



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 04:11 AM UTC

PDB ID : 9OL4 / pdb_00009ol4
EMDB ID : EMD-70589
Title : Cryo-EM Structure of Ryanodine Receptor 1: Drug Bound Open Conformation
Authors : Molinarolo, S.M.; Van Petegem, F.
Deposited on : 2025-05-12
Resolution : 3.37 Å(reported)
Based on initial model : 7TZC

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

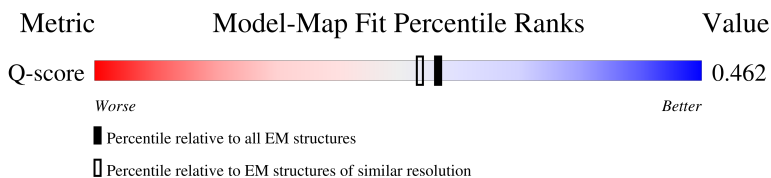
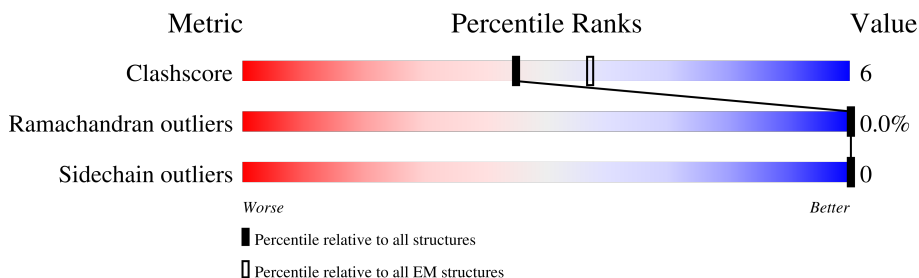
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.37 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	14287 (2.87 - 3.87)

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	5037	8% 70% 11% 19%
1	G	5037	8% 70% 11% 19%
1	M	5037	8% 70% 11% 19%
1	S	5037	8% 70% 11% 19%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	B	111	 86% 11% •
2	H	111	 86% 11% •
2	N	111	 86% 11% •
2	T	111	 86% 11% •

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 131292 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 Ryanodine receptor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	4064	Total	C	N	O	S	0	0
			31873	20385	5494	5773	221		
1	G	4064	Total	C	N	O	S	0	0
			31873	20385	5494	5773	221		
1	M	4064	Total	C	N	O	S	0	0
			31873	20385	5494	5773	221		
1	S	4064	Total	C	N	O	S	0	0
			31873	20385	5494	5773	221		

- Molecule 2 is a protein called Peptidyl-prolyl cis-trans isomerase FKBP1B.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	107	Total	C	N	O	S	0	0
			811	510	143	154	4		
2	H	107	Total	C	N	O	S	0	0
			811	510	143	154	4		
2	N	107	Total	C	N	O	S	0	0
			811	510	143	154	4		
2	T	107	Total	C	N	O	S	0	0
			811	510	143	154	4		

There are 12 discrepancies between the modelled and reference sequences:

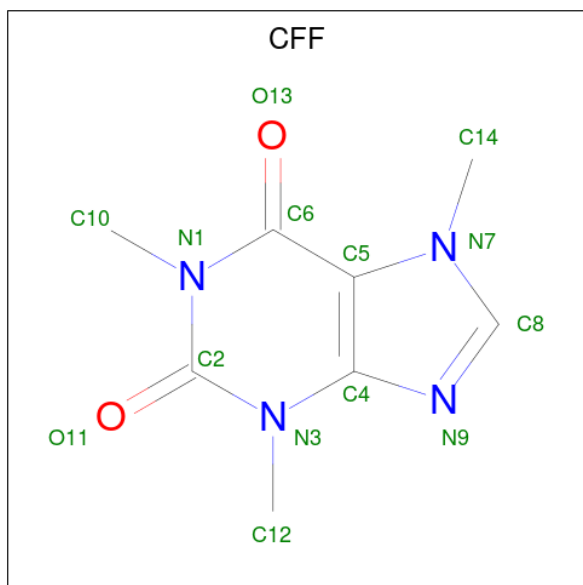
Chain	Residue	Modelled	Actual	Comment	Reference
B	-2	SER	-	expression tag	UNP P68106
B	-1	ASN	-	expression tag	UNP P68106
B	0	ALA	-	expression tag	UNP P68106
H	-2	SER	-	expression tag	UNP P68106
H	-1	ASN	-	expression tag	UNP P68106
H	0	ALA	-	expression tag	UNP P68106
N	-2	SER	-	expression tag	UNP P68106
N	-1	ASN	-	expression tag	UNP P68106
N	0	ALA	-	expression tag	UNP P68106

