



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 03:18 PM UTC

PDB ID : 5GO9 / pdb_00005go9
EMDB ID : EMD-9528
Title : Cryo-EM structure of RyR2 in closed state
Authors : Peng, W.; Wu, J.P.; Yan, N.
Deposited on : 2016-07-26
Resolution : 4.40 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

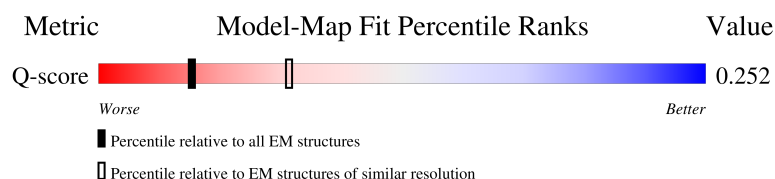
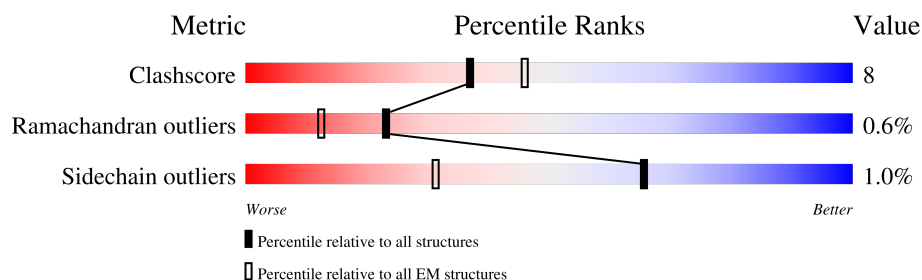
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 4.40 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	3132 (3.91 - 4.90)

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	4968	15% 53% 15% 31%
1	B	4968	15% 53% 15% 31%
1	C	4968	15% 53% 15% 31%
1	D	4968	15% 53% 15% 31%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 105068 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 RyR2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	3423	Total 26266	C 16740	N 4498	O 4874	S 154	0	0
1	B	3423	Total 26266	C 16740	N 4498	O 4874	S 154	0	0
1	C	3423	Total 26266	C 16740	N 4498	O 4874	S 154	0	0
1	D	3423	Total 26266	C 16740	N 4498	O 4874	S 154	0	0

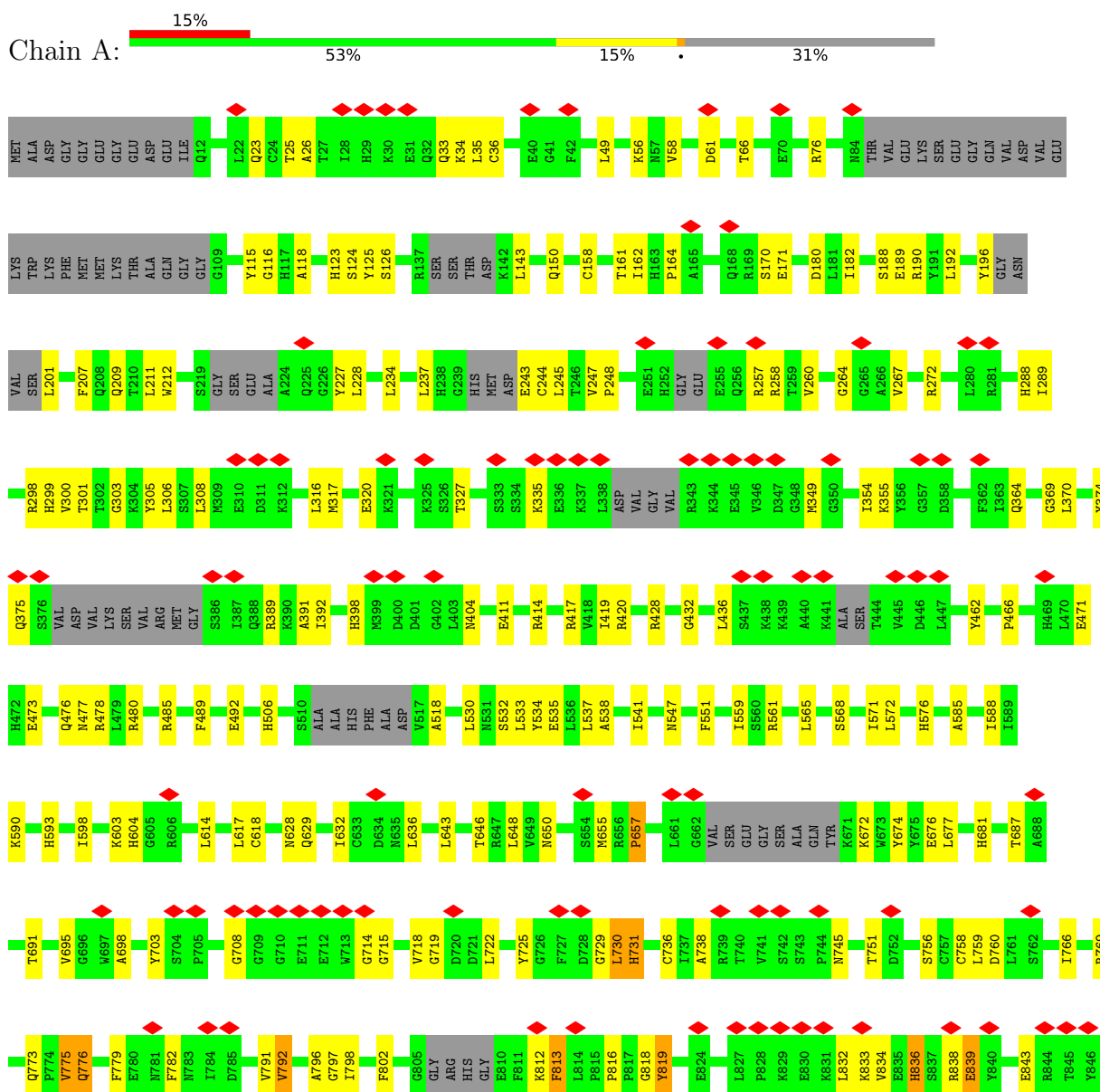
- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

