1275	K1215	V1154	G1090	L1028	R967	G906	V846	VAL
N1457	K1397	E1337	T1276	L1216	K1155	N1091	I1029	R968	K907	A847	HIS
H1458	V1398	L1338	V1277	L1217	Q1158	L1092	L1030	R969	Y908	E848	PHE
N1459	F1399	F1339	W1278	Y1218	M1159	D1093	T1031	P970	Y909	E849	ALA
N1460	N1400	W1340	H1279	N1219	A1160	R1094	A1032	P971	C909	V850	ILE
V1461	V1401	S1341	A1280	N1220	R1161	A1095	I1033	D972	E910	Y851	GLN
S1462	L1402	V1342	D1281	V1221	K1162	Y1096	K1034	Q973	ASN	R852	ALA
V1463	L1403	V1343	E1282	N1223	K1163	F1098	D1036	Q974	ASN	R853	ILE
Y1464	Y1404	I1345	L1283	F1224	A1164	A1099	R1037	Y975	LEU	N854	GLN
E1465	Y1405	P1346	E1284	G1225	R1165	E1100	R1037	Q976	LYS	L855	THR
R1406	R1406	K1347	E1285	G1226	E1166	R1101	T1038	Q977	LYS	K856	GLY
A1407	L1407	V1348	L1286	L1227	S1167	C1102	R1039	A978	ILE	L857	GLN
T1408	T1408	L1349	I1287	L1228	Y1168	M1103	V1040	L979	GLU	L858	ILE
Q1409	Q1409	R1350	M1288	A1228	Y1169	E1104	M1041	S980	TYR	L859	VAL
F1410	F1410	A1351	Y1289	S1229	Y1170	E1104	E1042	E981	VAL	P860	GLY
Y1411	Y1411	A1352	Y1290	T1230	E1170	P1105	Y1042	T982	LYS	W861	ALA
L1412	L1412	E1353	Q1291	L1231	T1171	S1109	I1044	Q983	ASN	L862	ILE
E1413	E1413	Q1354	D1292	V1232	E1172	Q1110	N1045	D984	LYS	R863	THR
F1414	F1414	A1355	R1293	H1233	L1173	K1118	R1046	P985	ARG	G864	GLU
K1415	K1415	H1356	G1294	L1234	I1174	A1112	L1047	E986	ASN	R865	GLY
P1416	P1416	L1357	Y1295	G1235	F1175	A1113	D1048	E987	CYS	I866	GLN
L1417	L1417	W1358	F1296	E1236	L1176		N1049	Y988	TYR	D927	LEU
L1418	L1418	A1359	E1297	Y1237	L1177		Y1050	S989	ASP	H867	THR
L1419	L1419	E1360	E1298	Q1238	A1178	L1116	D1051	V990	PRO	P813	GLN
N1420	N1420	L1361	L1299	A1239	K1179	Q1117	A1052	T991	GLY	V815	SER
D1421	D1421	Y1362	T1300	H1240	T1180	K1118	P1053	Y992	ARG	G869	LEU
L1422	L1422	F1363	T1301	Y1241	N1181	G1119	A1054	K993	VAL	C870	ILE
L1423	L1423	L1364	M1302	D1242	R1182	V1121	I1055	A994	LYS	E871	GLU
M1424	M1424	Y1365	E1304	G1243	L1183	E1125	A1056	P995	GLY	P819	PHE
V1425	V1425	K1366	A1305	A1244	E1185	K1122	N1057	M996	LEU	L820	LEU
L1426	L1426	K1367	A1306	R1245	A1184	E1123		T997	ALA	V822	ALA
S1427	S1427	Y1368	L1307	K1246	L1186	S1127	N1062	D999	LYS	D823	LYS
P1428	P1428	E1369	L1307	A1247	E1187	Y1128	E1063	P1001	THR	C824	THR
R1429	R1429	E1370	G1308	N1248	E1188	I1129	L1064	N1002	ASP	S825	ASP
L1430	L1430	Y1371	L1309	S1249	F1189	I1129	L1064	N1002	GLN	E826	GLN
D1431	D1431	N1373	E1310	T1250	I1190	K1130	F1065	E1003	LEU	D827	LEU
H1432	H1432	A1374	R1311	T1251	N1191	A1131	E1066	L1004	PRO	V828	PRO
T1433	T1433	I1375	H1313	T1252	G1192	D1132	E1067	I1005	ILE	I829	ILE
R1434	R1434	I1376	M1314	K1254	N1194	D1133	A1068	E1006	GLY	K830	GLY
A1435	A1435	T1377	G1315	E1255	N1195	P1134	F1069	L1007	VAL	N831	VAL
V1436	V1436	M1378	M1316	V1256	A1196	S1135	A1070	L1008	CYS	L832	CYS
N1437	N1437	M1379	F1317	V1257	H1197	S1136	I1071	E1009	ASP	I833	ASP
V1438	V1438	M1379	T1318	F1258	I1198	Y1137	R1072	K1010	LEU	L834	LEU
F1439	F1439	H1381	E1319	A1259	Q1199	M1138	K1074	V1012	GLY	V835	GLY
S1440	S1440	P1382	L1320	C1260	Q1200	E1139	F1075	L1013	ARG	V836	ARG
K1441	K1441	T1383	A1321	G1261	G1201	Q1142	D1076	D1014	LYS	R837	LYS
V1442	V1442	L1384	I1322	V1261	G1202	A1143	V1077	N1015	ASN	Q838	ASN
K1443	K1443	A1385	L1323	D1262	D1203	A1144	N1078	S1016	GLN	Q839	GLN
Q1444	Q1444	W1386	Y1324	G1263	R1204	A1145	T1079	V1017	LEU	F840	LEU
L1445	L1445	K1387	S1325	K1264	C1205	N1145	N1080	F1018	VAL		
P1446	P1446	E1388	K1326	E1265	Y1206	T1146	Q1083	S1019	ILE		
L1447	L1447	Q1389	F1327	F1266	D1207	G1148	V1084	E1020	ASP		
L1448	L1448			R1267	E1208			H1021	ARG		
K1449	K1449			L1268	K1209						
P1450	P1450			A1269							



PRO	ILE	VAL	TYR	GLY	GLN	PRO	GLN	LEU	MET	LEU	THR	ALA	GLY	PRO	SER	VAL	ALA	VAL	PRO	PRO	GLN	ALA	PRO	PHE	GLY	TYR	GLY	TYR	THR	ALA	PRO	PRO	TYR	GLY	GLN	PRO	GLN	PRO	PRO	GLY	PHE	GLY	TYR	SER	MET
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- Molecule 1: Clathrin heavy chain



GLU PRO LEU LEU ALA ASP ILE THR GLN ILE VAL VAL ASP PHE MET GLU TYR ASN LEU LEU ILE GLN GLN CYS THR THR ALA ALA PHE LEU LEU LEU ASP ALA LEU LEU LYS ASN ASN ARG ARG SER PRO GLU GLY PRO PRO LEU LEU GLN THR ARG ARG LEU LEU GLU MET MET ASN LEU MET HIS ALA ALA PRO ALA GLN VAL ASP ALA ALA ILE LEU

GLY	ASN	GLN	NET	PHE	THR	HIS	TYR	ASP	ARG	ALA	HIS	ILE	ALA	GLN	LEU	CYS	GLY	LYS	ALA	GLY	LEU	LEU	GLN	ARG	ALA	LEU	GLU	HIS	PHE	THR	THR	ASP	LEU	TYR	D635	D636	D637	D638	A639	V640	V641	H642	T643	H644	L645	L646	N647	P648	E649	V650	L651	V652	N653	V654	F655	G656	S657	L658	S659	V660
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D661	D662	D663	D664	D665	D666	D667	D668	D669	D670	D671	D672	D673	D674	D675	D676	D677	D678	D679	D680	D681	D682	D683	D684	D685	D686	D687	D688	D689	D690	D691	D692	D693	D694	D695	D696	D697	D698	D699	D700	D701	D702	D703	D704	D705	D706	D707	D708	D709	D710	D711	D712	D713	D714	D715	D716	D717	D718	D719	D720
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F721	S722	Q723	D724	F725	D726	F727	H728	F729	Q730	Y731	I732	Q733	A734	A735	Q736	K737	I738	G739	Q740	I741	K742	E743	F744	E745	R746	I747	C748	R749	E750	S751	N752	C753	Y754	D755	P756	E757	F758	Y759	K760	N761	F762	L763	K764	E765	A766	K767	L768	T769	D770	Q771	L772	P773	L774	I775	I776	V777	C778	D779
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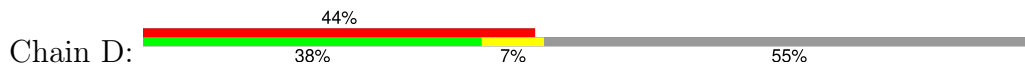
F781	F782	F783	F784	F785	F786	F789	F790	F791	F792	F793	F794	F795	F796	F797	F798	F799	F800	E801	E802	Q805	Q806	Q807	Q808	Q809	S810	R811	L812	P813	B814	V815	B816	G817	G818	L819	L820	D821	V822	D823	C824	S825	E826	D827	V828	K829	L830	N831	L832	L833	L834	V835	V836	R837	G838	Q839	F840	S841	T842
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------





[illegible]

- Molecule 2: Clathrin light chain

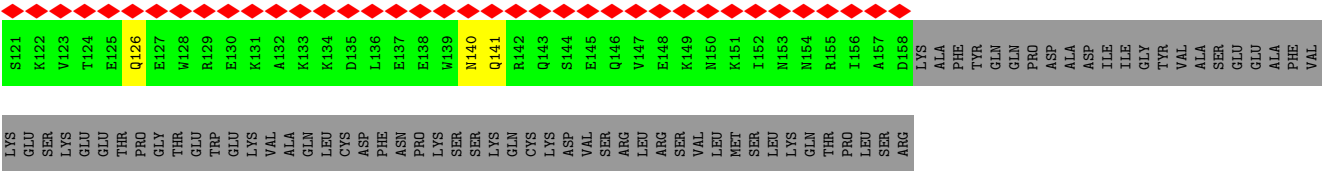


LYS	G189	T190	E191	W192	E193	K194	V195	A196	Q197	L198	C199	F201	M202	P203	K204	S205	S206	K207	Q208	C209	K210	D211	V212	S213	R214	L215	R216	S217	V218	L219	M220	S221	L222	K223	Q224	T225	PRO	LEU	SER	ARG																
\$121	K122	V123	T124	E125	Q126	E127	W128	R129	E130	K131	A132	K133	K134	D135	L136	E137	E138	W139	N140	Q141	R142	Q143	S144	E145	Q146	E148	K149	M150	K151	I152	M153	M154	R155	I156	A157	D158	K159	A160	F161	Y162	Q163	Q164	P165	D166	ALA	ASP	ILE	GLY	TYR	VAL	ALA	SER	GLU	GLU	PHE	VAL
SER	GLY	ALA	GLY	PRO	GLU	ASP	MET	THR	VAL	ASN	GLY	ASP	VAL	PHE	GLN	ASP	ALA	GLU	TYR	ALA	ALA	ILE	ALA	GLN	GLN	ALA	LEU	THR	GLN	GLU	P100	E101	S102	I103	R104	K105	W106	R107	E108	E109	Q110	R111	K112	R113	L114	Q115	E116	L117	D118	A119	A120					
MET	ALA	ASP	PHE	GLY	PHE	SER	SER	GLU	SER	GLY	ALA	PRO	GLU	VAL	ALA	GLU	GLU	ASP	PHE	ALA	LEU	GLN	GLN	GLN	GLN	ALA	LEU	THR	GLN	GLU	ASN	ASP	GLY	PHE	GLY	ALA	PRO	GLY	SER	GLN	LEU	ALA	GLN	PRO	GLY	PRO	ALA									

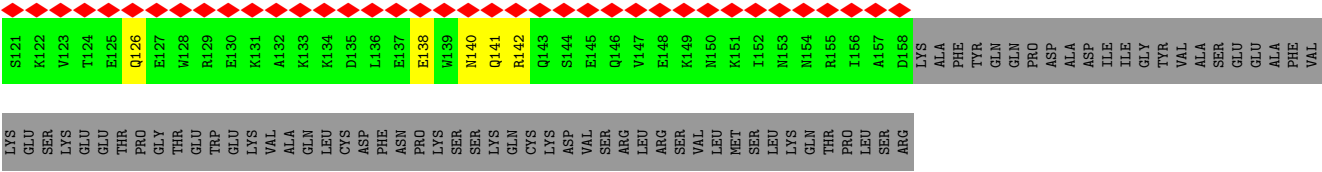
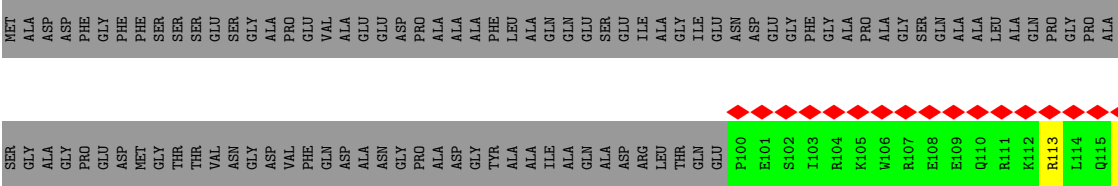
- Molecule 2: Clathrin light chain