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
T	-2	SER	-	expression tag	UNP P68106
T	-1	ASN	-	expression tag	UNP P68106
T	0	ALA	-	expression tag	UNP P68106

- Molecule 3 is CAFFEINE (CCD ID: CFF) (formula: $C_8H_{10}N_4O_2$).

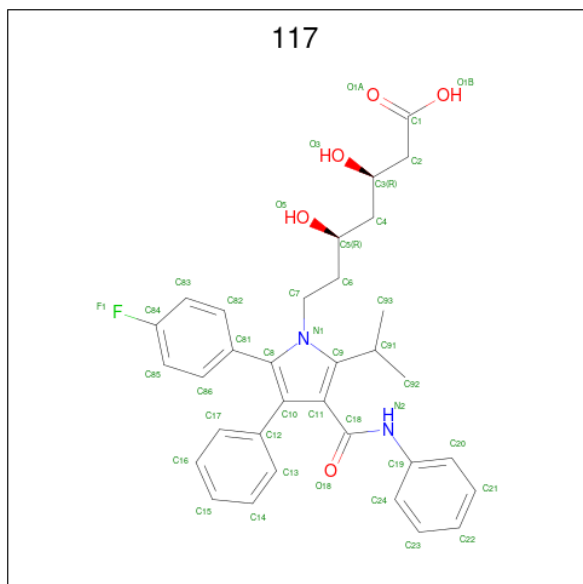


Mol	Chain	Residues	Atoms				AltConf
3	A	1	Total	C	N	O	0
			14	8	4	2	
3	G	1	Total	C	N	O	0
			14	8	4	2	
3	M	1	Total	C	N	O	0
			14	8	4	2	
3	S	1	Total	C	N	O	0
			14	8	4	2	

- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		AltConf
4	A	1	Total	Ca	0
			1	1	
4	G	1	Total	Ca	0
			1	1	
4	M	1	Total	Ca	0
			1	1	
4	S	1	Total	Ca	0
			1	1	

- Molecule 5 is 7-[2-(4-FLUORO-PHENYL)-5-ISOPROPYL-3-PHENYL-4-PHENYLCARBA MOYL-PYRROL-1-YL]- 3,5-DIHYDROXY-HEPTANOIC ACID (CCD ID: 117) (formula: $C_{33}H_{35}FN_2O_5$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
5	A	1	Total	C	F	N	O	0
			41	33	1	2	5	
5	A	1	Total	C	F	N	O	0
			41	33	1	2	5	
5	A	1	Total	C	F	N	O	0
			41	33	1	2	5	
5	G	1	Total	C	F	N	O	0
			41	33	1	2	5	
5	G	1	Total	C	F	N	O	0
			41	33	1	2	5	
5	G	1	Total	C	F	N	O	0
			41	33	1	2	5	
5	M	1	Total	C	F	N	O	0
			41	33	1	2	5	
5	M	1	Total	C	F	N	O	0
			41	33	1	2	5	
5	M	1	Total	C	F	N	O	0
			41	33	1	2	5	
5	S	1	Total	C	F	N	O	0
			41	33	1	2	5	
5	S	1	Total	C	F	N	O	0
			41	33	1	2	5	
5	S	1	Total	C	F	N	O	0
			41	33	1	2	5	