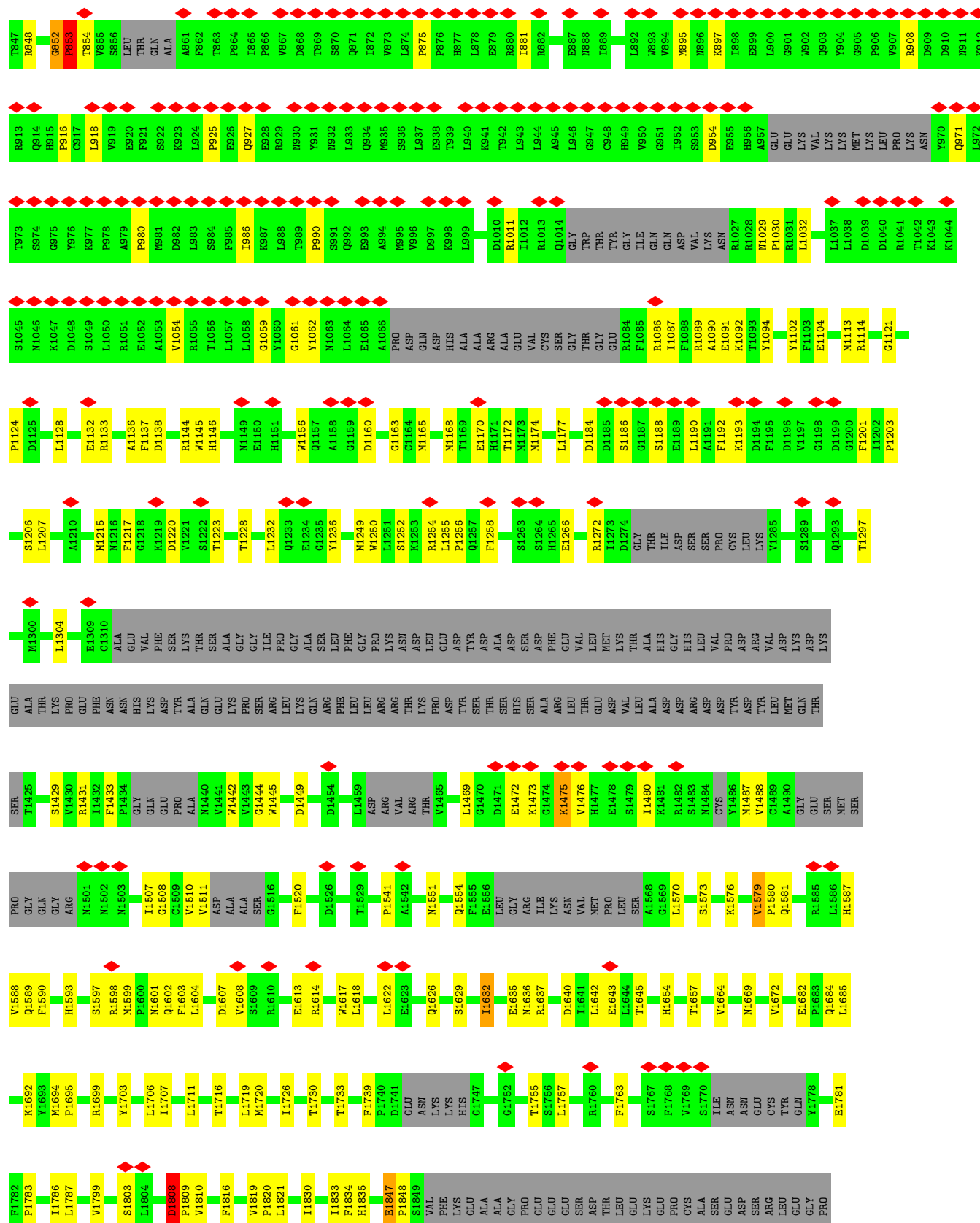
Mol	Chain	Residues	Atoms		AltConf
2	A	1	Total 1	Zn 1	0
2	B	1	Total 1	Zn 1	0
2	C	1	Total 1	Zn 1	0
2	D	1	Total 1	Zn 1	0

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: RyR2





G2907	PHE	E2847	G2787	G2788	F2663	GLY	A3404	E2316	N2196	N2199	L2062	L2063	ALA
	LYS	N2848	V2788	R2789	L2326	ILE	PRO	E2316	N2196	R2199	L2063	L2063	GLU
	ASP	Y2849	R2789	P2668	L2326	GLU	GLU	E2316	N2196	R2199	L2063	L2063	GLU
	LEU	H2850	R2790	C2669	L2326	GLN	MET	E2316	N2196	R2199	L2063	L2063	SER
	GLU	N2851	E2791	C2669	L2326	LEU	ILE	E2316	N2196	R2199	L2063	L2063	LYS
	ASP	I2852	R2792	C2669	L2326	ILE	ILE	E2316	N2196	R2199	L2063	L2063	GLY
	THR	G2853	T2793	C2669	L2326	HIS	HIS	E2316	N2196	R2199	L2063	L2063	LYS
	PRO	A2854	R2794	C2669	L2326	ALA	ALA	E2316	N2196	R2199	L2063	L2063	GLY
	SER	K2855	E2795	C2669	L2326	LYS	LYS	E2316	N2196	R2199	L2063	L2063	LYS
	ILE	K2856	G2796	C2669	L2326	ALA	ALA	E2316	N2196	R2199	L2063	L2063	ARG
	GLU	K2857	D2797	C2669	L2326	LEU	LEU	E2316	N2196	R2199	L2063	L2063	PRO
	LYS	K2858	SER	C2669	L2326	VAL	GLY	E2316	N2196	R2199	L2063	L2063	LYS
	ARG	K2858	ASP	C2669	L2326	VAL	E2416	E2316	N2196	R2199	L2063	L2063	GLU
	PHE	L2859	P2679	C2669	L2326	GLU	R2419	E2316	N2196	R2199	L2063	L2063	G1893
	ALA	E2860	TYR	C2669	L2326	ILE	I2420	E2316	N2196	R2199	L2063	L2063	E1901
	THR	L2861	GLU	C2669	L2326	ALA	R2421	E2316	N2196	R2199	L2063	L2063	L1905
	SER	E2862	GLU	C2669	L2326	ASP	L2424	E2316	N2196	R2199	L2063	L2063	L1911
	LEU	G2863	GLU	C2669	L2326	THR	R2425	E2316	N2196	R2199	L2063	L2063	V1934
	GLN	K2864	ASN	C2669	L2326	ALA	S2426	E2316	N2196	R2199	L2063	L2063	Q1938
	LEU	G2865	TYR	C2669	L2326	LEU	L2427	E2316	N2196	R2199	L2063	L2063	D1999
	ILE	G2866	VAL	C2669	L2326	LEU	ILE	E2316	N2196	R2199	L2063	L2063	D2013
	THR	G2867	SER	C2669	L2326	LEU	LEU	E2316	N2196	R2199	L2063	L2063	GLU
	GLN	H2868	MET	C2669	L2326	ALA	GLU	E2316	N2196	R2199	L2063	L2063	ASP
	ASP	H2869	GLU	C2669	L2326	ALA	ASP	E2316	N2196	R2199	L2063	L2063	GLY
	GLU	P2870	LYS	C2669	L2326	ALA	PRO	E2316	N2196	R2199	L2063	L2063	TYR
	ALA	L2871	GLN	C2669	L2326	ALA	V2434	E2316	N2196	R2199	L2063	L2063	ASN
	HIS	L2871	VAL	C2669	L2326	ALA	I2439	E2316	N2196	R2199	L2063	L2063	LEU
	GLN	L2872	SER	C2669	L2326	ALA	A2440	E2316	N2196	R2199	L2063	L2063	GLY
	THR	V2873	ASP	C2669	L2326	ALA	F2441	E2316	N2196	R2199	L2063	L2063	ASP