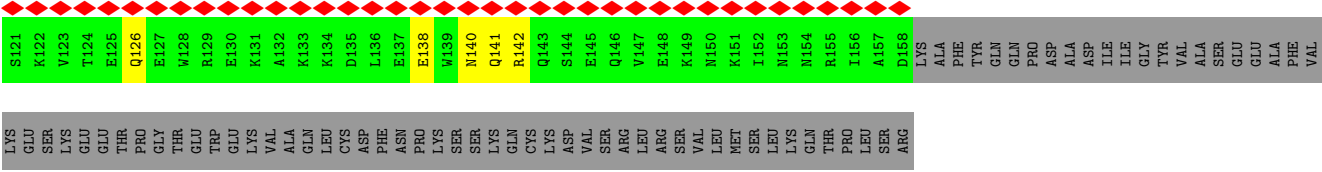
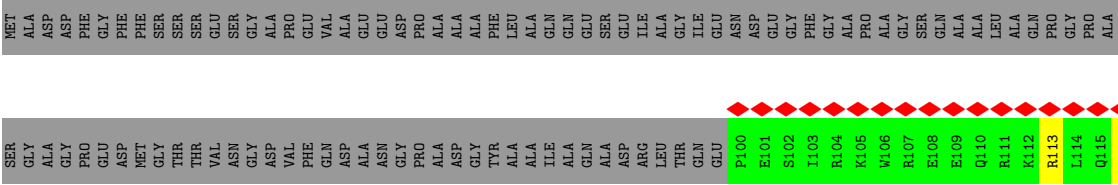
SER	GLY	ALA
GLY	ASP	ALA
PRO	PHE	GLY
GLU	PHE	GLY
ASP	PHE	GLY
MET	GLY	SER
THR	THR	SER
VAL	VAL	GLU
ASN	ASN	SER
GLY	GLY	GLY
ASP	ASP	ALA
VAL	PHE	PRO
PHE	PHE	GLU
GLN	GLN	VAL
ASP	ASP	ALA
ALA	ALA	GLU
ASN	ASN	GLU
GLY	GLY	ASP
PRO	PRO	ALA
ALA	ALA	ALA
ASP	ASP	ALA
GLY	GLY	ALA
TYR	TYR	PHE
ALA	ALA	LEU
ALA	ALA	ALA
ILE	ILE	GLN
ALA	ALA	GLN
GLN	GLN	GLU
ALA	ALA	SER
ASP	ASP	GLU
ARG	ARG	ILE
LEU	LEU	ALA
THR	THR	GLY
GLN	GLN	ILE
GLU	GLU	ASN
P100	P100	ASP
E101	E101	GLU
S102	S102	GLY
I103	I103	PHE
R104	R104	GLY
K105	K105	ALA
W106	W106	PRO
R107	R107	ALA
E108	E108	GLY
E109	E109	SER
Q110	Q110	GLN
R111	R111	ALA
K112	K112	LEU
R113	R113	GLN
L114	L114	PRO
Q115	Q115	GLY
E116	E116	ALA
L117	L117	ALA
D118	D118	ALA
A119	A119	ALA
L120	L120	ALA



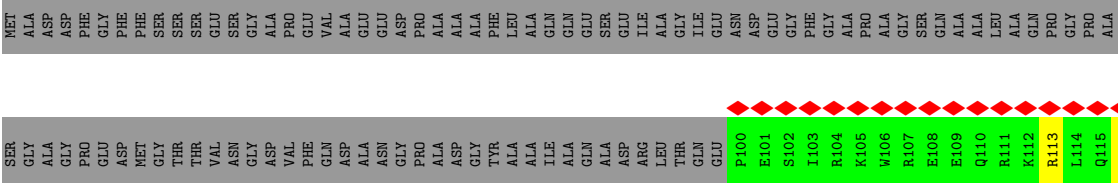
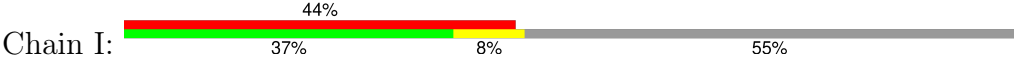
• Molecule 2: Clathrin light chain



• Molecule 2: Clathrin light chain



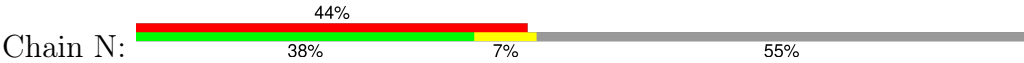
• Molecule 2: Clathrin light chain



S121	K122	V123	T124	E125	Q126	E127	W128	R129	E130	K131	A132	K133	K134	D135	L136	E137	E138	W139	N140	Q141	R142	Q143	S144	E145	Q146	V147	E148	K149	N150	K151	I152	N153	R154	R155	I156	A157	D158	K159	A160	F161	Y162	Q163	Q164	P165	D166	ALA	ASP	ILE	ILE	GLY	TYR	VAL	ALA	SER	GLU	GLU	ALA	PHE	VAL
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LYS	GLU	SER	LYS	GLU	GLU	THR	PRO	G189	T190	E191	W192	E193	K194	V195	A196	Q197	L198	C199	D200	F201	N202	P203	K204	S205	S206	K207	Q208	C209	K210	D211	V212	S213	R214	L215	R216	S217	V218	L219	M220	S221	L222	K223	Q224	T225	PRO	LEU	SER	ARG
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• Molecule 2: Clathrin light chain



MET	ALA	ASP	GLY	PHE	GLY	PHE	SER	SER	THR	GLU	SER	GLY	ALA	GLU	VAL	GLU	ALA	ASP	PRO	ALA	ALA	ALA	PHE	LEU	ALA	GLN	GLU	SER	GLU	ASP	ILE	GLY	ALA	GLN	GLU	PRO	GLY	ALA
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SER	GLY	ALA	GLY	PRO	GLU	ASP	MET	THR	VAL	ASN	GLY	VAL	PHE	GLN	ASP	ALA	GLY	TYR	ALA	ILE	ALA	GLN	GLU	P100	E101	S102	I103	R104	K105	W106	R107	E108	E109	Q110	R111	K112	R113	L114	Q115	E116	L117	D118	A119	A120
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S121	K122	V123	T124	E125	Q126	E127	W128	R129	E130	K131	A132	K133	K134	D135	L136	E137	E138	W139	N140	Q141	R142	Q143	S144	E145	Q146	V147	E148	K149	N150	K151	I152	N153	R154	R155	I156	A157	D158	K159	A160	F161	Y162	Q163	Q164	P165	D166	ALA	ASP	ILE	ILE	GLY	TYR	VAL	ALA	SER	GLU	GLU	ALA	PHE	VAL
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LYS	GLU	SER	LYS	GLU	GLU	THR	PRO	G189	T190	E191	W192	E193	K194	V195	A196	Q197	L198	C199	D200	F201	N202	P203	K204	S205	S206	K207	Q208	C209	K210	D211	V212	S213	R214	L215	R216	S217	V218	L219	M220	S221	L222	K223	Q224	T225	PRO	LEU	SER	ARG
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## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	313406	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 ( $e^-/\text{\AA}^2$ )	69	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	2800	Depositor
Magnification	82111	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.374	Depositor
Minimum map value	-0.157	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.016	Depositor
Recommended contour level	0.195	Depositor
Map size ( $\text{\AA}$ )	436.48, 436.48, 436.48	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.705, 1.705, 1.705	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	0.30	0/3240	0.50	0/4375
1	B	0.28	0/5513	0.49	0/7468
1	C	0.29	0/3667	0.52	0/4970
1	F	0.30	0/3240	0.50	0/4375
1	G	0.29	0/5513	0.49	0/7468
1	H	0.29	0/3667	0.52	0/4970
1	K	0.30	0/3240	0.50	0/4375
1	L	0.29	0/5513	0.49	0/7468
1	M	0.29	0/3667	0.52	0/4970
2	D	0.28	0/887	0.51	0/1183
2	E	0.27	0/520	0.57	0/692
2	I	0.28	0/887	0.51	0/1183
2	J	0.28	0/520	0.56	0/692
2	N	0.28	0/887	0.51	0/1183
2	O	0.28	0/520	0.56	0/692
All	All	0.29	0/41481	0.51	0/56064

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	3168	0	3118	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	5405	0	5359	61	0
1	C	3598	0	3592	58	0
1	F	3168	0	3118	35	0
1	G	5405	0	5359	65	0
1	H	3598	0	3592	53	0
1	K	3168	0	3118	36	0
1	L	5405	0	5359	65	0
1	M	3598	0	3592	56	0
2	D	875	0	872	8	0
2	E	514	0	508	4	0
2	I	875	0	872	9	0
2	J	514	0	508	5	0
2	N	875	0	872	8	0
2	O	514	0	508	5	0
All	All	40680	0	40347	488	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 6.