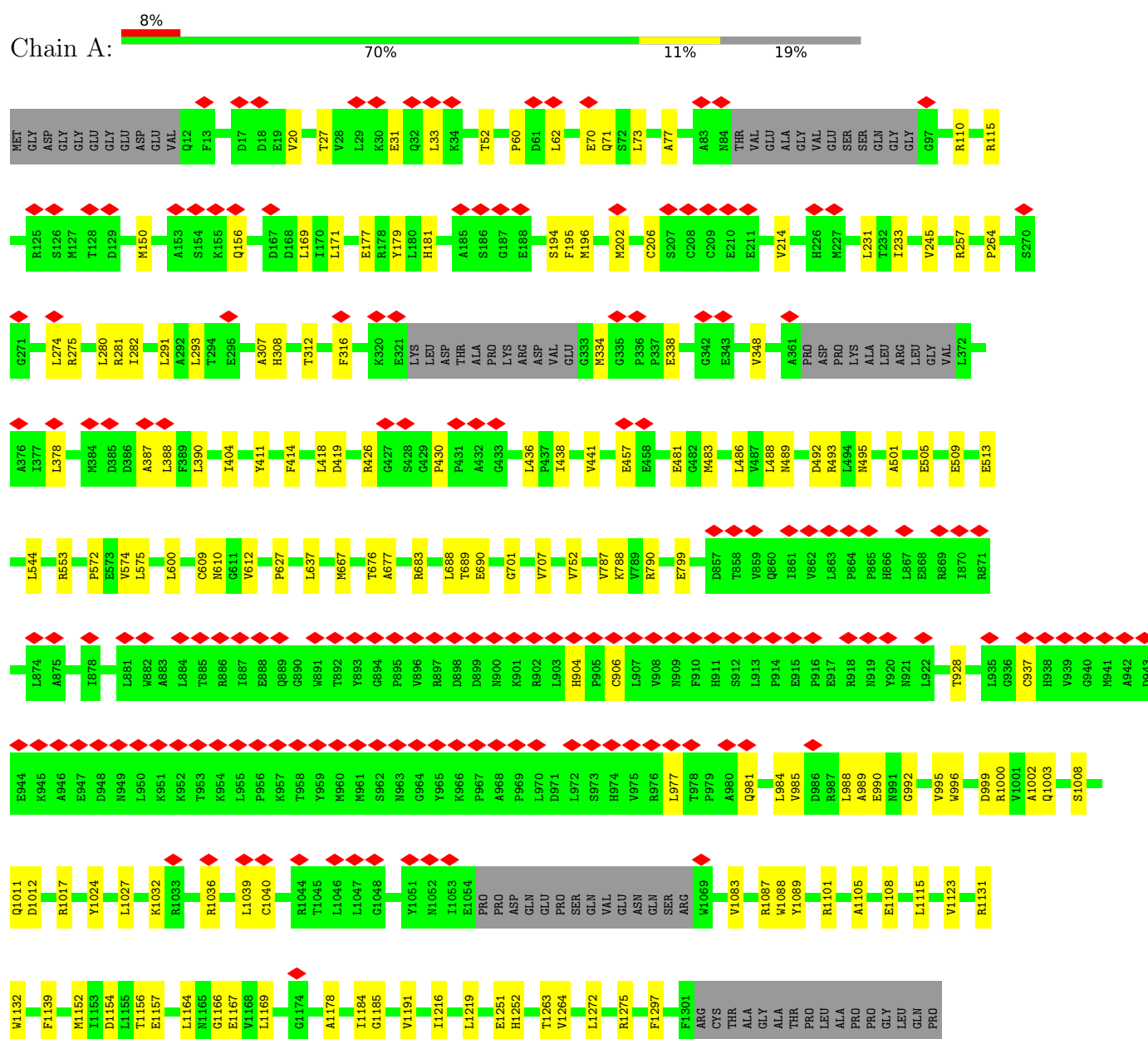
- Molecule 6 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
6	A	1	Total 1	Zn 1	0
6	G	1	Total 1	Zn 1	0
6	M	1	Total 1	Zn 1	0
6	S	1	Total 1	Zn 1	0