	ILE	P2874	GLU	C2669	L2326	ALA	Q2442	E2316	N2196	R2199	L2063	L2063	ARG
	LEU	V2875	GLY	C2669	L2326	ALA	MET	E2316	N2196	R2199	L2063	L2063	MET
	GLU	P2876	ASN	C2669	L2326	ALA	THR	E2316	N2196	R2199	L2063	L2063	ASN
	PHE	D2877	PHE	C2669	L2326	ALA	THR	E2316	N2196	R2199	L2063	L2063	LYS
	ASP	A2878	GLY	C2669	L2326	ALA	ILE	E2316	N2196	R2199	L2063	L2063	ALA
	GLY	T2877	ALA	C2669	L2326	ALA	ALA	E2316	N2196	R2199	L2063	L2063	ALA
	GLY	L2878	ALA	C2669	L2326	ALA	LYS	E2316	N2196	R2199	L2063	L2063	THR
	SER	T2879	ASP	C2669	L2326	ALA	ASP	E2316	N2196	R2199	L2063	L2063	THR
	ARG	A2880	THR	C2669	L2326	ALA	GLY	E2316	N2196	R2199	L2063	L2063	ARG
	SER	K2881	THR	C2669	L2326	ALA	VAL	E2316	N2196	R2199	L2063	L2063	GLN
	LYS	E2882	THR	C2669	L2326	ALA	VAL	E2316	N2196	R2199	L2063	L2063	LYS
	GLY	K2883	THR	C2669	L2326	ALA	GLU	E2316	N2196	R2199	L2063	L2063	ALA
	HIS	A2884	THR	C2669	L2326	ALA	PRO	E2316	N2196	R2199	L2063	L2063	THR
	PHE	K2885	THR	C2669	L2326	ALA	ASP	E2316	N2196	R2199	L2063	L2063	LYS
	PRO	D2886	THR	C2669	L2326	ALA	ASP	E2316	N2196	R2199	L2063	L2063	LEU
	THR	A2887	THR	C2669	L2326	ALA	ASP	E2316	N2196	R2199	L2063	L2063	VAL
	GLN	E2888	THR	C2669	L2326	ALA	ASP	E2316	N2196	R2199	L2063	L2063	PHE
	ILE	K2889	THR	C2669	L2326	ALA	ASP	E2316	N2196	R2199	L2063	L2063	ARG
	LYS	A2890	THR	C2669	L2326	ALA	ASP	E2316	N2196	R2199	L2063	L2063	SER
	PHE	Q2891	THR	C2669	L2326	ALA	ASP	E2316	N2196	R2199	L2063	L2063	PRO
	PHE	D2892	THR	C2669	L2326	ALA	ASP	E2316	N2196	R2199	L2063	L2063	GLN
	ALA	E2893	THR	C2669	L2326	ALA	ASP	E2316	N2196	R2199	L2063	L2063	LYS
	LYS	L2894	THR	C2669	L2326	ALA	ASP	E2316	N2196	R2199	L2063	L2063	GLU
		K2895	THR	C2669	L2326	ALA	ASP	E2316	N2196	R2199	L2063	L2063	THR
		L2897	THR	C2669	L2326	ALA	ASP	E2316	N2196	R2199	L2063	L2063	ILE
		Q2898	THR	C2669	L2326	ALA	ASP	E2316	N2196	R2199	L2063	L2063	ASN
		I2899	THR	C2669	L2326	ALA	ASP	E2316	N2196	R2199	L2063	L2063	MET
		M2844	THR	C2669	L2326	ALA	ASP	E2316	N2196	R2199	L2063	L2063	LEU
		Y2901	THR	C2669	L2326	ALA	ASP	E2316	N2196	R2199	L2063	L2063	Q2061
		Y2902	THR	C2669	L2326	ALA	ASP	E2316	N2196	R2199	L2063	L2063	Q2060
		A2903	THR	C2669	L2326	ALA	ASP	E2316	N2196	R2199	L2063	L2063	T2058
		S2905	THR	C2669	L2326	ALA	ASP	E2316	N2196	R2199	L2063	L2063	L2059
		R2906	THR	C2669	L2326	ALA	ASP	E2316	N2196	R2199	L2063	L2063	Q2061