All (488) 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:C:772:LEU:H	1:C:773:PRO:HD2	1.22	1.03
1:H:772:LEU:H	1:H:773:PRO:HD2	1.22	1.00
1:M:772:LEU:H	1:M:773:PRO:HD2	1.22	1.00
1:H:763:LEU:HB3	1:H:768:LEU:HD11	1.46	0.97
1:C:763:LEU:HB3	1:C:768:LEU:HD11	1.46	0.97
1:M:763:LEU:HB3	1:M:768:LEU:HD11	1.46	0.96
1:C:772:LEU:H	1:C:773:PRO:CD	1.89	0.85
1:M:768:LEU:HD12	1:M:768:LEU:H	1.43	0.84
1:H:772:LEU:H	1:H:773:PRO:CD	1.89	0.84
1:M:772:LEU:H	1:M:773:PRO:CD	1.89	0.83
1:C:768:LEU:HD12	1:C:768:LEU:H	1.43	0.82
1:H:768:LEU:HD12	1:H:768:LEU:H	1.43	0.82
1:H:771:GLN:H	1:H:771:GLN:CD	1.87	0.77
1:A:1408:ILE:HD12	1:A:1419:LEU:HD11	1.68	0.75
1:M:771:GLN:H	1:M:771:GLN:CD	1.87	0.75
1:C:771:GLN:CD	1:C:771:GLN:H	1.87	0.75
1:K:1408:ILE:HD12	1:K:1419:LEU:HD11	1.68	0.75
1:F:1408:ILE:HD12	1:F:1419:LEU:HD11	1.68	0.74
1:B:908:TYR:O	1:B:912:ARG:NH1	2.22	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:908:TYR:O	1:G:912:ARG:NH1	2.22	0.73
1:C:749:ARG:O	1:C:780:ARG:NH2	2.22	0.73
1:H:749:ARG:O	1:H:780:ARG:NH2	2.22	0.73
1:L:1380:ASN:OD1	1:L:1381:HIS:ND1	2.22	0.72
1:G:1380:ASN:OD1	1:G:1381:HIS:ND1	2.22	0.72
1:M:772:LEU:N	1:M:773:PRO:HD2	2.03	0.72
1:M:749:ARG:O	1:M:780:ARG:NH2	2.22	0.72
1:L:908:TYR:O	1:L:912:ARG:NH1	2.21	0.72
1:M:848:GLU:OE2	1:M:852:ARG:NH1	2.24	0.71
1:C:848:GLU:OE2	1:C:852:ARG:NH1	2.24	0.71
1:H:848:GLU:OE2	1:H:852:ARG:NH1	2.24	0.70
1:C:635:ASP:O	1:C:638:ARG:NH1	2.25	0.70
1:B:1380:ASN:OD1	1:B:1381:HIS:ND1	2.22	0.70
1:H:771:GLN:N	1:H:771:GLN:OE1	2.25	0.70
1:L:1199:GLN:OE1	1:L:1226:ARG:NH1	2.25	0.70
1:H:635:ASP:O	1:H:638:ARG:NH1	2.25	0.70
1:B:1199:GLN:OE1	1:B:1226:ARG:NH1	2.25	0.70
1:M:771:GLN:N	1:M:771:GLN:OE1	2.25	0.70
1:K:1461:LYS:NZ	1:K:1465:GLU:OE2	2.26	0.69
1:A:1461:LYS:NZ	1:A:1465:GLU:OE2	2.26	0.69
1:C:771:GLN:N	1:C:771:GLN:OE1	2.25	0.69
1:C:772:LEU:N	1:C:773:PRO:HD2	2.03	0.69
1:G:1199:GLN:OE1	1:G:1226:ARG:NH1	2.25	0.69
1:F:1461:LYS:NZ	1:F:1465:GLU:OE2	2.26	0.69
1:M:635:ASP:O	1:M:638:ARG:NH1	2.25	0.69
1:A:1278:VAL:O	1:A:1311:ARG:NH1	2.27	0.68
1:B:1248:ASN:OD1	1:C:854:ARG:NH2	2.26	0.68
1:K:1278:VAL:O	1:K:1311:ARG:NH1	2.27	0.68
1:F:1278:VAL:O	1:F:1311:ARG:NH1	2.27	0.68
2:I:146:GLN:O	2:I:150:ASN:ND2	2.27	0.68
1:C:865:ARG:NH1	1:C:872:GLU:OE1	2.27	0.67
1:H:865:ARG:NH1	1:H:872:GLU:OE1	2.27	0.67
1:H:772:LEU:N	1:H:773:PRO:CD	2.58	0.67
1:B:1097:GLU:N	1:B:1097:GLU:OE1	2.28	0.66
1:L:1097:GLU:N	1:L:1097:GLU:OE1	2.28	0.66
1:M:865:ARG:NH1	1:M:872:GLU:OE1	2.27	0.66
1:C:723:GLN:N	1:C:723:GLN:OE1	2.29	0.66
1:G:1097:GLU:N	1:G:1097:GLU:OE1	2.28	0.66
1:K:1519:ASN:ND2	1:L:1101:ARG:O	2.29	0.66
1:L:1012:VAL:O	1:L:1016:SER:OG	2.14	0.66
1:M:723:GLN:N	1:M:723:GLN:OE1	2.29	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:772:LEU:N	1:C:773:PRO:CD	2.58	0.65
1:G:1012:VAL:O	1:G:1016:SER:OG	2.14	0.65
1:G:936:GLU:OE2	1:G:936:GLU:N	2.30	0.65
1:L:936:GLU:N	1:L:936:GLU:OE2	2.30	0.65
1:H:723:GLN:N	1:H:723:GLN:OE1	2.29	0.65
1:G:1304:GLU:OE2	1:G:1324:TYR:OH	2.15	0.65
1:B:1304:GLU:OE2	1:B:1324:TYR:OH	2.15	0.65
1:B:936:GLU:OE2	1:B:936:GLU:N	2.30	0.64
1:B:1012:VAL:O	1:B:1016:SER:OG	2.14	0.64
1:H:772:LEU:N	1:H:773:PRO:HD2	2.03	0.64
1:M:825:SER:OG	1:M:827:ASP:OD2	2.11	0.64
1:F:1464:ASN:O	1:F:1468:ASN:ND2	2.31	0.64
1:H:825:SER:OG	1:H:827:ASP:OD2	2.11	0.64
1:L:1304:GLU:OE2	1:L:1324:TYR:OH	2.15	0.64
1:G:837:ARG:NH1	1:G:838:GLY:O	2.32	0.63
1:L:837:ARG:NH1	1:L:838:GLY:O	2.32	0.63
1:K:1464:ASN:O	1:K:1468:ASN:ND2	2.31	0.63
1:L:852:ARG:O	1:L:854:ARG:NH1	2.32	0.63
1:F:1519:ASN:ND2	1:G:1101:ARG:O	2.31	0.63
1:B:852:ARG:O	1:B:854:ARG:NH1	2.32	0.62
1:A:1464:ASN:O	1:A:1468:ASN:ND2	2.31	0.62
1:F:1457:ASN:OD1	1:F:1458:HIS:ND1	2.31	0.62
1:G:852:ARG:O	1:G:854:ARG:NH1	2.32	0.62
1:A:1457:ASN:OD1	1:A:1458:HIS:ND1	2.31	0.62
2:E:113:ARG:NH2	2:E:116:GLU:OE1	2.33	0.62
1:B:1220:ASN:O	1:C:793:ARG:NH1	2.32	0.62
1:B:837:ARG:NH1	1:B:838:GLY:O	2.32	0.62
2:O:113:ARG:NH2	2:O:116:GLU:OE1	2.33	0.62
1:L:1170:GLU:N	1:L:1170:GLU:OE1	2.33	0.62
1:H:768:LEU:HD12	1:H:768:LEU:N	2.15	0.61
2:J:113:ARG:NH2	2:J:116:GLU:OE1	2.33	0.61
1:C:778:CYS:O	1:C:782:ASP:N	2.34	0.61
1:L:1248:ASN:OD1	1:M:854:ARG:NH2	2.34	0.61
1:M:778:CYS:O	1:M:782:ASP:N	2.34	0.61
1:G:1170:GLU:N	1:G:1170:GLU:OE1	2.33	0.61
1:M:986:GLU:N	1:M:986:GLU:OE1	2.34	0.61
1:C:986:GLU:OE1	1:C:986:GLU:N	2.34	0.61
1:G:1411:TYR:O	1:G:1415:LYS:N	2.34	0.61
1:H:986:GLU:OE1	1:H:986:GLU:N	2.34	0.61
1:B:1170:GLU:N	1:B:1170:GLU:OE1	2.33	0.60
1:G:1248:ASN:OD1	1:H:854:ARG:NH2	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1519:ASN:ND2	1:B:1101:ARG:O	2.34	0.60
1:H:778:CYS:O	1:H:782:ASP:N	2.34	0.60
1:K:1457:ASN:OD1	1:K:1458:HIS:ND1	2.31	0.60
1:B:1411:TYR:O	1:B:1415:LYS:N	2.34	0.60
1:F:1584:GLU:OE2	1:F:1588:ARG:NH2	2.35	0.60
1:C:768:LEU:HD12	1:C:768:LEU:N	2.15	0.60
1:A:1584:GLU:OE2	1:A:1588:ARG:NH2	2.35	0.59
1:G:1220:ASN:O	1:H:793:ARG:NH1	2.34	0.59
1:K:1584:GLU:OE2	1:K:1588:ARG:NH2	2.35	0.59
1:L:1388:GLU:N	1:L:1388:GLU:OE1	2.36	0.59
1:C:825:SER:OG	1:C:827:ASP:OD2	2.11	0.59
1:L:1393:ASP:O	1:L:1397:LYS:NZ	2.36	0.59
1:H:794:ASN:OD1	1:H:795:ASN:N	2.35	0.59
1:L:1411:TYR:O	1:L:1415:LYS:N	2.34	0.59
1:B:1388:GLU:N	1:B:1388:GLU:OE1	2.36	0.59
1:A:1284:GLU:O	1:A:1288:ASN:ND2	2.35	0.58
2:D:217:SER:O	2:D:221:SER:N	2.36	0.58
1:F:1284:GLU:O	1:F:1288:ASN:ND2	2.35	0.58
1:L:1120:MET:O	1:L:1124:ALA:N	2.36	0.58
1:M:768:LEU:HD12	1:M:768:LEU:N	2.15	0.58
2:N:217:SER:O	2:N:221:SER:N	2.36	0.58
1:B:1393:ASP:O	1:B:1397:LYS:NZ	2.36	0.58
1:K:1284:GLU:O	1:K:1288:ASN:ND2	2.36	0.58
1:B:1120:MET:O	1:B:1124:ALA:N	2.36	0.58
2:I:217:SER:O	2:I:221:SER:N	2.36	0.58
1:M:794:ASN:OD1	1:M:795:ASN:N	2.35	0.58
1:B:1352:ALA:HB3	1:B:1361:LEU:HD21	1.86	0.57
1:G:1120:MET:O	1:G:1124:ALA:N	2.36	0.57
1:L:1352:ALA:HB3	1:L:1361:LEU:HD21	1.86	0.57
1:L:1220:ASN:O	1:M:793:ARG:NH1	2.37	0.57
1:M:954:GLU:OE2	1:M:954:GLU:N	2.38	0.57
1:G:1393:ASP:O	1:G:1397:LYS:NZ	2.36	0.57
1:G:1388:GLU:N	1:G:1388:GLU:OE1	2.36	0.57
1:H:954:GLU:OE2	1:H:954:GLU:N	2.38	0.57
1:C:954:GLU:OE2	1:C:954:GLU:N	2.38	0.56
1:M:772:LEU:N	1:M:773:PRO:CD	2.58	0.56
1:G:1352:ALA:HB3	1:G:1361:LEU:HD21	1.86	0.56
1:C:794:ASN:OD1	1:C:795:ASN:N	2.35	0.56
1:C:768:LEU:H	1:C:768:LEU:CD1	2.18	0.56
1:C:771:GLN:CD	1:C:771:GLN:N	2.59	0.56
1:H:908:TYR:O	1:H:912:ARG:NH1	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:724:ASP:OD2	1:C:726:ASP:N	2.40	0.55
1:C:849:VAL:O	1:C:853:ASN:N	2.40	0.55
1:F:1508:ARG:NH1	1:F:1531:ASP:OD2	2.40	0.55
1:F:1523:GLN:O	1:F:1527:LEU:N	2.38	0.55
1:H:724:ASP:OD2	1:H:726:ASP:N	2.40	0.55
1:L:1333:ARG:NH1	1:L:1359:ALA:O	2.40	0.55
1:M:724:ASP:OD2	1:M:726:ASP:N	2.40	0.55
1:L:971:ILE:HA	1:L:974:VAL:HG12	1.88	0.55
1:M:921:TYR:O	1:M:925:GLN:N	2.39	0.55
1:K:1508:ARG:NH1	1:K:1531:ASP:OD2	2.40	0.55
1:L:954:GLU:OE2	1:L:954:GLU:N	2.39	0.55
1:L:1304:GLU:OE2	1:L:1331:LYS:NZ	2.35	0.55
1:B:1460:ASN:ND2	1:B:1461:LYS:N	2.55	0.55
1:C:908:TYR:O	1:C:912:ARG:NH1	2.39	0.55
1:G:954:GLU:OE2	1:G:954:GLU:N	2.39	0.55
1:H:921:TYR:O	1:H:925:GLN:N	2.40	0.55
2:I:213:SER:OG	2:I:216:ARG:NH1	2.40	0.55
1:A:1298:GLU:OE1	1:A:1298:GLU:N	2.40	0.55
1:K:1298:GLU:OE1	1:K:1298:GLU:N	2.40	0.55
1:G:971:ILE:HA	1:G:974:VAL:HG12	1.89	0.55
1:H:772:LEU:O	1:H:776:ILE:HD12	2.07	0.55
1:M:772:LEU:O	1:M:776:ILE:HD12	2.07	0.55
2:D:213:SER:OG	2:D:216:ARG:NH1	2.40	0.55
1:H:849:VAL:O	1:H:853:ASN:N	2.40	0.55
1:A:1508:ARG:NH1	1:A:1531:ASP:OD2	2.40	0.54
1:M:849:VAL:O	1:M:853:ASN:N	2.40	0.54
1:F:1298:GLU:OE1	1:F:1298:GLU:N	2.40	0.54
1:G:1460:ASN:ND2	1:G:1461:LYS:N	2.55	0.54
1:M:768:LEU:H	1:M:768:LEU:CD1	2.17	0.54
1:M:908:TYR:O	1:M:912:ARG:NH1	2.39	0.54
1:A:1520:ARG:NH2	1:A:1523:GLN:OE1	2.41	0.54
2:I:113:ARG:NH2	2:I:116:GLU:OE1	2.41	0.54
1:B:971:ILE:HA	1:B:974:VAL:HG12	1.89	0.54
2:N:113:ARG:NH2	2:N:116:GLU:OE1	2.41	0.54
1:C:772:LEU:O	1:C:776:ILE:HD12	2.07	0.54
1:L:1460:ASN:ND2	1:L:1461:LYS:N	2.55	0.54
1:L:1460:ASN:O	1:L:1464:ASN:N	2.40	0.54
1:G:1460:ASN:O	1:G:1464:ASN:N	2.40	0.54
1:C:1063:GLU:N	1:C:1063:GLU:OE1	2.41	0.54
2:D:113:ARG:NH2	2:D:116:GLU:OE1	2.41	0.54
1:F:1520:ARG:NH2	1:F:1523:GLN:OE1	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:213:SER:OG	2:N:216:ARG:NH1	2.40	0.54
1:K:1520:ARG:NH2	1:K:1523:GLN:OE1	2.41	0.54
1:G:1194:ASN:OD1	1:G:1195:ASN:N	2.42	0.53
1:A:1523:GLN:O	1:A:1527:LEU:N	2.38	0.53
1:B:913:ASP:OD1	1:B:916:LEU:N	2.41	0.53
1:G:1333:ARG:NH1	1:G:1359:ALA:O	2.40	0.53
1:M:743:GLU:N	1:M:743:GLU:OE1	2.42	0.53
1:C:921:TYR:O	1:C:925:GLN:N	2.40	0.53
1:B:1054:ASP:OD1	1:B:1055:ILE:N	2.42	0.53
1:H:1063:GLU:N	1:H:1063:GLU:OE1	2.41	0.53
1:M:771:GLN:CD	1:M:771:GLN:N	2.59	0.53
1:B:1194:ASN:OD1	1:B:1195:ASN:N	2.42	0.52
2:O:126:GLN:O	2:O:126:GLN:NE2	2.42	0.52
1:G:913:ASP:OD1	1:G:916:LEU:N	2.41	0.52
1:G:1054:ASP:OD1	1:G:1055:ILE:N	2.42	0.52
1:L:1250:THR:OG1	1:L:1251:ARG:NH1	2.43	0.52
1:L:1460:ASN:ND2	1:L:1461:LYS:H	2.07	0.52
1:M:1063:GLU:N	1:M:1063:GLU:OE1	2.41	0.52
2:I:149:LYS:O	2:I:153:ASN:ND2	2.42	0.52
1:C:743:GLU:OE1	1:C:743:GLU:N	2.42	0.52
1:K:1523:GLN:O	1:K:1527:LEU:N	2.38	0.52
1:G:1460:ASN:ND2	1:G:1461:LYS:H	2.07	0.52
1:L:1253:TRP:HB2	1:L:1276:ILE:HD11	1.91	0.52
1:M:900:TYR:O	1:M:923:ARG:NH2	2.41	0.52
1:A:1605:GLU:O	1:A:1608:THR:OG1	2.21	0.52
1:B:1460:ASN:O	1:B:1464:ASN:N	2.40	0.52
1:M:850:GLU:OE2	1:M:881:LYS:NZ	2.43	0.52
1:B:1333:ARG:NH1	1:B:1359:ALA:O	2.40	0.52
1:L:1054:ASP:OD1	1:L:1055:ILE:N	2.42	0.52
2:E:126:GLN:O	2:E:126:GLN:NE2	2.42	0.52
1:G:1250:THR:OG1	1:G:1251:ARG:NH1	2.43	0.52
1:L:1194:ASN:OD1	1:L:1195:ASN:N	2.42	0.52
1:H:743:GLU:OE1	1:H:743:GLU:N	2.42	0.52
1:B:1250:THR:OG1	1:B:1251:ARG:NH1	2.43	0.52
1:K:1460:ASN:OD1	1:K:1461:LYS:N	2.42	0.52
1:L:1460:ASN:HD22	1:L:1461:LYS:H	1.58	0.52
1:B:1322:ILE:O	1:B:1325:SER:OG	2.14	0.52
1:B:1460:ASN:ND2	1:B:1461:LYS:H	2.07	0.52
1:C:900:TYR:O	1:C:923:ARG:NH2	2.41	0.52
1:H:850:GLU:OE2	1:H:881:LYS:NZ	2.43	0.52
2:J:126:GLN:O	2:J:126:GLN:NE2	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1460:ASN:OD1	1:A:1461:LYS:N	2.42	0.51
1:F:1460:ASN:OD1	1:F:1461:LYS:N	2.42	0.51
1:L:913:ASP:OD1	1:L:916:LEU:N	2.41	0.51
1:H:768:LEU:H	1:H:768:LEU:CD1	2.18	0.51
1:H:971:ILE:HA	1:H:974:VAL:HG22	1.92	0.51
1:B:1253:TRP:HB2	1:B:1276:ILE:HD11	1.91	0.51
1:B:1304:GLU:OE2	1:B:1331:LYS:NZ	2.35	0.51
1:H:900:TYR:O	1:H:923:ARG:NH2	2.41	0.51
1:M:877:ASN:OD1	1:M:878:ALA:N	2.44	0.51
1:G:1460:ASN:HD22	1:G:1461:LYS:H	1.58	0.51
1:G:1304:GLU:OE2	1:G:1331:LYS:NZ	2.35	0.51
1:M:724:ASP:O	1:M:728:HIS:ND1	2.44	0.51
1:G:1253:TRP:HB2	1:G:1276:ILE:HD11	1.91	0.51
1:C:877:ASN:OD1	1:C:878:ALA:N	2.44	0.51
1:G:1322:ILE:O	1:G:1325:SER:OG	2.14	0.51
1:M:971:ILE:HA	1:M:974:VAL:HG22	1.92	0.51
1:H:877:ASN:OD1	1:H:878:ALA:N	2.44	0.51
1:A:1439:PHE:O	1:A:1443:LYS:N	2.43	0.50
1:A:1411:TYR:O	1:A:1415:LYS:N	2.45	0.50
1:B:1460:ASN:HD22	1:B:1461:LYS:H	1.58	0.50
1:C:971:ILE:HA	1:C:974:VAL:HG22	1.92	0.50