3 Residue-property plots

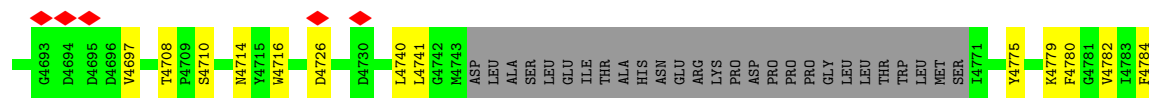
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Ryanodine receptor 1

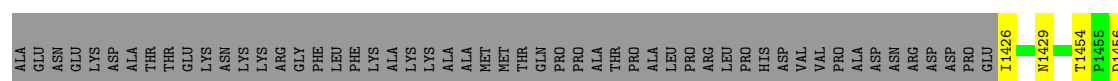
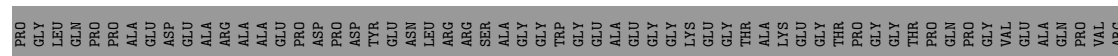
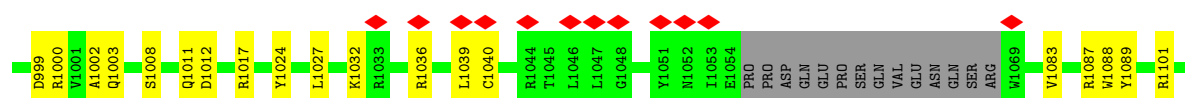
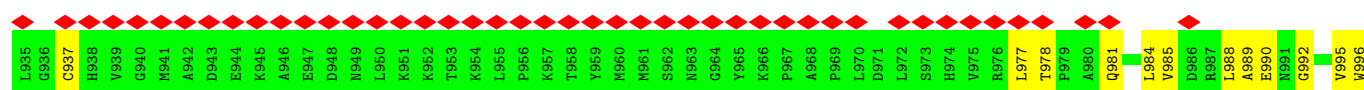
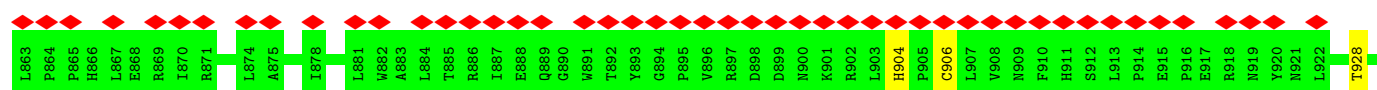
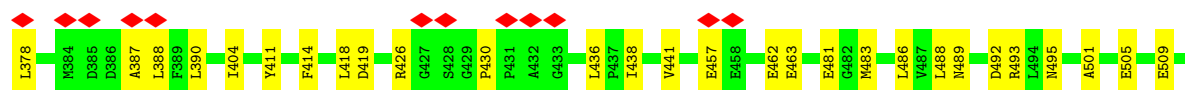
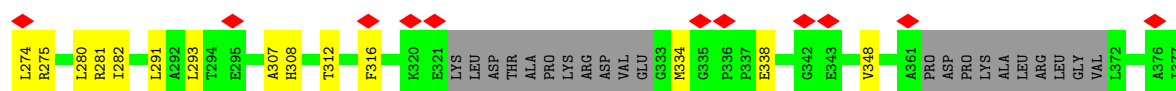
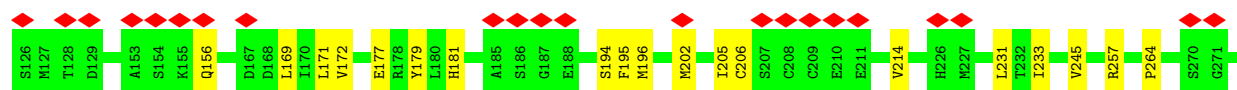