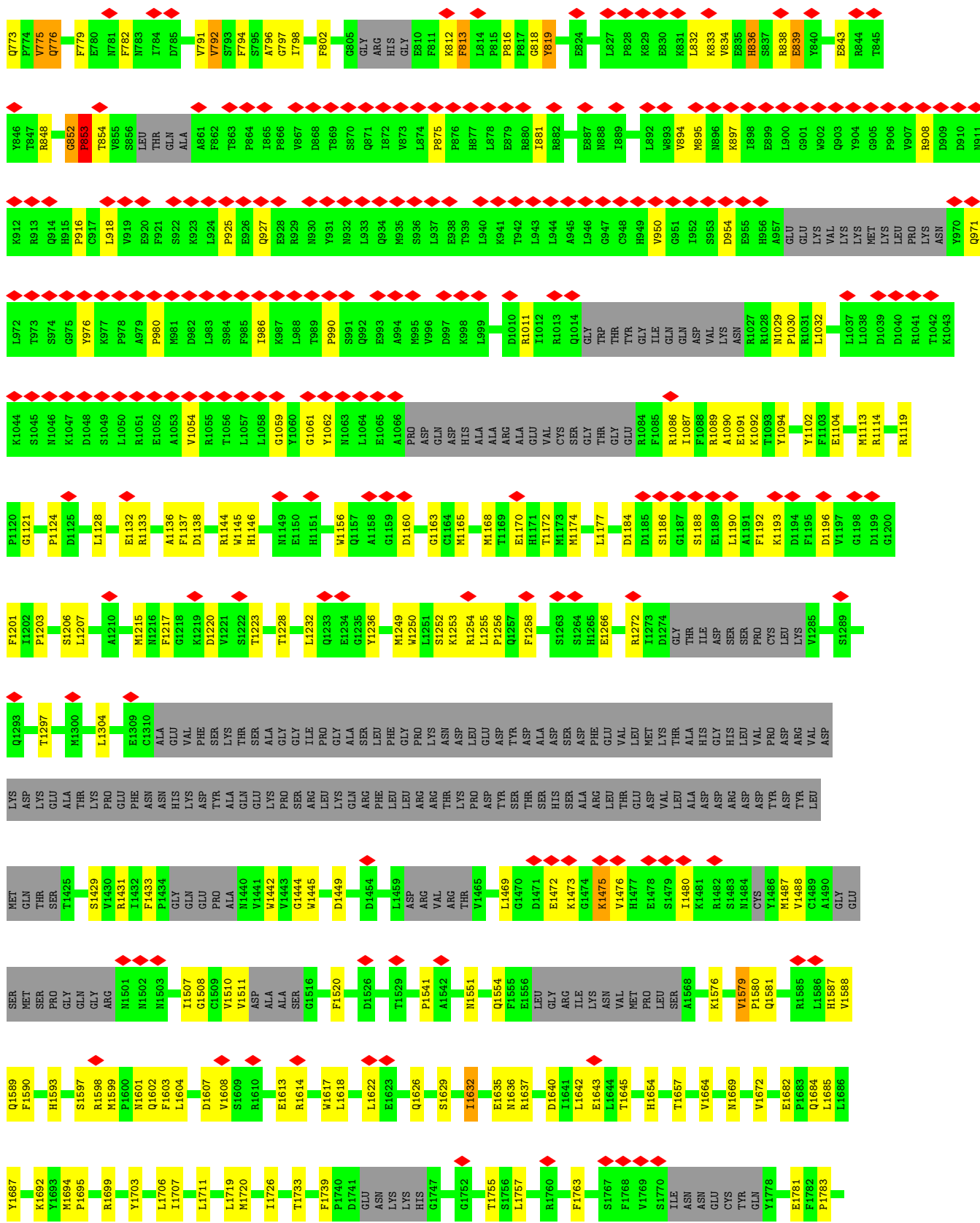
Q3976	L3846	L3760	GLU	CYS	ASP	GLN	GLU	GLY	ASN	TYR	PRO	VAL
V3980	L3847	G3763	ASP	MET	PRO	GLU	ASP	ILE	ILE	V3149	LYS	VAL
L3983	C3848		GLY	ARG	ASN	ARG	ASN	PRO	SER	E3150	ILE	SER
L3984	N3852	L3766	THR	ARG	PRO	LYS	GLY	PRO	GLU	R3151	VAL	PRO
L3985	L3859	L3767	LYS	TYR	LYS	MET	ALA	ALA	GLU	Q3152	ASN	LEU
L3986	L3861		LYS	TYR	LYS	LYS	VAL	VAL	MET	R3153	CYS	ILE
L3987	D3663		LYS	SER	ASP	ARG	ASP	GLU	ASN	S3154	LYS	ASP
L3988	D3662		LYS	SER	GLY	GLY	GLY	GLY	GLU	R3155	GLN	GLN
L3989	L3671		LYS	VAL	GLY	ASP	PHE	GLY	GLU	L3156	TYR	TYR
L3990	L3779		LYS	GLY	GLY	ARG	GLY	GLY	GLY	L3157	LYS	LYS
L3991	L3872		LYS	HIS	LYS	ARG	MET	ASP	ILE	A3158	ASN	ASN
L3992	L3873		GLN	GLN	GLY	VAL	VAL	VAL	VAL	E3159	ARG	ARG
L3992	S3874		GLN	GLN	GLY	VAL	ALA	ALA	ASP	V3100	LYS	LYS
L3996	T3875		GLN	ARG	ASP	GLY	GLY	GLY	GLY	A3101	LEU	LEU
L3996	V3876		GLN	ARG	ASP	GLY	GLY	GLY	GLY	L3102	LEU	LEU
M4000	V3876		GLN	ARG	ASP	GLY	GLY	GLY	GLY	L3103	LEU	LEU
M4003	V3891		GLN	LYS	ASP	GLY	GLY	GLY	GLY	P3104	LEU	LEU
M4003	L3797		GLN	VAL	TRP	VAL	ILE	ILE	ILE	M3105	LEU	LEU
L4004	K3798		GLN	TRP	GLN	VAL	ILE	ILE	ILE	L3106	LEU	LEU
L4004	Q3799		GLN	TRP	GLN	VAL	ILE	ILE	ILE	L3107	LEU	LEU
S4007	S3800		GLN	HIS	ASP	ALA	ALA	ALA	ALA	L3108	LEU	LEU
S4007	C3801		GLN	HIS	ASP	ALA	ALA	ALA	ALA	E3111	LEU	LEU
V4011	S3802		GLU	LYS	GLY	LEU	LEU	LEU	LEU	H3112	LEU	LEU
V4012	V3803		GLU	LYS	GLY	LEU	LEU	LEU	LEU	T3113	LEU	LEU
V4012	K3915		GLU	SER	LYS	ARG	LYS	LYS	LYS	G3114	LEU	LEU
M4013	Q3916		GLU	LYS	ASP	GLY	GLY	GLY	GLY	L3115	LEU	LEU
M4013	Q3917		GLU	GLN	ASP	GLY	GLY	GLY	GLY	Q3116	LEU	LEU
L4014	N3918		GLU	GLN	ASP	GLY	GLY	GLY	GLY	H3117	LEU	LEU
L4015	N3919		GLU	GLN	ASP	GLY	GLY	GLY	GLY	L3118	LEU	LEU
L4016	N3920		GLU	GLN	ASP	GLY	GLY	GLY	GLY	GLY	LEU	LEU
F4017	L3921		GLU	GLN	ASP	GLY	GLY	GLY	GLY	ALA	LEU	LEU
F4017	T3922		GLU	GLN	ASP	GLY	GLY	GLY	GLY	ALA	LEU	LEU
S4030	E3923		GLU	GLN	ASP	GLY	GLY	GLY	GLY	ALA	LEU	LEU
D4031	Y3924		GLU	GLN	ASP	GLY	GLY	GLY	GLY	ALA	LEU	LEU
D4031	I3925		GLU	GLN	ASP	GLY	GLY	GLY	GLY	ALA	LEU	LEU
E4035	Q3926		GLU	GLN	ASP	GLY	GLY	GLY	GLY	ALA	LEU	LEU
E4035	Y4036		GLU	GLN	ASP	GLY	GLY	GLY	GLY	ALA	LEU	LEU
D4037	Y4036		GLU	GLN	ASP	GLY	GLY	GLY	GLY	ALA	LEU	LEU
P4038	C3929		GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
P4038	T3930		GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
D4039	N3931		GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
N3932	G3931		GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
G4040	N3932		GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
Q3933	Q3933		GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
K4041	Q3933		GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
S4045	H3938		GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
K4046	SER		GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
R4047	D3943		GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
D4048	A3944		GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
F4049	F4049		GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
H4050	F4051		GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
K4051	K4051		GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
A4052	A4052		GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
H4056	H4056		GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
L4068	S3666		GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
S4069	Q3961		GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
C4070	E3971		GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
A4071	E3971		GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
E4072	L3975		GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
T4073	L3975		GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
T3028	SER		GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
ILE	ILE		GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
VAL	VAL		GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
PRO	PRO		GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
LEU	LEU		GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
VAL	VAL		GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
ASN	ASN		GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
LEU	LEU		GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
GLN	GLN		GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
ASP	ASP		GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
GLN	GLN		GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
TYR	TYR		GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
LYS	LYS		GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
ASN	ASN		GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
HIS	HIS		GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
ARG	ARG		GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
LEU	LEU		GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
Y2982			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
F2983			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
L2984			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
A2987			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
S2988			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
R2989			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
P2990			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
L2991			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
C2992			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
S2993			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
G2994			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
G2995			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
H2996			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
A2997			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
S2998			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
N2999			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
K3000			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
E3001			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
K3002			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
E3003			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
K3004			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
V3005			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
THR			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
LEU			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
F3009			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
C3010			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
K3011			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
L3012			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
G3013			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
V3014			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
L3015			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
V3016			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
R3017			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
H3018			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
R3019			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
T3020			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
S3021			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
L3022			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
F3023			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
G3024			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
H3025			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
D3026			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU
A3027			GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	LEU	LEU