1:A:1253:TRP:HB2	1:A:1276:ILE:HD11	1.94	0.50
1:B:981:GLU:OE1	1:B:982:THR:N	2.45	0.50
1:C:724:ASP:O	1:C:728:HIS:ND1	2.44	0.50
1:L:981:GLU:OE1	1:L:982:THR:N	2.45	0.50
1:H:724:ASP:O	1:H:728:HIS:ND1	2.44	0.50
2:N:146:GLN:O	2:N:150:ASN:OD1	2.30	0.50
1:B:851:LYS:O	1:B:853:ASN:ND2	2.45	0.50
1:G:981:GLU:OE1	1:G:982:THR:N	2.45	0.50
1:G:1349:LEU:HD13	1:G:1361:LEU:HD23	1.94	0.50
1:K:1603:MET:O	1:K:1607:LEU:HD13	2.12	0.49
1:K:1605:GLU:O	1:K:1608:THR:OG1	2.21	0.49
1:G:851:LYS:O	1:G:853:ASN:ND2	2.45	0.49
1:L:1396:THR:O	1:L:1429:ARG:NH1	2.45	0.49
1:L:851:LYS:O	1:L:853:ASN:ND2	2.45	0.49
1:A:1603:MET:O	1:A:1607:LEU:HD13	2.12	0.49
1:B:1349:LEU:HD13	1:B:1361:LEU:HD23	1.94	0.49
1:C:782:ASP:OD1	1:C:811:ARG:NH2	2.46	0.49
1:F:1603:MET:O	1:F:1607:LEU:HD13	2.12	0.49
1:G:849:VAL:O	1:G:853:ASN:N	2.44	0.49
2:D:146:GLN:O	2:D:150:ASN:OD1	2.30	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:1411:TYR:O	1:F:1415:LYS:N	2.45	0.49
1:B:954:GLU:OE2	1:B:954:GLU:N	2.39	0.49
1:K:1411:TYR:O	1:K:1415:LYS:N	2.45	0.49
1:B:849:VAL:O	1:B:853:ASN:N	2.44	0.49
1:F:1605:GLU:O	1:F:1608:THR:OG1	2.21	0.49
1:L:1349:LEU:HD13	1:L:1361:LEU:HD23	1.94	0.49
1:L:1464:ASN:O	1:L:1468:ASN:OD1	2.31	0.49
1:H:782:ASP:OD1	1:H:811:ARG:NH2	2.46	0.49
1:M:666:CYS:SG	1:M:667:LEU:N	2.86	0.49
1:K:1397:LYS:O	1:L:976:GLN:NE2	2.46	0.49
1:A:1460:ASN:O	1:A:1464:ASN:OD1	2.31	0.48
1:C:666:CYS:SG	1:C:667:LEU:N	2.86	0.48
1:F:1253:TRP:HB2	1:F:1276:ILE:HD11	1.94	0.48
1:K:1253:TRP:HB2	1:K:1276:ILE:HD11	1.94	0.48
1:M:782:ASP:OD1	1:M:811:ARG:NH2	2.46	0.48
1:F:1439:PHE:O	1:F:1443:LYS:N	2.43	0.48
1:K:1460:ASN:O	1:K:1464:ASN:OD1	2.31	0.48
1:H:666:CYS:SG	1:H:667:LEU:N	2.86	0.48
1:C:883:TYR:O	1:C:886:SER:OG	2.25	0.48
1:G:1464:ASN:O	1:G:1468:ASN:OD1	2.31	0.48
1:H:903:ARG:NE	1:H:926:CYS:SG	2.87	0.48
1:C:850:GLU:OE2	1:C:881:LYS:NZ	2.43	0.48
1:L:934:CYS:O	1:L:938:SER:OG	2.26	0.48
1:A:1360:GLU:OE1	1:A:1360:GLU:N	2.44	0.48
1:M:903:ARG:NE	1:M:926:CYS:SG	2.87	0.48
1:B:1152:GLU:N	1:B:1152:GLU:OE1	2.47	0.47
1:B:1396:THR:O	1:B:1429:ARG:NH1	2.45	0.47
1:C:903:ARG:NE	1:C:926:CYS:SG	2.87	0.47
1:F:1460:ASN:O	1:F:1464:ASN:OD1	2.31	0.47
1:H:770:ASP:O	1:H:772:LEU:HB2	2.14	0.47
1:C:770:ASP:O	1:C:772:LEU:HB2	2.14	0.47
1:L:1152:GLU:N	1:L:1152:GLU:OE1	2.48	0.47
1:A:1330:GLN:OE1	1:A:1330:GLN:N	2.45	0.47
1:M:770:ASP:O	1:M:772:LEU:HB2	2.14	0.47
1:B:1310:GLU:OE1	1:B:1310:GLU:N	2.48	0.47
2:J:118:ASP:OD1	2:J:119:ALA:N	2.48	0.47
1:L:1310:GLU:N	1:L:1310:GLU:OE1	2.48	0.47
1:K:1488:ASP:OD1	1:K:1488:ASP:N	2.47	0.47
1:A:1488:ASP:OD1	1:A:1488:ASP:N	2.47	0.47
1:G:1152:GLU:N	1:G:1152:GLU:OE1	2.47	0.47
1:B:1060:ILE:HD13	1:B:1084:VAL:HG13	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:1310:GLU:OE1	1:F:1310:GLU:N	2.45	0.46
1:G:1310:GLU:N	1:G:1310:GLU:OE1	2.48	0.46
1:G:1365:TYR:O	1:G:1370:GLU:N	2.44	0.46
1:M:640:VAL:O	1:M:643:THR:HG22	2.16	0.46
1:B:1464:ASN:O	1:B:1468:ASN:OD1	2.31	0.46
1:B:1139:GLU:OE1	1:B:1139:GLU:N	2.48	0.46
1:C:640:VAL:O	1:C:643:THR:HG22	2.16	0.46
2:O:118:ASP:OD1	2:O:119:ALA:N	2.48	0.46
1:B:1365:TYR:O	1:B:1370:GLU:N	2.44	0.46
1:L:1060:ILE:HD13	1:L:1084:VAL:HG13	1.97	0.46
1:C:866:ILE:HD12	1:C:876:HIS:CE1	2.51	0.46
1:G:1002:ASN:ND2	1:G:1034:LYS:O	2.48	0.46
1:A:1248:ASN:OD1	1:A:1253:TRP:NE1	2.49	0.46
1:B:1002:ASN:ND2	1:B:1034:LYS:O	2.48	0.46
1:H:640:VAL:O	1:H:643:THR:HG22	2.16	0.46
1:F:1397:LYS:O	1:G:976:GLN:NE2	2.46	0.46
1:K:1310:GLU:OE1	1:K:1310:GLU:N	2.45	0.46
1:G:1009:GLU:HA	1:G:1012:VAL:HG12	1.98	0.46
1:L:1139:GLU:N	1:L:1139:GLU:OE1	2.48	0.46
1:L:1300:ILE:O	1:L:1304:GLU:N	2.49	0.46
1:B:1300:ILE:O	1:B:1304:GLU:N	2.49	0.46
1:F:1488:ASP:OD1	1:F:1488:ASP:N	2.47	0.46
1:H:866:ILE:HD12	1:H:876:HIS:CE1	2.51	0.46
1:A:1257:CYS:SG	1:A:1258:PHE:N	2.90	0.45
1:B:1009:GLU:HA	1:B:1012:VAL:HG12	1.98	0.45
1:C:690:HIS:O	1:C:694:SER:OG	2.33	0.45
1:K:1257:CYS:SG	1:K:1258:PHE:N	2.90	0.45
1:K:1356:HIS:NE2	2:N:114:LEU:HD22	2.32	0.45
1:G:1139:GLU:N	1:G:1139:GLU:OE1	2.48	0.45
1:F:1248:ASN:OD1	1:F:1253:TRP:NE1	2.49	0.45
1:L:1322:ILE:O	1:L:1325:SER:OG	2.14	0.45
1:G:1060:ILE:HD13	1:G:1084:VAL:HG13	1.97	0.45
1:F:1532:SER:O	1:F:1532:SER:OG	2.33	0.45
1:H:767:LYS:HE3	1:H:767:LYS:HB2	1.72	0.45
1:K:1304:GLU:OE2	1:K:1324:TYR:OH	2.32	0.45
1:L:1002:ASN:ND2	1:L:1034:LYS:O	2.48	0.45
1:L:1365:TYR:O	1:L:1370:GLU:N	2.44	0.45
2:D:143:GLN:O	2:D:147:VAL:HG23	2.17	0.45
1:F:1372:ASP:OD1	1:F:1373:ASN:N	2.50	0.45
1:M:866:ILE:HD12	1:M:876:HIS:CE1	2.51	0.45
1:M:910:GLU:HG2	1:M:933:VAL:HG13	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:143:GLN:O	2:N:147:VAL:HG23	2.17	0.45
2:E:118:ASP:OD1	2:E:119:ALA:N	2.48	0.45
1:F:1433:THR:OG1	1:F:1460:ASN:ND2	2.50	0.45
1:G:1396:THR:O	1:G:1429:ARG:NH1	2.45	0.45
1:A:1372:ASP:OD1	1:A:1373:ASN:N	2.50	0.45
1:F:1257:CYS:SG	1:F:1258:PHE:N	2.90	0.45
1:K:1439:PHE:O	1:K:1443:LYS:N	2.43	0.45
1:H:762:PHE:O	1:H:766:ALA:N	2.43	0.45
1:K:1372:ASP:OD1	1:K:1373:ASN:N	2.50	0.45
1:L:1009:GLU:HA	1:L:1012:VAL:HG12	1.98	0.45
2:D:118:ASP:OD1	2:D:119:ALA:N	2.50	0.44
1:H:910:GLU:HG2	1:H:933:VAL:HG13	1.99	0.44
1:K:1360:GLU:OE1	1:K:1360:GLU:N	2.44	0.44
2:N:118:ASP:OD1	2:N:119:ALA:N	2.50	0.44
1:K:1330:GLN:OE1	1:K:1330:GLN:N	2.45	0.44
1:M:988:VAL:O	1:M:992:VAL:HG23	2.17	0.44
2:I:143:GLN:O	2:I:147:VAL:HG23	2.17	0.44
1:F:1304:GLU:OE2	1:F:1324:TYR:OH	2.32	0.44
1:L:849:VAL:O	1:L:853:ASN:N	2.44	0.44
1:C:642:HIS:O	1:C:646:LEU:N	2.48	0.44
1:C:988:VAL:O	1:C:992:VAL:HG23	2.17	0.44
1:G:1091:ASN:OD1	1:G:1094:ARG:N	2.49	0.44
1:H:988:VAL:O	1:H:992:VAL:HG23	2.17	0.44
1:A:1433:THR:OG1	1:A:1460:ASN:ND2	2.50	0.44
1:G:839:GLN:N	1:G:839:GLN:OE1	2.49	0.44
1:G:1300:ILE:O	1:G:1304:GLU:N	2.49	0.44
1:M:690:HIS:O	1:M:694:SER:OG	2.33	0.44
2:I:118:ASP:OD1	2:I:119:ALA:N	2.50	0.44
1:A:1310:GLU:OE1	1:A:1310:GLU:N	2.45	0.44
1:F:1582:VAL:HG11	1:F:1598:TYR:CE2	2.53	0.44
1:B:1405:TYR:CE1	1:B:1430:LEU:HD11	2.54	0.43
1:M:767:LYS:HE2	1:M:767:LYS:H	1.83	0.43
1:C:767:LYS:HE3	1:C:767:LYS:HB2	1.72	0.43
1:M:968:ARG:HD2	1:M:971:ILE:HD11	2.00	0.43
1:C:925:GLN:OE1	1:C:946:TYR:OH	2.29	0.43
1:K:1433:THR:OG1	1:K:1460:ASN:ND2	2.49	0.43
1:L:1405:TYR:CE1	1:L:1430:LEU:HD11	2.54	0.43
1:H:767:LYS:HE2	1:H:767:LYS:H	1.83	0.43
1:M:827:ASP:OD2	1:M:828:VAL:N	2.51	0.43
1:A:1582:VAL:HG11	1:A:1598:TYR:CE2	2.53	0.43
1:F:1360:GLU:OE1	1:F:1360:GLU:N	2.44	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:1431:ASP:OD1	1:G:1432:HIS:N	2.51	0.43
1:H:827:ASP:OD2	1:H:828:VAL:N	2.51	0.43
1:M:762:PHE:O	1:M:766:ALA:N	2.43	0.43
1:A:1356:HIS:NE2	2:D:114:LEU:HD22	2.33	0.43
1:L:839:GLN:OE1	1:L:839:GLN:N	2.49	0.43
1:C:827:ASP:OD2	1:C:828:VAL:N	2.51	0.43
1:B:1431:ASP:OD1	1:B:1432:HIS:N	2.51	0.43
1:C:968:ARG:HD2	1:C:971:ILE:HD11	2.00	0.43
1:G:1405:TYR:CE1	1:G:1430:LEU:HD11	2.53	0.43
1:H:883:TYR:O	1:H:886:SER:OG	2.25	0.43
1:B:839:GLN:OE1	1:B:839:GLN:N	2.49	0.43
1:K:1582:VAL:HG11	1:K:1598:TYR:CE2	2.53	0.43
1:G:1253:TRP:CB	1:G:1276:ILE:HD11	2.49	0.43
1:H:968:ARG:HD2	1:H:971:ILE:HD11	2.00	0.43
1:B:1253:TRP:CB	1:B:1276:ILE:HD11	2.49	0.43
1:C:910:GLU:HG2	1:C:933:VAL:HG13	1.99	0.43
1:L:1431:ASP:OD1	1:L:1432:HIS:N	2.51	0.43
1:C:767:LYS:HE2	1:C:767:LYS:H	1.83	0.42
1:C:949:ARG:NH2	1:G:896:GLU:OE2	2.50	0.42
1:K:1248:ASN:OD1	1:K:1253:TRP:NE1	2.49	0.42
1:B:1091:ASN:OD1	1:B:1094:ARG:N	2.49	0.42
1:A:1304:GLU:OE2	1:A:1324:TYR:OH	2.32	0.42
1:G:877:ASN:OD1	1:G:878:ALA:N	2.53	0.42
1:L:988:VAL:O	1:L:992:VAL:HG22	2.19	0.42
1:H:937:ASN:OD1	1:H:937:ASN:N	2.53	0.42
2:N:214:ARG:O	2:N:218:VAL:HG12	2.20	0.42
1:B:896:GLU:OE2	1:M:949:ARG:NH2	2.52	0.42
1:G:988:VAL:O	1:G:992:VAL:HG22	2.19	0.42
2:I:138:GLU:OE2	2:I:142:ARG:NH2	2.50	0.42
1:C:937:ASN:N	1:C:937:ASN:OD1	2.53	0.42
1:F:1330:GLN:OE1	1:F:1330:GLN:N	2.45	0.42
1:L:1253:TRP:CB	1:L:1276:ILE:HD11	2.49	0.42
1:H:771:GLN:HB3	1:H:774:LEU:HD21	2.01	0.42
1:L:877:ASN:OD1	1:L:878:ALA:N	2.53	0.42
2:O:138:GLU:OE2	2:O:142:ARG:NH2	2.44	0.42
1:G:1030:LEU:HA	1:G:1033:ILE:HD12	2.02	0.42
1:G:1360:GLU:OE1	1:G:1360:GLU:N	2.53	0.42
1:L:1298:GLU:HA	1:L:1301:THR:HG22	2.02	0.42
1:B:877:ASN:OD1	1:B:878:ALA:N	2.53	0.42
1:C:771:GLN:HB3	1:C:774:LEU:HD21	2.01	0.42
2:D:214:ARG:O	2:D:218:VAL:HG12	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1582:VAL:HG11	1:A:1598:TYR:CD2	2.55	0.41
1:B:1360:GLU:OE1	1:B:1360:GLU:N	2.53	0.41
1:F:1582:VAL:HG11	1:F:1598:TYR:CD2	2.55	0.41
1:G:1298:GLU:HA	1:G:1301:THR:HG22	2.02	0.41
1:B:901:ASP:OD1	1:B:901:ASP:N	2.53	0.41
1:B:988:VAL:O	1:B:992:VAL:HG22	2.19	0.41
1:B:1298:GLU:HA	1:B:1301:THR:HG22	2.02	0.41
1:K:1582:VAL:HG11	1:K:1598:TYR:CD2	2.55	0.41
1:G:1013:LEU:HD22	1:G:1028:LEU:HD22	2.03	0.41
1:B:1030:LEU:HA	1:B:1033:ILE:HD12	2.02	0.41
1:L:1360:GLU:OE1	1:L:1360:GLU:N	2.53	0.41
2:J:138:GLU:OE2	2:J:142:ARG:NH2	2.44	0.41
1:L:901:ASP:OD1	1:L:901:ASP:N	2.53	0.41
1:H:690:HIS:O	1:H:694:SER:OG	2.33	0.41
1:A:1397:LYS:O	1:B:976:GLN:NE2	2.49	0.41
1:A:1502:HIS:O	1:A:1502:HIS:ND1	2.54	0.41
1:C:950:ARG:O	1:C:952:ASP:N	2.54	0.41
1:M:925:GLN:OE1	1:M:946:TYR:OH	2.29	0.41
1:M:950:ARG:O	1:M:952:ASP:N	2.54	0.41
1:L:1177:LEU:HD23	1:L:1182:ARG:HB2	2.02	0.41
1:L:1423:LEU:HD21	1:L:1451:TYR:CD2	2.56	0.41
1:H:950:ARG:O	1:H:952:ASP:N	2.54	0.41
1:M:771:GLN:HB3	1:M:774:LEU:HD21	2.01	0.41
2:I:214:ARG:O	2:I:218:VAL:HG12	2.20	0.41
1:B:1013:LEU:HD22	1:B:1028:LEU:HD22	2.02	0.41
1:F:1502:HIS:ND1	1:F:1502:HIS:O	2.54	0.41
1:K:1502:HIS:ND1	1:K:1502:HIS:O	2.54	0.41
2:E:140:ASN:OD1	2:E:141:GLN:N	2.54	0.41
1:M:642:HIS:O	1:M:646:LEU:N	2.48	0.41
1:A:1457:ASN:OD1	1:A:1458:HIS:N	2.54	0.41
1:C:762:PHE:O	1:C:766:ALA:N	2.43	0.41
1:K:1457:ASN:OD1	1:K:1458:HIS:N	2.54	0.41
1:G:1177:LEU:HD23	1:G:1182:ARG:HB2	2.02	0.41
1:L:1030:LEU:HA	1:L:1033:ILE:HD12	2.02	0.41
1:L:1323:LEU:O	1:L:1327:PHE:N	2.45	0.41
1:M:937:ASN:OD1	1:M:937:ASN:N	2.53	0.41
1:M:1041:MET:O	1:M:1045:ASN:OD1	2.39	0.41
1:F:1547:THR:HG22	1:F:1548:GLU:N	2.36	0.41
1:F:1574:TYR:OH	1:F:1601:GLN:OE1	2.10	0.41
1:K:1547:THR:HG22	1:K:1548:GLU:N	2.36	0.41
1:G:1423:LEU:HD21	1:G:1451:TYR:CD2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:140:ASN:OD1	2:O:141:GLN:N	2.54	0.40
1:G:1319:GLU:O	1:G:1323:LEU:HD13	2.22	0.40
1:B:1423:LEU:HD21	1:B:1451:TYR:CD2	2.56	0.40
1:G:1323:LEU:O	1:G:1327:PHE:N	2.45	0.40
1:G:1336:LEU:HD11	1:G:1364:LEU:HD21	2.03	0.40
1:L:1319:GLU:O	1:L:1323:LEU:HD13	2.22	0.40
1:L:1091:ASN:OD1	1:L:1094:ARG:N	2.49	0.40
1:H:1041:MET:O	1:H:1045:ASN:OD1	2.39	0.40
1:M:752:ASN:OD1	1:M:780:ARG:NH2	2.54	0.40
1:A:1411:TYR:HB2	1:A:1419:LEU:HD13	2.04	0.40
1:A:1420:ASN:HA	1:A:1423:LEU:HD12	2.04	0.40
1:C:1041:MET:O	1:C:1045:ASN:OD1	2.39	0.40
2:J:140:ASN:OD1	2:J:141:GLN:N	2.54	0.40
1:L:1013:LEU:HD22	1:L:1028:LEU:HD22	2.02	0.40
1:C:956:TRP:HA	1:C:959:VAL:HG12	2.04	0.40
1:K:1369:GLU:OE1	1:K:1371:TYR:OH	2.35	0.40
1:G:921:TYR:O	1:G:925:GLN:N	2.55	0.40
1:L:973:GLN:O	1:L:977:THR:HG23	2.22	0.40