F2929	R2869	I2809	E2749	R2624	ASP	Y2256	W2101	ALA	GLU	P1773	N1482	ASP	PRO
L2930	E2870	K2810	K2750	R2625	ARG	L2257	D2109	ASP	LYS	L1786	V1501	ALA	GLU
Q2931	L2871	E2811	L2751	L2626	ARG	L2258	S2113	ASP	GLU	PRO	SER	THR	
M2932	Q2872	S2812	D2752	V2627	GLU	G2262	L2116	C2021	ALA	ALA	PRO	LYS	
Q2934	A2873	L2813	S2753	F2628	HIS	L2259	W2117	P2022	LYS	GLY	GLN	ASN	
A2936	W2874	K2814	F2754	D2629	PHE	L2260	L2117	L2023	GLU	VAL	GLN	ALA	
V2937	A2875	A2815	L2755	V2630	GLY	L2261	M2120	L2044	GLU	ALA	GLY	LYS	
A2938	E2876	M2816	L2756	P2631	GLU	L2262	W2121	L2045	GLU	ALA	GLY	ALA	
T2938	Q2877	L2817	K2757	E2635	PRO	L2263	L2122	L2046	GLU	ALA	GLY	ARG	
R2939	L2878	A2818	F2758	M2639	GLU	L2264	L2123	L2047	GLU	ALA	GLY	PRO	
GLY	A2879	W2819	A2759	P2640	GLU	L2265	L2124	L2048	GLU	ALA	GLY	ASP	
LEU	E2880	E2820	E2760	L2643	GLU	L2266	L2125	L2049	GLU	ALA	GLY	THR	
LYS	M2881	W2821	T2761	L2644	GLU	L2267	R2126	L2050	GLU	ALA	GLY	ALA	
ASP	Y2882	T2822	T2762	R2650	PRO	L2268	Y2128	L2051	GLU	ALA	GLY	LYS	
GLU	H2883	I2823	H2763	C2651	GLU	L2269	D2151	L2052	GLU	ALA	GLY	LYS	
MET	N2884	E2824	E2764	E2670	GLY	L2270	W2153	L2053	GLU	ALA	GLY	ARG	
LEU	T2885	K2825	K2765	L2678	LYS	L2271	L2159	L2054	GLU	ALA	GLY	MET	
ASP	W2886	A2826	W2766	L2679	ASP	L2272	Q2161	L2055	GLU	ALA	GLY	MET	
THR	G2887	R2827	A2767	R2687	GLY	L2273	R2163	L2056	GLU	ALA	GLY	THR	
SER	G2888	E2828	F2768	D2716	ALA	L2274	L2164	L2057	GLU	ALA	GLY	THR	
SER	R2889	G2829	D2769	D2717	THR	L2275	L2165	L2058	GLU	ALA	GLY	THR	
L2960	K2890	E2830	I2771	D2718	LYS	L2276	P2172	L2059	GLU	ALA	GLY	THR	
R2965	G2891	GLU	Q2772	SER	THR	L2277	E2175	L2060	GLU	ALA	GLY	THR	
W2966	Q2892	ARG	N2773	THR	THR	L2278	L2176	L2061	GLU	ALA	GLY	THR	
M2967	E2893	GLU	M2774	SER	SER	L2279	P2325	L2062	GLU	ALA	GLY	THR	
D2968	L2894	LYS	W2775	LYS	LYS	L2280	L2177	L2063	GLU	ALA	GLY	THR	
S2970	E2895	LYS	S2776	ALA	GLU	L2281	W2178	L2064	GLU	ALA	GLY	THR	
Q2971	A2896	LYS	Q2777	GLU	GLU	L2282	R2189	L2065	GLU	ALA	GLY	THR	
E2972	K2897	THR	Y2777	LYS	LYS	L2283	L2196	L2066	GLU	ALA	GLY	THR	