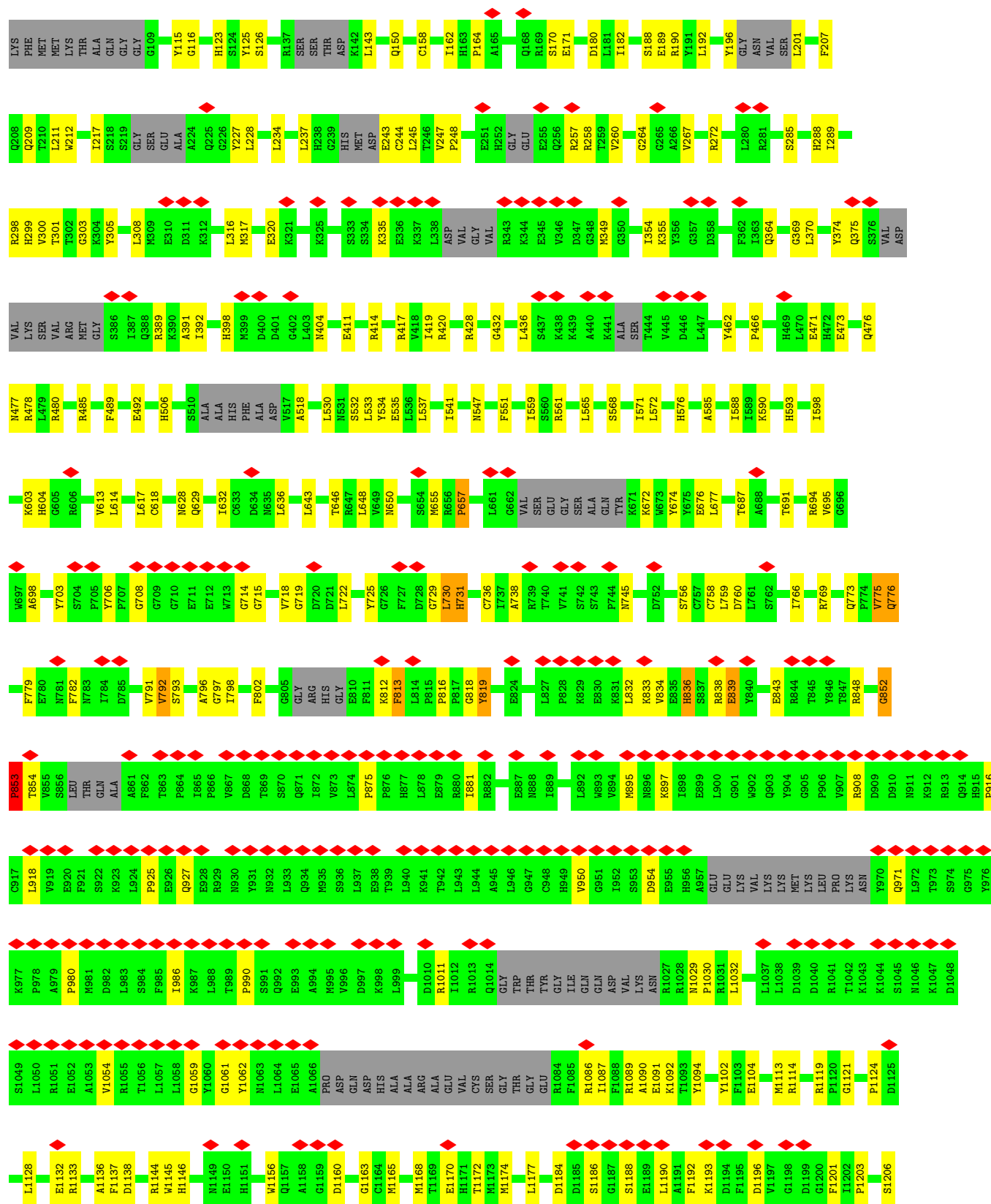






Frequency	Percentage
Daily	15%
Often	53%
Sometimes	15%
Never	31%













4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	48454	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 ($e^-/\text{\AA}^2$)	44	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.173	Depositor
Minimum map value	-0.090	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	546.0, 546.0, 546.0	wwPDB
Map dimensions	520, 520, 520	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.05, 1.05, 1.05	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	1.30	136/26751 (0.5%)	1.06	69/36149 (0.2%)
1	B	1.30	136/26751 (0.5%)	1.06	69/36149 (0.2%)
1	C	1.30	136/26751 (0.5%)	1.06	69/36149 (0.2%)
1	D	1.30	136/26751 (0.5%)	1.06	69/36149 (0.2%)
All	All	1.30	544/107004 (0.5%)	1.06	276/144596 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	30
1	B	0	30
1	C	0	30
1	D	0	30
All	All	0	120

The worst 5 of 544 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	4954	PRO	CA-C	-11.29	1.41	1.52
1	B	4954	PRO	CA-C	-11.29	1.41	1.52
1	C	4954	PRO	CA-C	-11.29	1.41	1.52
1	D	4954	PRO	CA-C	-11.29	1.41	1.52
1	A	4955	ALA	CA-C	-11.00	1.41	1.53

The worst 5 of 276 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1847	GLU	CA-C-N	12.84	135.89	119.84
1	A	1847	GLU	C-N-CA	12.84	135.89	119.84
1	B	1847	GLU	CA-C-N	12.84	135.89	119.84
1	B	1847	GLU	C-N-CA	12.84	135.89	119.84
1	C	1847	GLU	CA-C-N	12.84	135.89	119.84

There are no chirality outliers.

5 of 120 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	471	GLU	Peptide
1	A	657	PRO	Peptide
1	A	729	GLY	Peptide
1	A	775	VAL	Peptide
1	A	791	VAL	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	26266	0	24898	424	0
1	B	26266	0	24898	432	0
1	C	26266	0	24898	428	0
1	D	26266	0	24898	412	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
All	All	105068	0	99592	1555	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 8.

The worst 5 of 1555 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:4873:GLU:HA	1:B:4875:ARG:NH1	1.62	1.15

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4875:ARG:NH1	1:D:4873:GLU:HA	1.62	1.14
1:B:4873:GLU:HA	1:C:4875:ARG:NH1	1.62	1.13
1:C:4873:GLU:OE1	1:D:4875:ARG:HD3	1.49	1.12
1:C:4873:GLU:HA	1:D:4875:ARG:NH1	1.62	1.12

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	3289/4968 (66%)	2983 (91%)	285 (9%)	21 (1%)	21	58
1	B	3289/4968 (66%)	2983 (91%)	285 (9%)	21 (1%)	21	58
1	C	3289/4968 (66%)	2983 (91%)	285 (9%)	21 (1%)	21	58
1	D	3289/4968 (66%)	2983 (91%)	285 (9%)	21 (1%)	21	58
All	All	13156/19872 (66%)	11932 (91%)	1140 (9%)	84 (1%)	23	58

5 of 84 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	4071	ALA
1	B	4071	ALA
1	C	4071	ALA
1	D	4071	ALA
1	A	730	LEU

5.3.2 Protein sidechains [i](#)

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	2659/4355 (61%)	2634 (99%)	25 (1%)	70	76
1	B	2658/4355 (61%)	2633 (99%)	25 (1%)	70	76
1	C	2659/4355 (61%)	2633 (99%)	26 (1%)	68	76
1	D	2660/4355 (61%)	2634 (99%)	26 (1%)	68	76
All	All	10636/17420 (61%)	10534 (99%)	102 (1%)	65	76

5 of 102 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	1054	VAL
1	C	4515	ASN
1	D	4875	ARG
1	C	1632	ILE
1	C	3813	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 209 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	531	ASN
1	C	3954	HIS
1	D	3956	GLN
1	C	628	ASN
1	C	1921	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

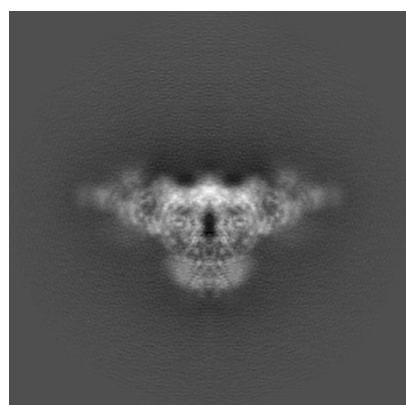
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9528. These allow visual inspection of the internal detail of the map and identification of artifacts.

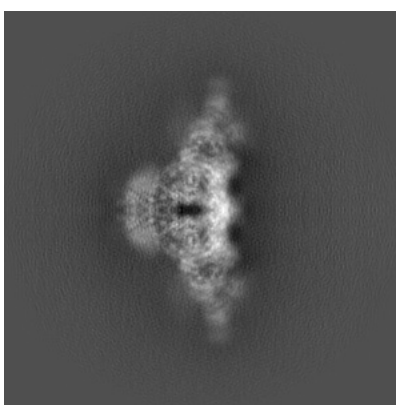
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

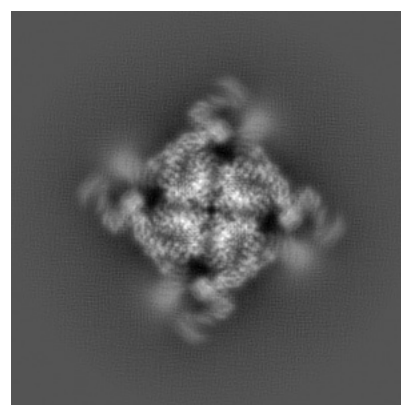
6.1.1 Primary map



X



Y

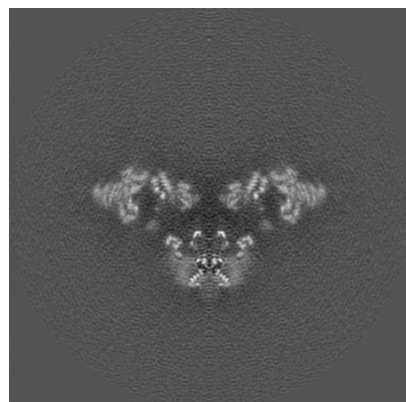


Z

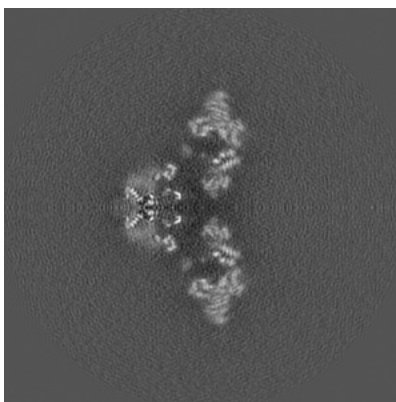
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