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	377/1675 (22%)	351 (93%)	26 (7%)	0	100	100
1	B	664/1675 (40%)	620 (93%)	44 (7%)	0	100	100
1	C	439/1675 (26%)	389 (89%)	48 (11%)	2 (0%)	25	64
1	F	377/1675 (22%)	351 (93%)	26 (7%)	0	100	100
1	G	664/1675 (40%)	620 (93%)	44 (7%)	0	100	100
1	H	439/1675 (26%)	391 (89%)	46 (10%)	2 (0%)	25	64

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	K	377/1675 (22%)	351 (93%)	26 (7%)	0	100	100
1	L	664/1675 (40%)	620 (93%)	44 (7%)	0	100	100
1	M	439/1675 (26%)	389 (89%)	48 (11%)	2 (0%)	25	64
2	D	100/229 (44%)	95 (95%)	5 (5%)	0	100	100
2	E	57/229 (25%)	57 (100%)	0	0	100	100
2	I	100/229 (44%)	95 (95%)	5 (5%)	0	100	100
2	J	57/229 (25%)	57 (100%)	0	0	100	100
2	N	100/229 (44%)	95 (95%)	5 (5%)	0	100	100
2	O	57/229 (25%)	57 (100%)	0	0	100	100
All	All	4911/16449 (30%)	4538 (92%)	367 (8%)	6 (0%)	50	83

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	772	LEU
1	H	772	LEU
1	M	772	LEU
1	C	773	PRO
1	H	773	PRO
1	M	773	PRO

### 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	342/1471 (23%)	341 (100%)	1 (0%)	91	92
1	B	587/1471 (40%)	585 (100%)	2 (0%)	91	92
1	C	405/1471 (28%)	401 (99%)	4 (1%)	73	82
1	F	342/1471 (23%)	341 (100%)	1 (0%)	91	92
1	G	587/1471 (40%)	585 (100%)	2 (0%)	91	92
1	H	405/1471 (28%)	401 (99%)	4 (1%)	73	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	K	342/1471 (23%)	341 (100%)	1 (0%)	91	92
1	L	587/1471 (40%)	585 (100%)	2 (0%)	91	92
1	M	405/1471 (28%)	401 (99%)	4 (1%)	73	82
2	D	96/184 (52%)	94 (98%)	2 (2%)	48	67
2	E	55/184 (30%)	55 (100%)	0	100	100
2	I	96/184 (52%)	95 (99%)	1 (1%)	73	82
2	J	55/184 (30%)	55 (100%)	0	100	100
2	N	96/184 (52%)	94 (98%)	2 (2%)	48	67
2	O	55/184 (30%)	55 (100%)	0	100	100
All	All	4455/14343 (31%)	4429 (99%)	26 (1%)	82	88

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1509	ARG
1	B	887	ASN
1	B	907	LYS
1	C	767	LYS
1	C	772	LEU
1	C	907	LYS
1	C	1045	ASN
2	D	150	ASN
2	D	205	SER
1	F	1509	ARG
1	K	1509	ARG
1	G	887	ASN
1	G	907	LYS
1	L	887	ASN
1	L	907	LYS
1	H	767	LYS
1	H	772	LEU
1	H	907	LYS
1	H	1045	ASN
1	M	767	LYS
1	M	772	LEU
1	M	907	LYS
1	M	1045	ASN
2	I	205	SER
2	N	150	ASN

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Mol	Chain	Res	Type
2	N	205	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	H	889	ASN
1	M	889	ASN
2	I	150	ASN
2	I	153	ASN

### 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](#)

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.