F2973	G2898	ARG	G2778	ARG	LYS	L2284	W2199	L2067	GLU	ALA	GLY	THR	
L2974	E2899	LYS	E2779	ALA	ALA	L2285	M2203	L2068	GLU	ALA	GLY	THR	
E2978	Q2900	ILE	M2780	THR	THR	L2286	V2212	L2069	GLU	ALA	GLY	THR	
ALA	V2901	GLN	V2781	VAL	VAL	L2287	G2216	L2070	GLU	ALA	GLY	THR	
VAL	H2902	THR	D2782	ASP	ASP	L2288	GLY	L2071	GLU	ALA	GLY	THR	
SER	T2903	GLN	E2783	ALA	ALA	L2289	GLY	L2072	GLU	ALA	GLY	THR	
SER	L2904	GLN	E2784	GLY	GLY	L2290	V2352	L2073	GLU	ALA	GLY	THR	
GLY	L2905	THR	E2785	ASN	ASN	L2291	V2353	L2074	GLU	ALA	GLY	THR	
ARG	L2906	TYR	L2786	PHE	PHE	L2292	V2354	L2075	GLU	ALA	GLY	THR	
VAL	V2907	ASP	K2786	ASP	ASP	L2293	R2354	L2076	GLU	ALA	GLY	THR	
GLU	T2908	PRO	T2787	P2737	P2737	L2294	R2355	L2077	GLU	ALA	GLY	THR	
LYS	D2909	ARG	H2788	R2738	R2738	L2295	L2368	L2078	GLU	ALA	GLY	THR	
S2989	T2910	GLY	P2789	P2739	P2739	L2296	D2389	L2079	GLU	ALA	GLY	THR	
E2992	L2911	LYS	M2790	V2740	V2740	L2297	P2395	L2080	GLU	ALA	GLY	THR	
L2995	T2912	LYS	L2791	E2741	E2741	L2298	GLY	L2081	GLU	ALA	GLY	THR	
L3003	A2913	LYS	R2792	T2742	T2742	L2299	GLY	L2082	GLU	ALA	GLY	THR	
P3004	K2914	LYS	R2793	L2743	L2743	L2300	VAL	L2083	GLU	ALA	GLY	THR	
L3005	E2915	LYS	V2794	N2744	N2744	L2301	ARG	L2084	GLU	ALA	GLY	THR	
L3006	E2916	LYS	K2795	V2745	V2745	L2302	ARG	L2085	GLU	ALA	GLY	THR	
N3007	A2917	LYS	T2796	I2746	I2746	L2303	ARG	L2086	GLU	ALA	GLY	THR	
F3010	R2918	LYS	F2797	I2747	I2747	L2304	ARG	L2087	GLU	ALA	GLY	THR	
	D2919	LYS	S2798	P2748	P2748	L2305	ARG	L2088	GLU	ALA	GLY	THR	
	R2920	LYS	E2799			L2306	ARG	L2089	GLU	ALA	GLY	THR	
	E2921	LYS	K2800			L2307	ARG	L2090	GLU	ALA	GLY	THR	
	K2922	LYS	D2801			L2308	ARG	L2091	GLU	ALA	GLY	THR	
	A2923	LYS	E2802			L2309	ARG	L2092	GLU	ALA	GLY	THR	
	Q2924	LYS	E2803			L2310	ARG	L2093	GLU	ALA	GLY	THR	
	E2925	LYS	I2804			L2311	ARG	L2094	GLU	ALA	GLY	THR	
	L2926	LYS	L2805			L2312	ARG	L2095	GLU	ALA	GLY	THR	
	L2927	LYS	R2806			L2313	ARG	L2096	GLU	ALA	GLY	THR	
	K2928	LYS	W2807			L2314	ARG	L2097	GLU	ALA	GLY	THR	