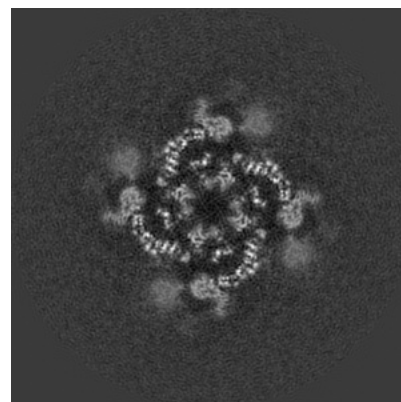
6.2.1 Primary map



X Index: 260



Y Index: 260

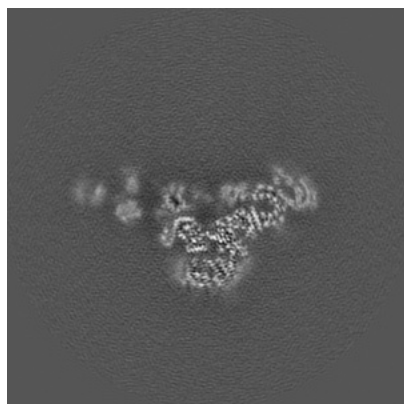


Z Index: 260

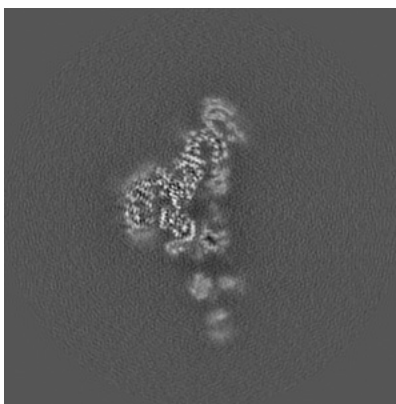
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

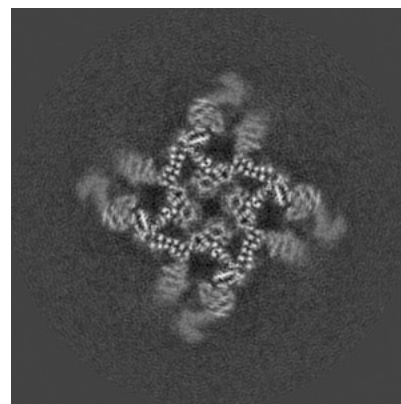
6.3.1 Primary map



X Index: 243



Y Index: 277

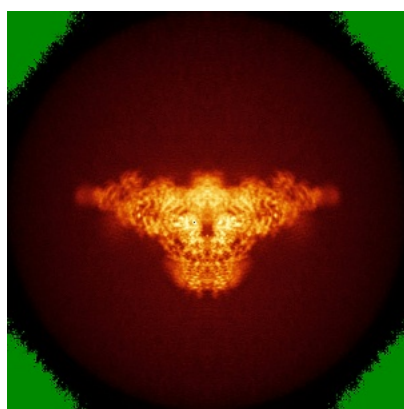


Z Index: 271

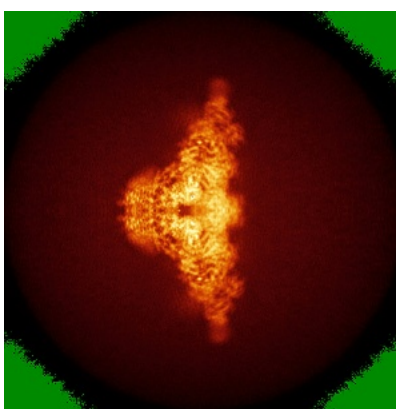
The images above show the largest variance slices of the map in three orthogonal directions.

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

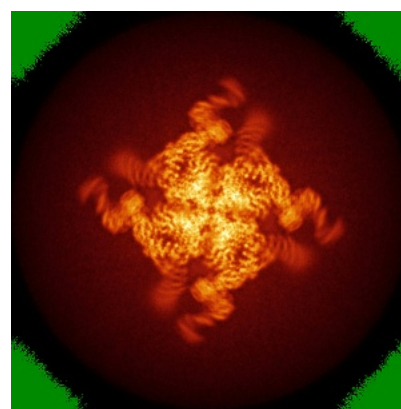
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views

This section was not generated.

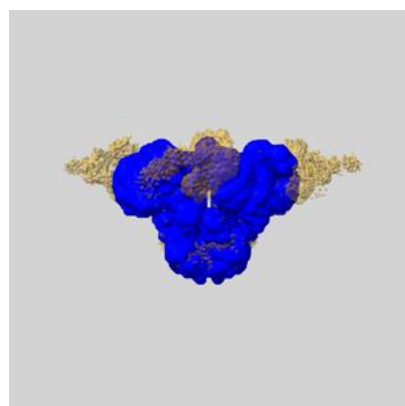
6.6 Mask visualisation [i](#)

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

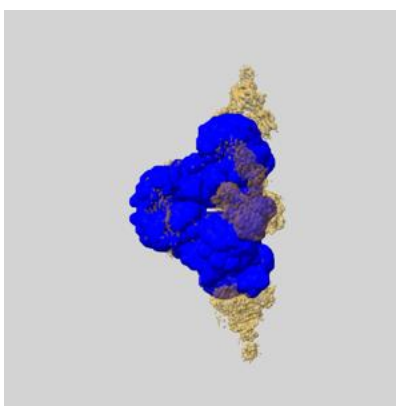
A mask typically either:

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

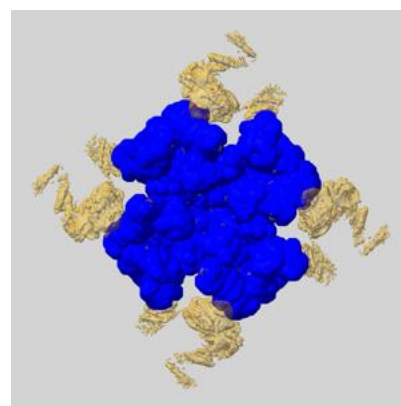
6.6.1 emd_9528_msk_1.map [i](#)