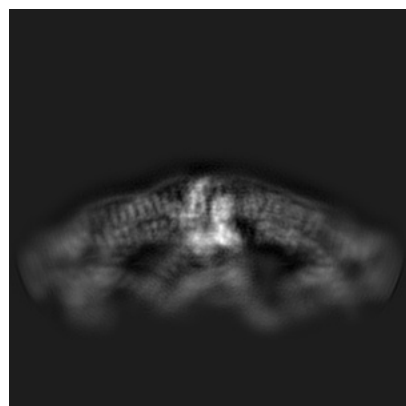
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0126. These allow visual inspection of the internal detail of the map and identification of artifacts.

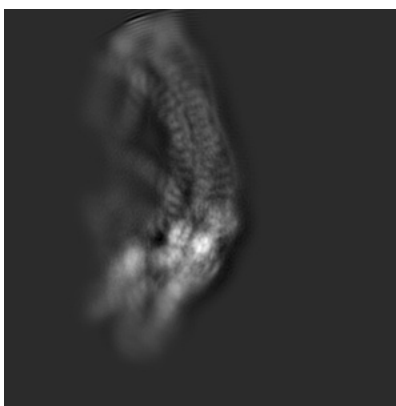
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

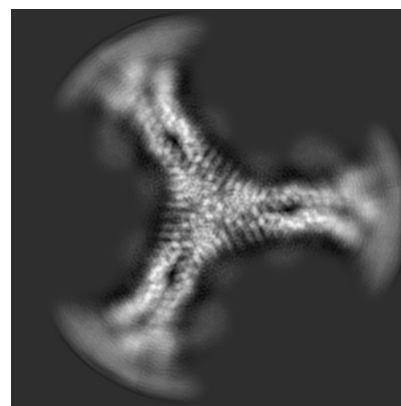
#### 6.1.1 Primary map



X



Y

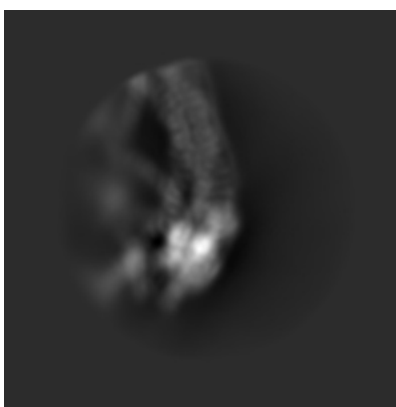


Z

#### 6.1.2 Raw map



X



Y

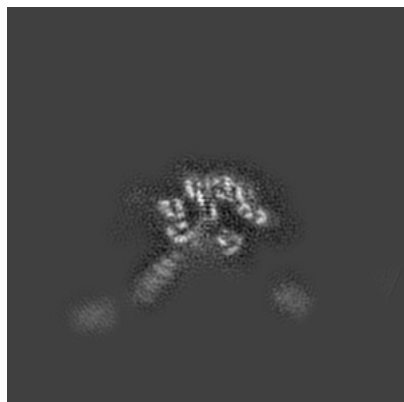


Z

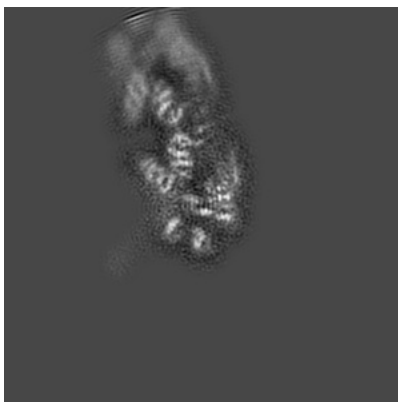
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

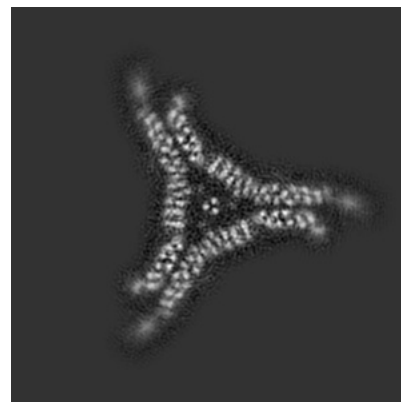
### 6.2.1 Primary map



X Index: 128

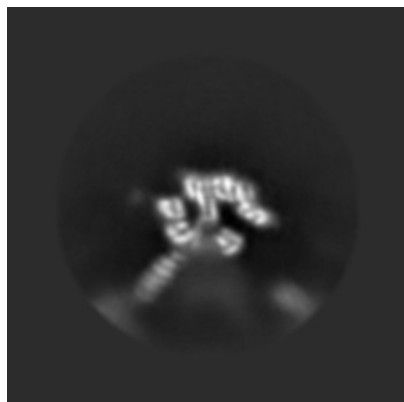


Y Index: 128

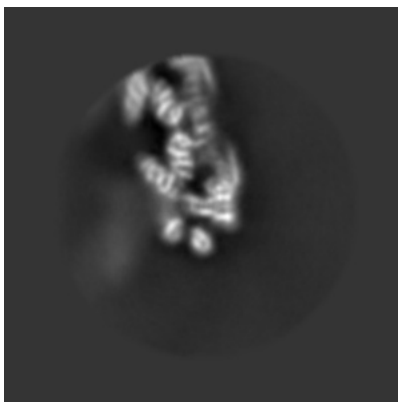


Z Index: 128

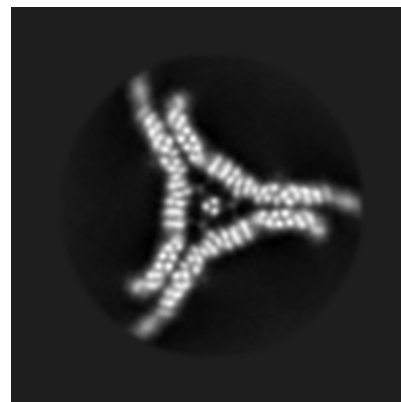
### 6.2.2 Raw map



X Index: 128



Y Index: 128

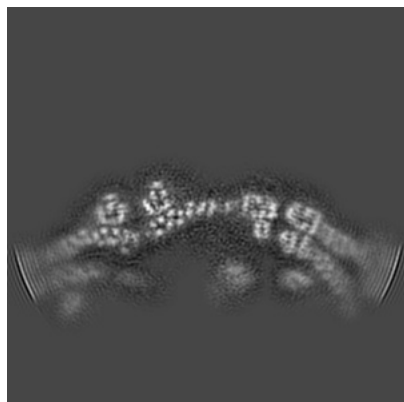


Z Index: 128

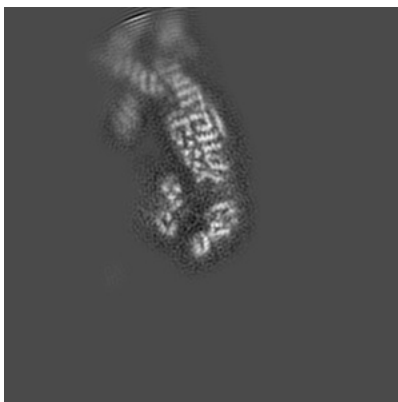
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

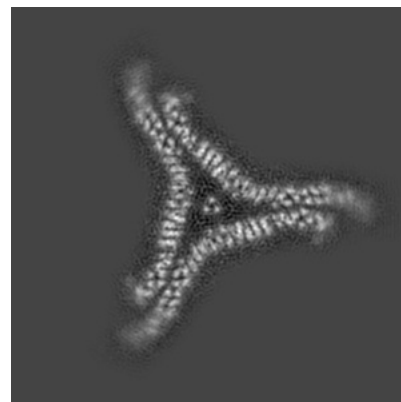
### 6.3.1 Primary map



X Index: 101



Y Index: 117



Z Index: 124

### 6.3.2 Raw map



X Index: 100



Y Index: 120



Z Index: 124

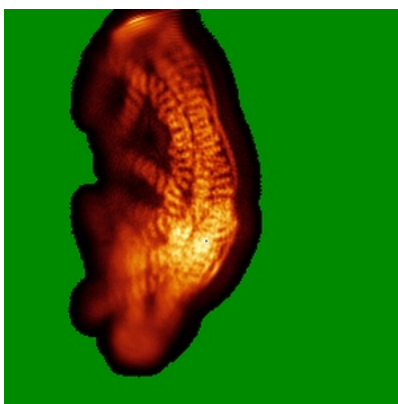
The images above show the largest variance slices of the map in three orthogonal directions.

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

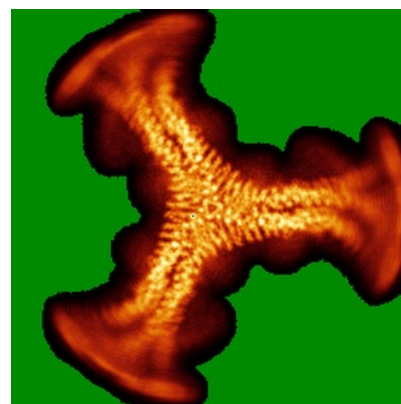
### 6.4.1 Primary map



X



Y

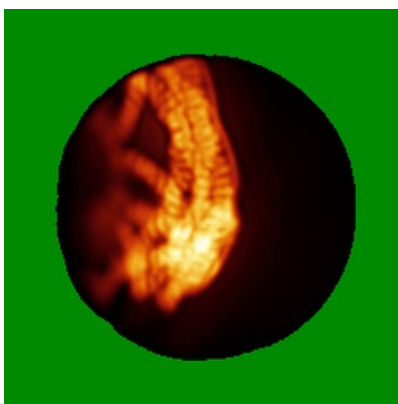


Z

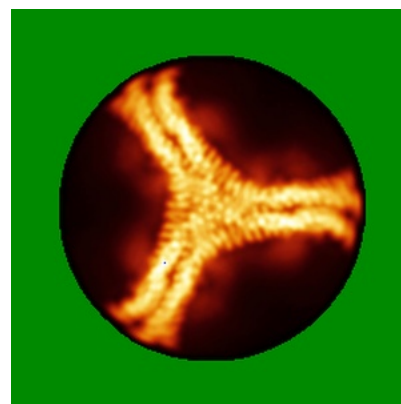
### 6.4.2 Raw map



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 0.195. 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.