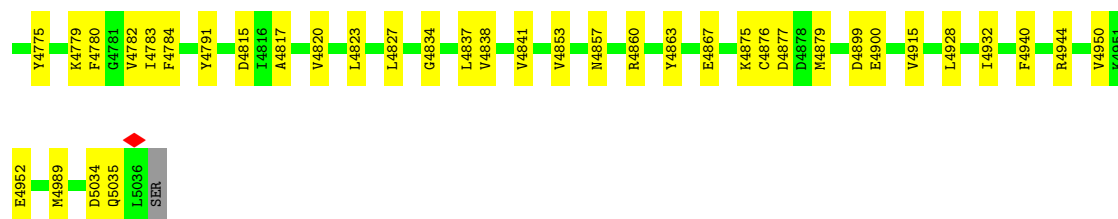


• Molecule 1: Ryanodine receptor 1

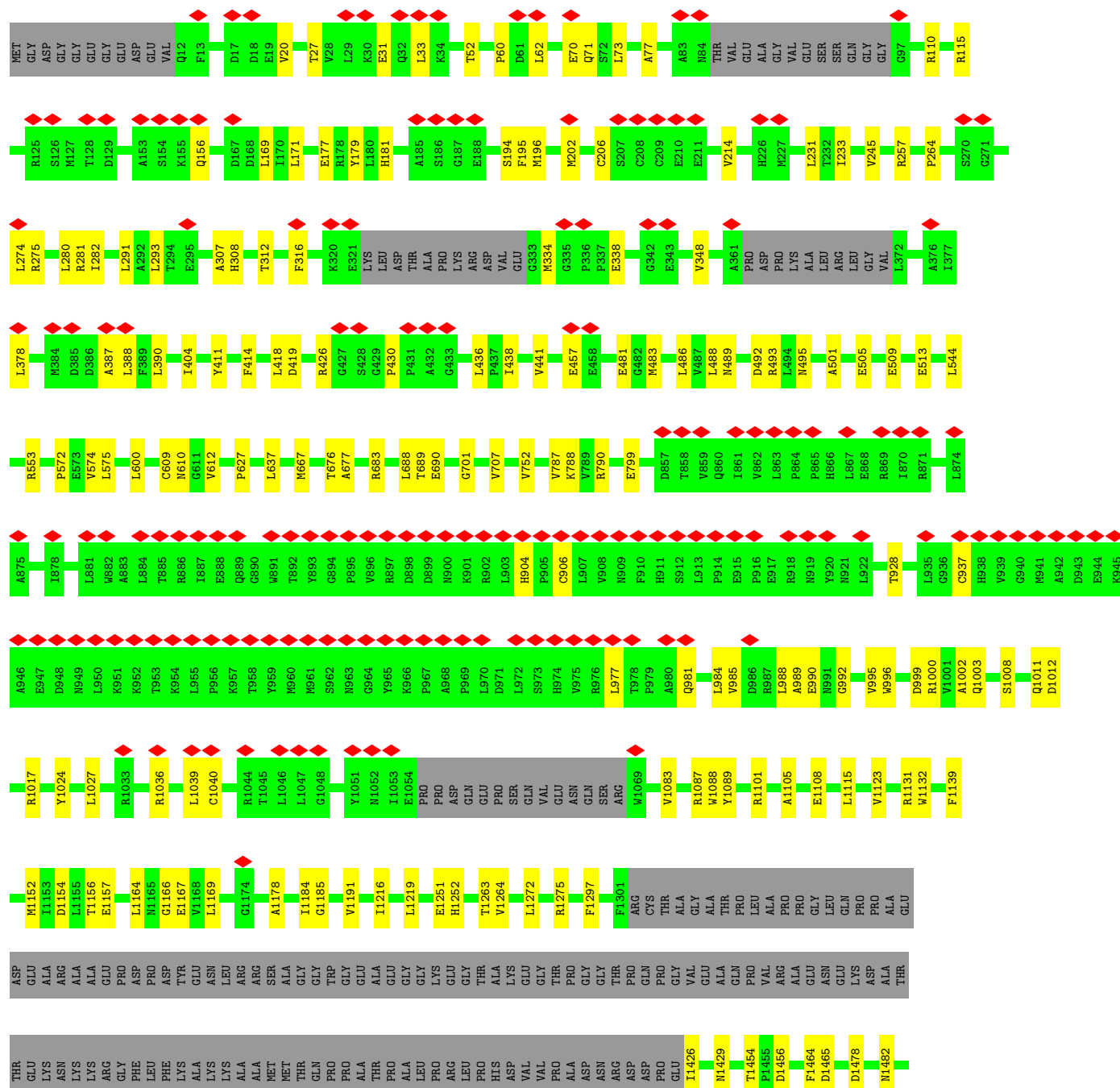


P3004	D2919	P2859	E2799	P2739	R2575	D2389	THR	GLU	Q2003	LYS	GLY	F1464
L3005	R2920	P2860	K2800	V2740	A2598	P2395	LYS	GLU	Q2003	GLU	GLY	D1465
N3007	E2921	D2861	D2801	E2741	Q2599	P2395	GLU	LYS	L2009	ASP	ALA	D1478
F3010	K2922	L2862	K2802	T2742	V2602	VAL	M2228	+	K2013	GLU	+	H1482
T3011	A2923	G2863	E2803	L2743	I2603	ARG	F2251	+	ASP	GLU	+	V1501
F3017	Q2924	G2864	T2804	N2744	V2602	ASP	Y2256	+	ALA	GLU	+	SER
E2925	V2865	V2865	Y2805	V2745	Q2620	ARG	L2257	+	ASP	LYS	+	PRO
T3020	T2866	T2866	K2806	I2746	R2624	ARG	L2258	+	GLU	ASP	+	GLY
P3021	L2927	L2867	W2807	I2747	R2624	ARG	G2262	+	GLU	ALA	+	GLN
+	K2928	S2868	P2808	P2748	R2625	GLU	G2262	+	ASP	GLU	+	GLN
K3036	F2929	R2869	T2809	E2749	L2626	HIS	ILE	+	C2021	GLU	+	ALA
E3037	L2930	E2870	K2810	K2750	V2627	PHE	GLY	+	P2022	LYS	+	GLY
M3038	Q2931	L2871	E2811	L2751	F2628	GLY	GLY	+	L2023	GLU	+	ILE