X



Y

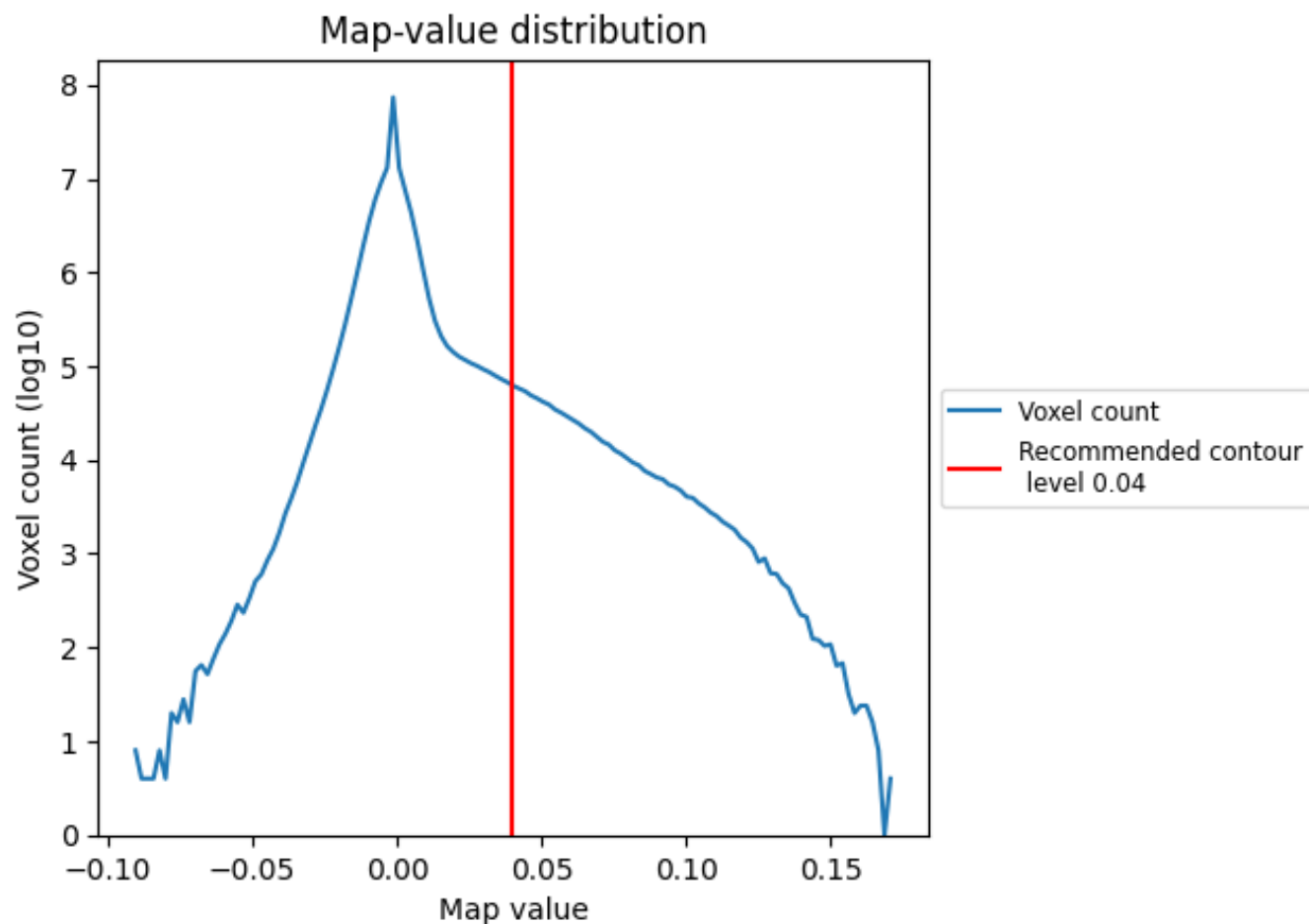


Z

7 Map analysis [i](#)

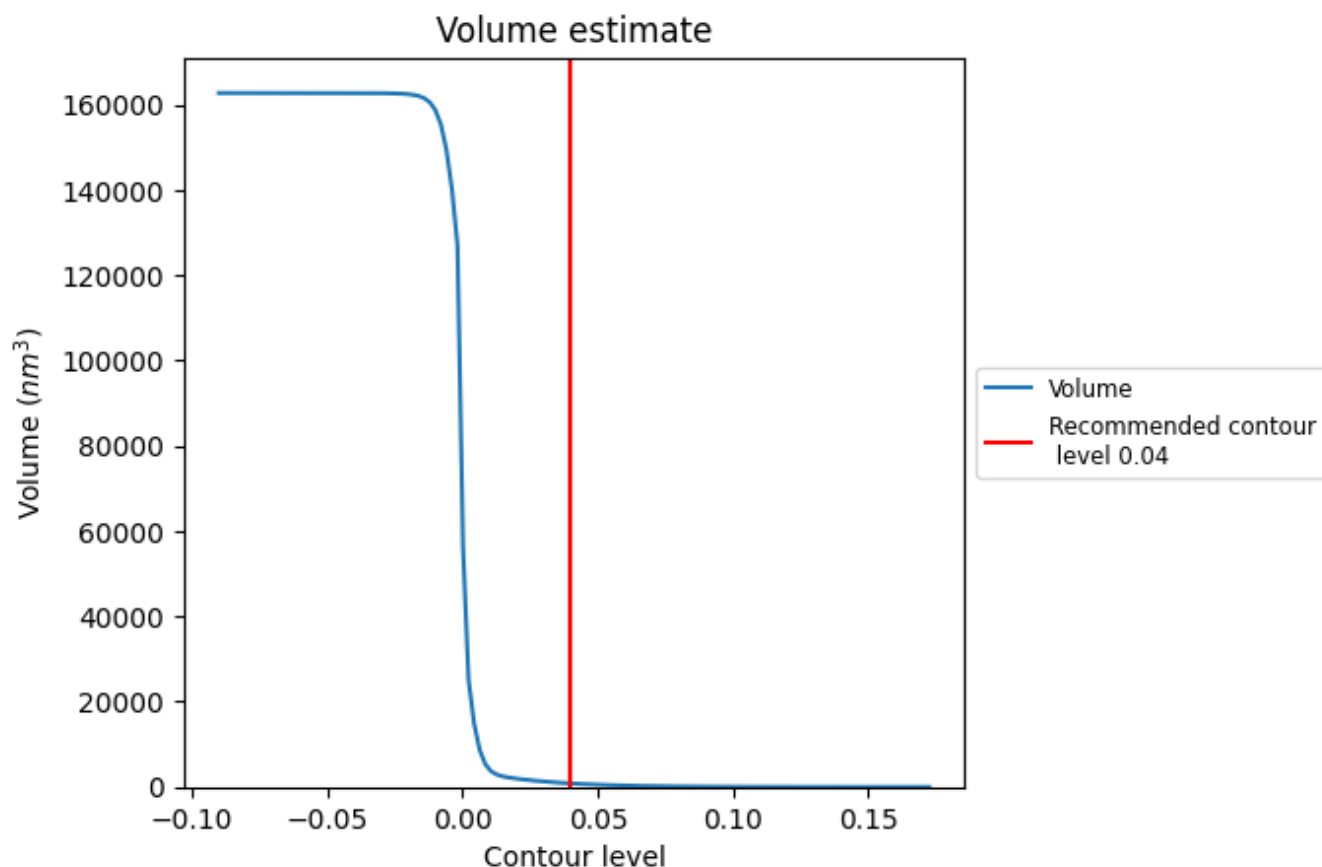
This section contains the results of statistical analysis of the map.

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.

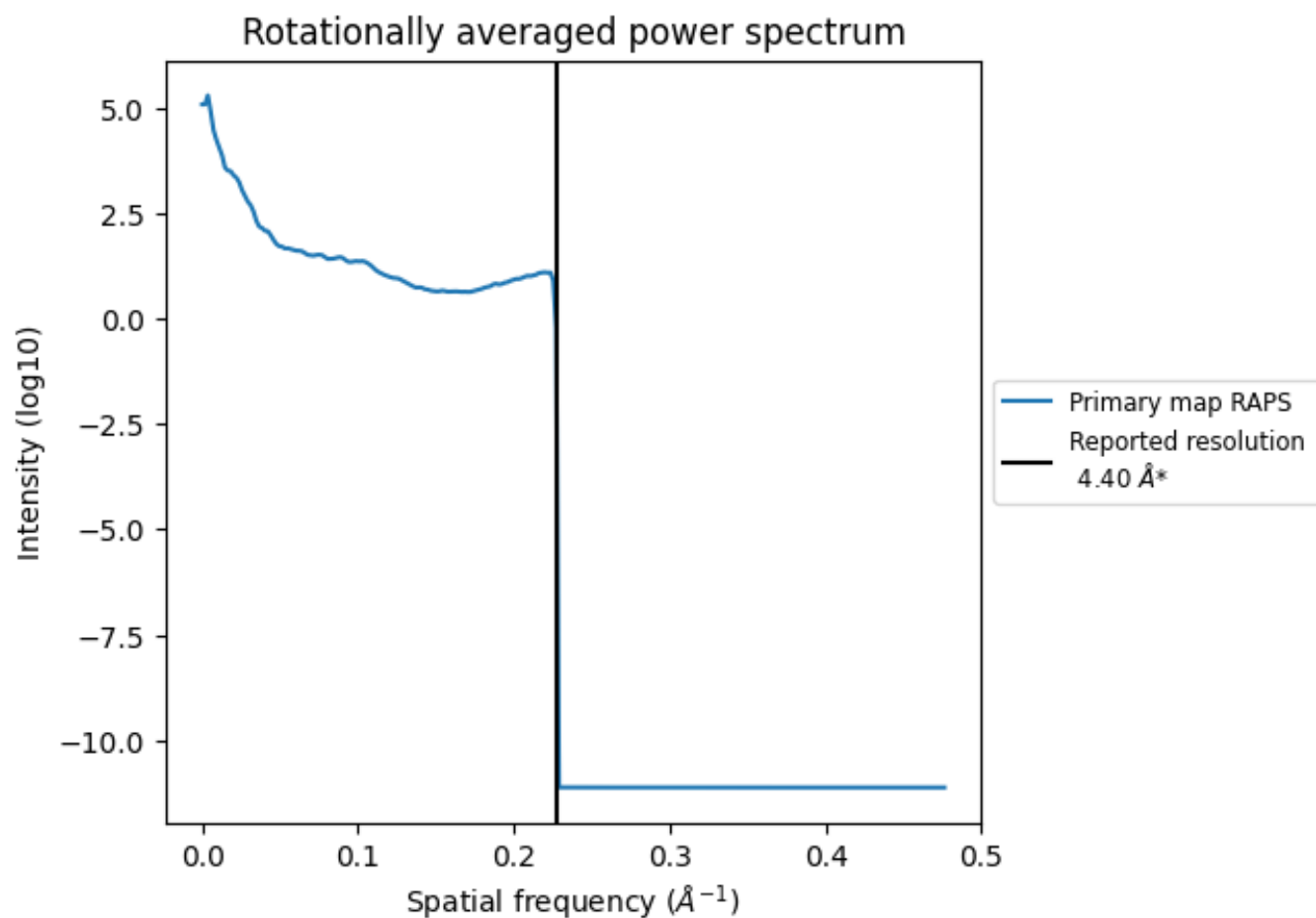
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 837 nm³; this corresponds to an approximate mass of 756 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 0.227 $\text{\AA}^{-1}$