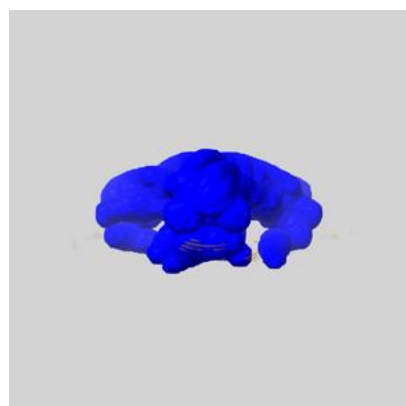
## 6.6 Mask visualisation [i](#)

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

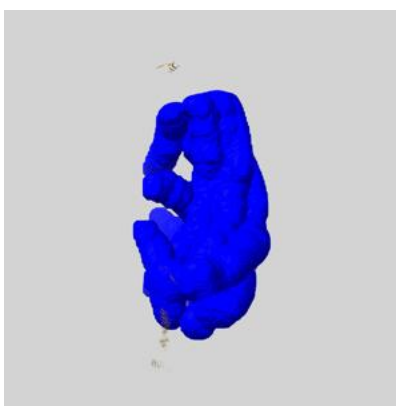
A mask typically either:

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

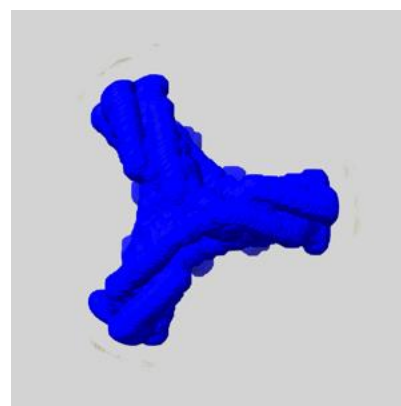
### 6.6.1 emd\_0126\_msk\_1.map [i](#)



X



Y

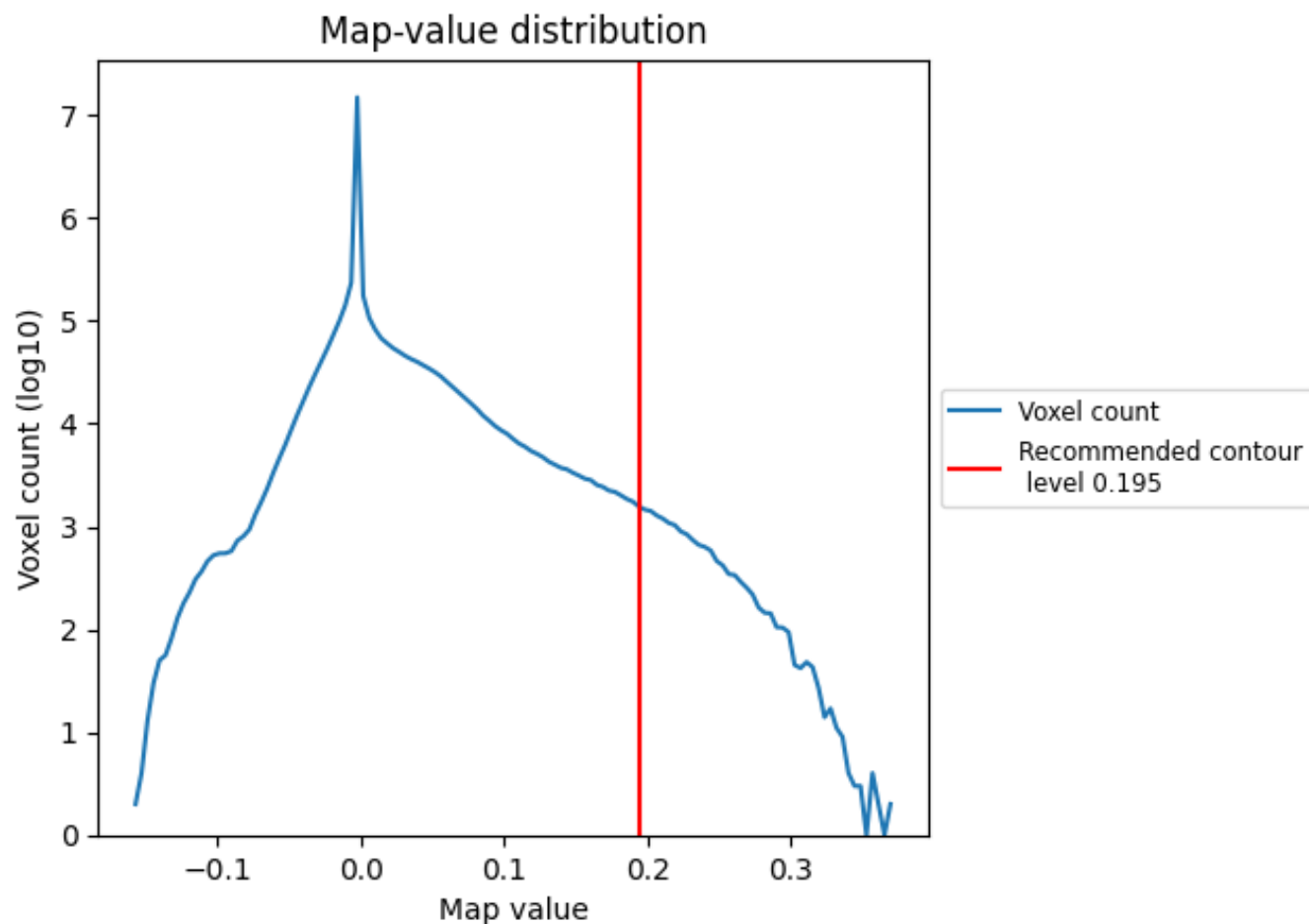


Z

## 7 Map analysis [i](#)

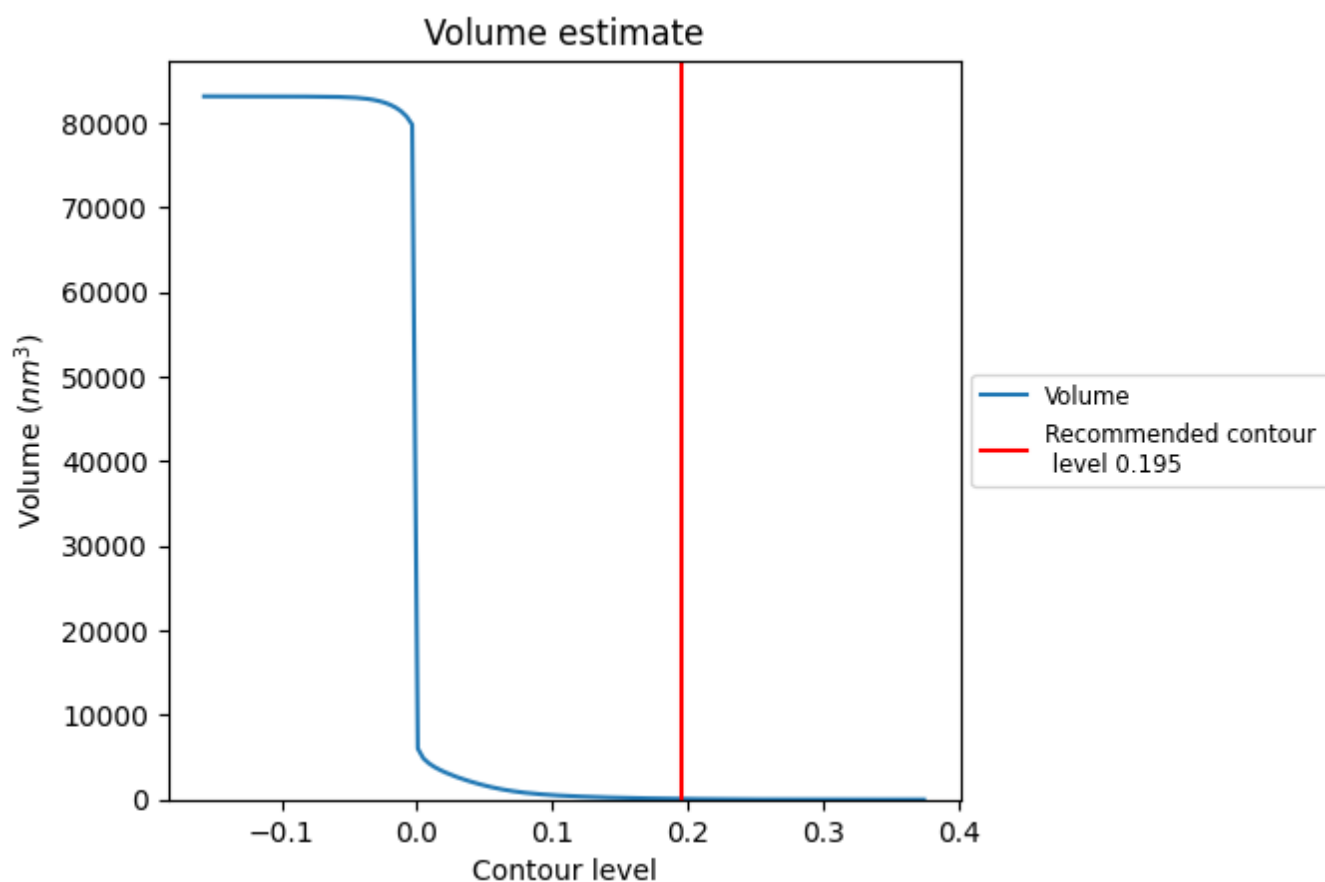
This section contains the results of statistical analysis of the map.

### 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](#)

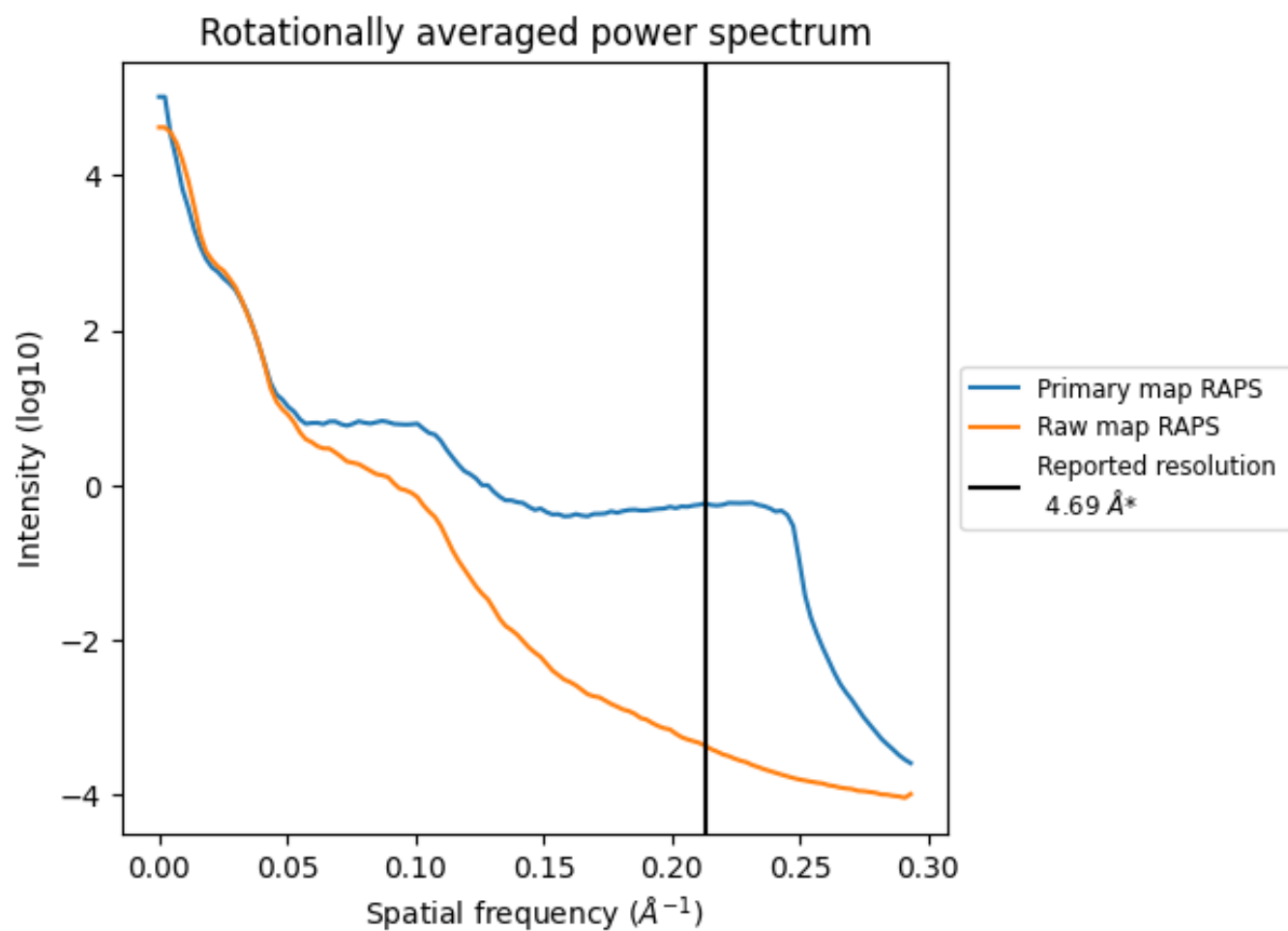


The volume at the recommended contour level is 82 nm<sup>3</sup>; this corresponds to an approximate mass of 74 kDa.

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 ⓘ

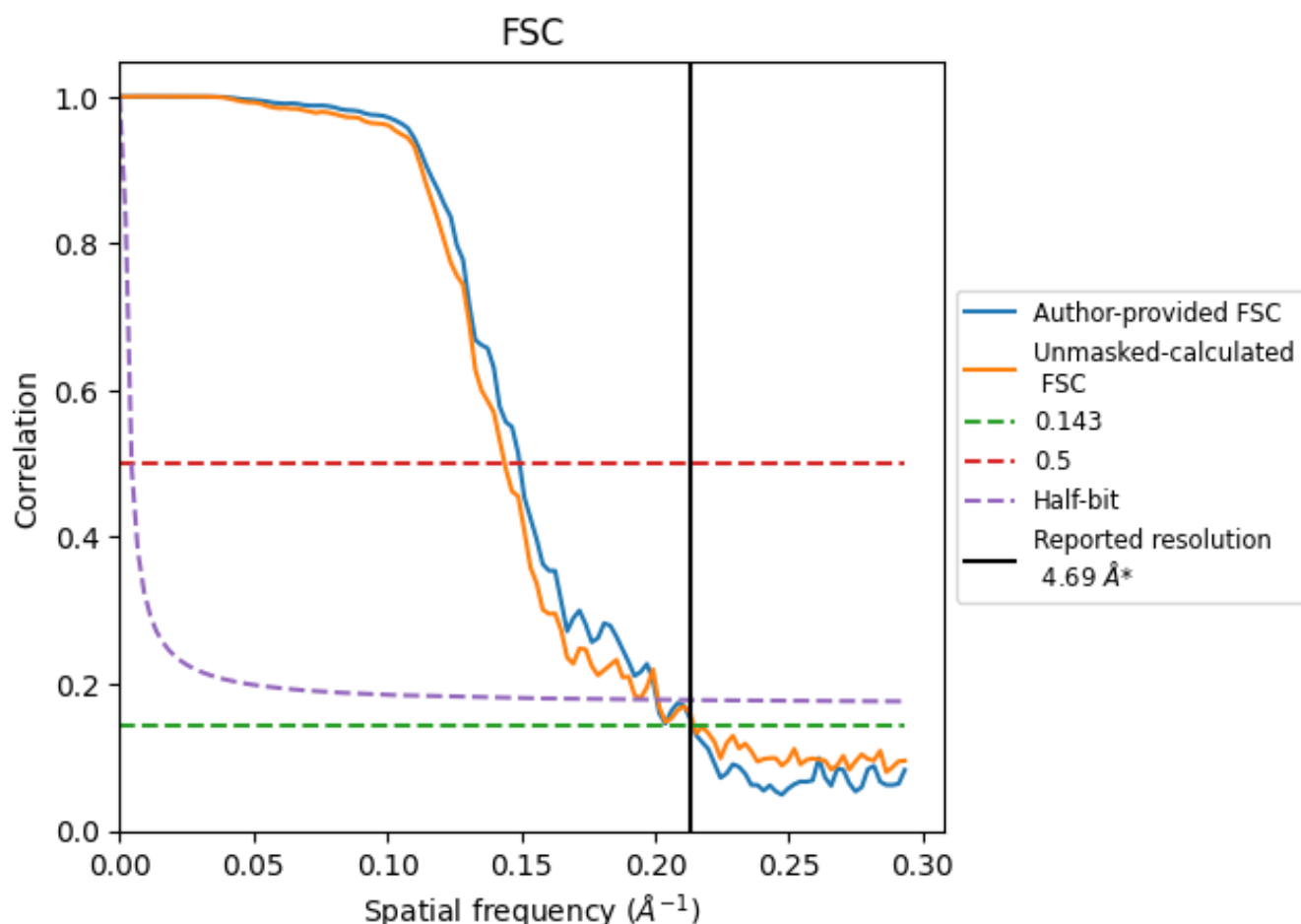


\*Reported resolution corresponds to spatial frequency of 0.213 Å<sup>-1</sup>

## 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 0.213 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

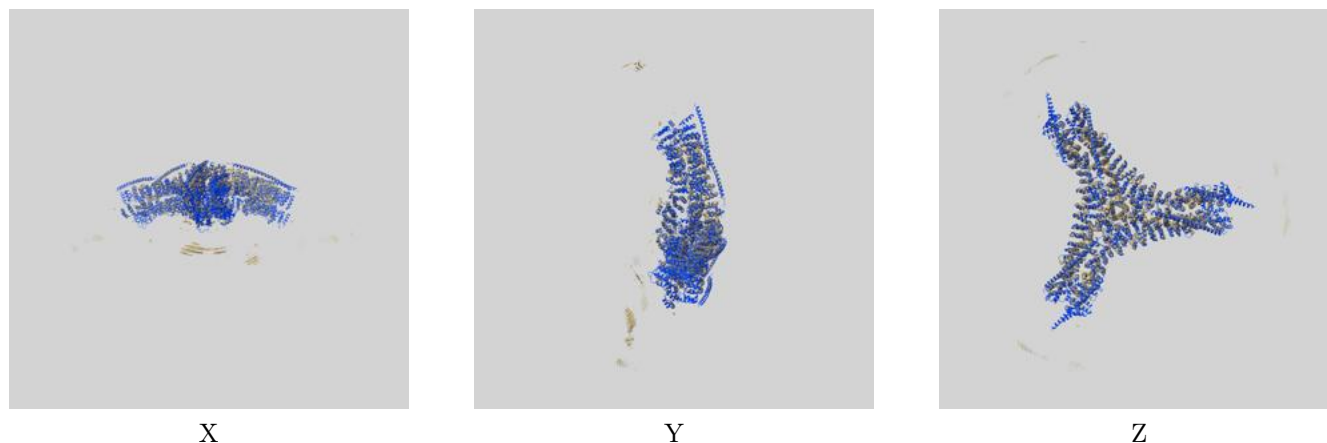
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.69	-	-
Author-provided FSC curve	4.67	6.69	4.98
Unmasked-calculated*	4.66	6.95	4.97

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

## 9 Map-model fit [i](#)

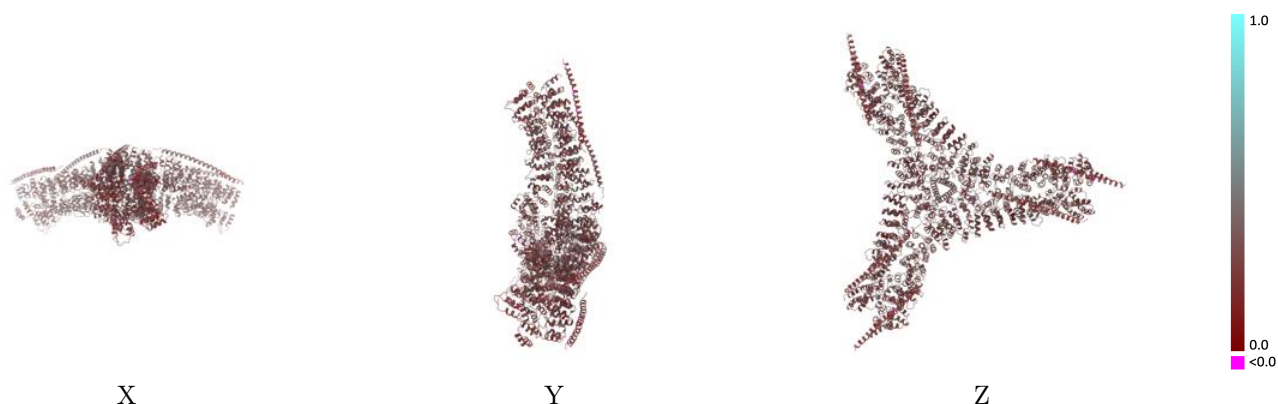
This section contains information regarding the fit between EMDB map EMD-0126 and PDB model 6SCT. Per-residue inclusion information can be found in section [3](#) on page [5](#).

### 9.1 Map-model overlay [i](#)



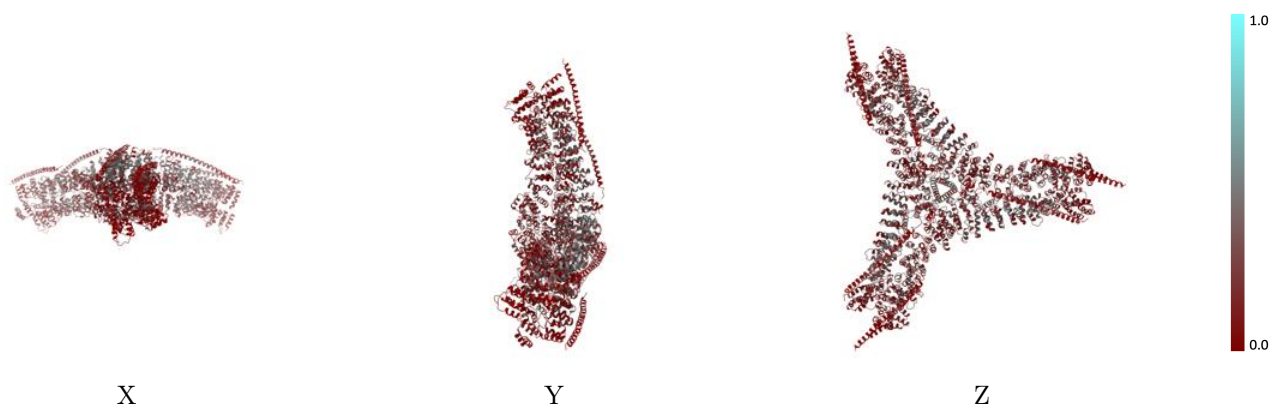
The images above show the 3D surface view of the map at the recommended contour level 0.195 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



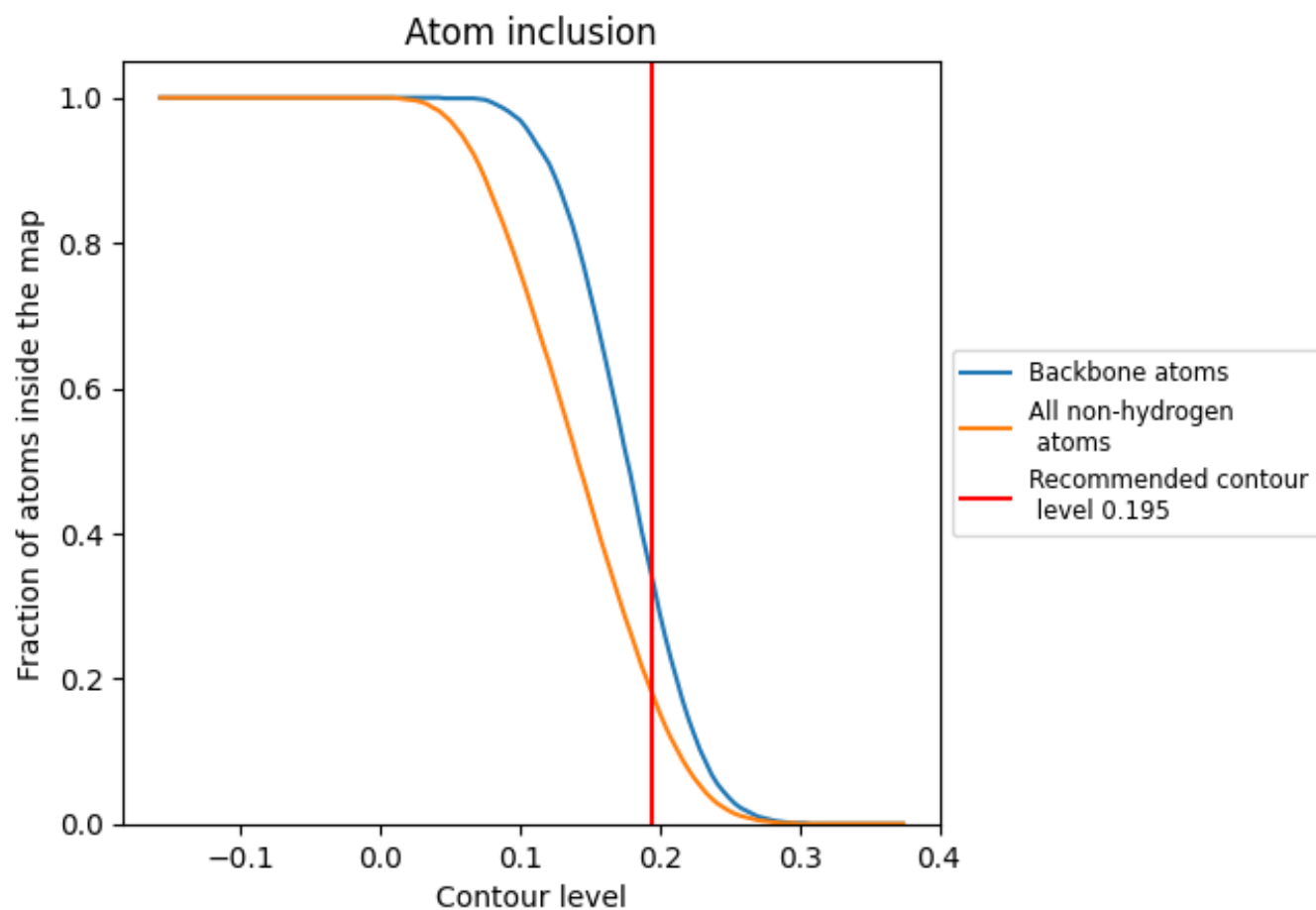
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.195).

## 9.4 Atom inclusion ⓘ



At the recommended contour level, 34% of all backbone atoms, 18% 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 (0.195) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.1780	<div></div> 0.2970
A	<div></div> 0.2840	<div></div> 0.3140
B	<div></div> 0.1680	<div></div> 0.2980
C	<div></div> 0.1370	<div></div> 0.2890
D	<div></div> 0.1160	<div></div> 0.2920
E	<div></div> 0.0220	<div></div> 0.2180
F	<div></div> 0.2860	<div></div> 0.3160
G	<div></div> 0.1690	<div></div> 0.2990
H	<div></div> 0.1360	<div></div> 0.2910
I	<div></div> 0.1150	<div></div> 0.2890
J	<div></div> 0.0260	<div></div> 0.2210
K	<div></div> 0.2860	<div></div> 0.3170
L	<div></div> 0.1680	<div></div> 0.2980
M	<div></div> 0.1390	<div></div> 0.2890
N	<div></div> 0.1100	<div></div> 0.2910
O	<div></div> 0.0340	<div></div> 0.2180

1.0

0.0

<0.0