8 Fourier-Shell correlation

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

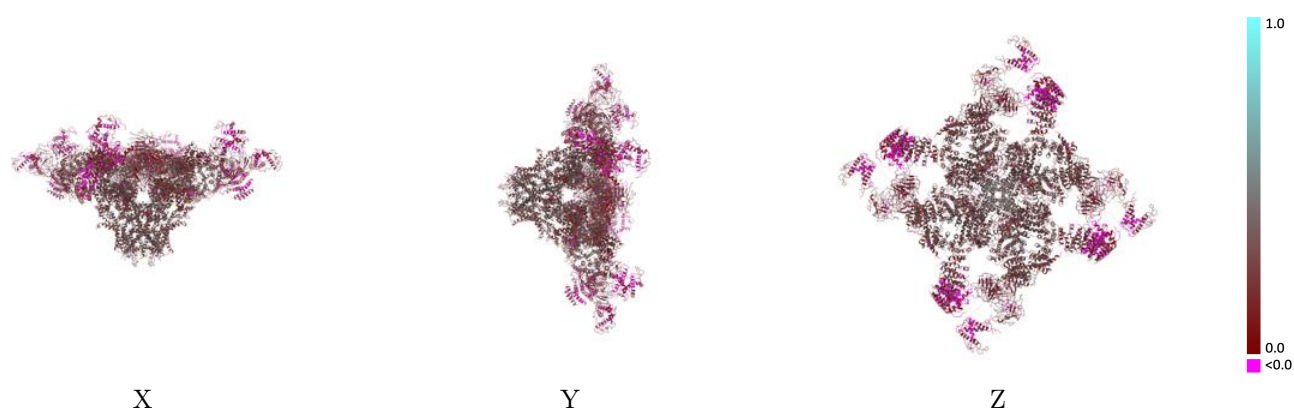
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-9528 and PDB model 5GO9. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlay [i](#)

This section was not generated.

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

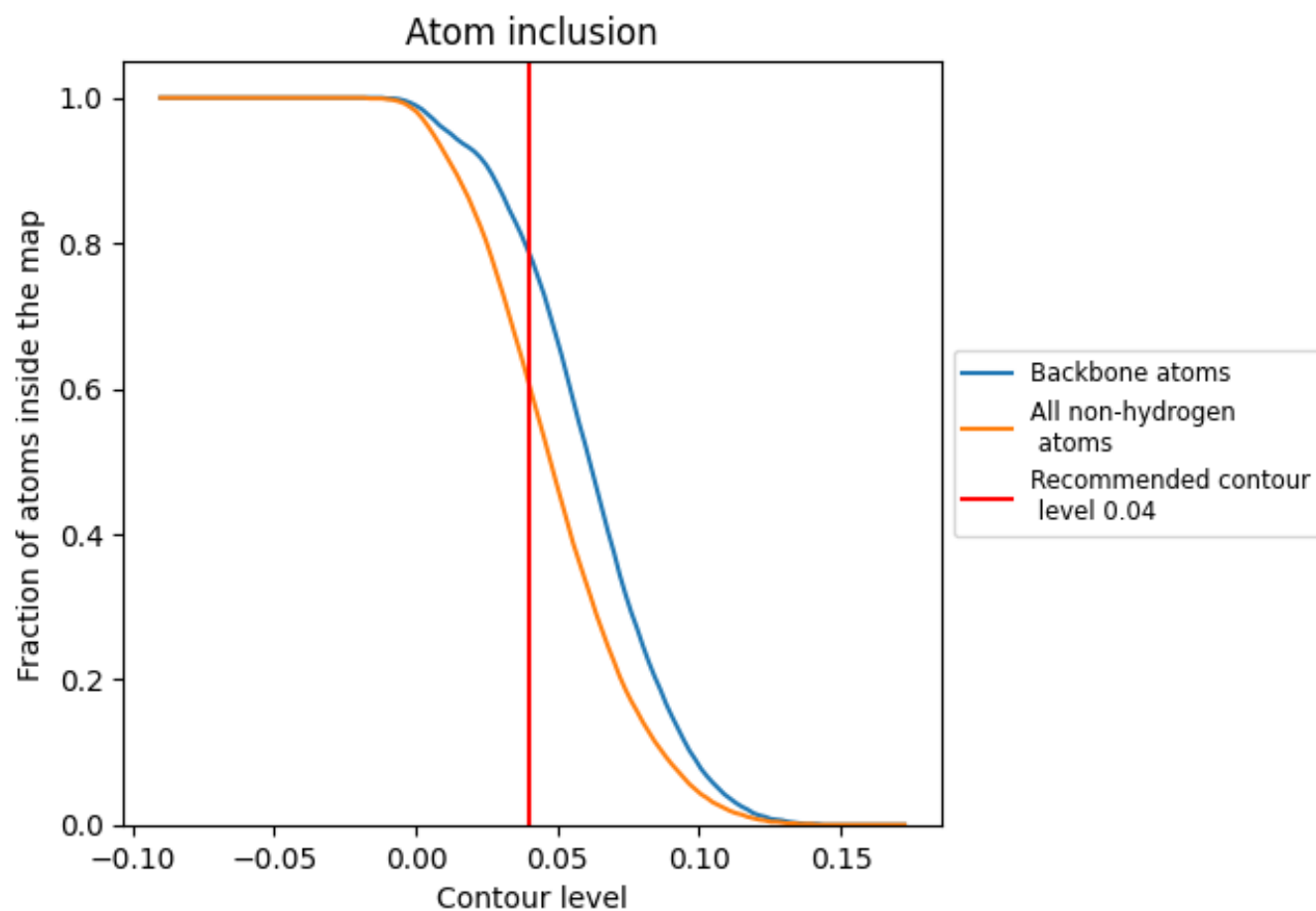


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 61% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6060	0.2520
A	0.6060	0.2520
B	0.6060	0.2530
C	0.6060	0.2520
D	0.6060	0.2520