L3046	M2932	Q2872	S2812	D2752	V2630	GLU	GLY	+	+	VAL	+	SER
V3050	N2933	A2873	L2813	S2753	V2631	PRO	MET	+	T2044	GLU	+	ALA
R3051	Q2934	A2875	K2814	F2754	E2635	PRO	GLN	+	GLN	PRO	+	ALA
H3052	Y2935	A2876	A2815	F2755	M2639	GLU	G2269	+	GLY	ALA	+	GLY
F3057	A2936	Q2877	W2816	T2756	P2640	GLU	S2270	+	GLY	GLY	+	THR
+	V2937	T2877	L2817	K2757	P2640	GLU	T2271	+	GLU	LYS	+	V1542
D3060	T2938	L2878	A2818	F2758	L2643	LEU	D2274	+	GLU	GLU	+	E1543
A3061	R2939	A2879	W2819	T2759	L2644	LEU	V2275	+	GLU	LYS	+	P1544
P3062	GLY	E2880	E2820	E2760	R2452	LEU	A2276	+	GLU	ASP	+	T1557
N3066	LYS	N2881	W2821	Y2761	R2452	LEU	V2280	+	GLU	GLU	+	V1561
+	ASP	Y2882	T2822	T2762	T2478	GLY	L2286	+	GLU	GLU	+	I1562
A3077	NET	H2883	L2823	H2763	E2670	LYS	E2292	+	THR	GLU	+	R1623
R3078	GLU	N2884	E2824	E2764	L2678	ASP	D2293	+	SER	LEU	+	Q1629
T3079	LEU	T2885	K2825	K2765	L2678	GLY	D2294	+	SER	LEU	+	V1845
V3080	ASP	T2886	K2826	W2766	R2697	ALA	L2295	+	ARG	GLU	+	E1867
+	THR	W2887	A2826	W2767	R2697	ALA	E2296	+	LEU	LYS	+	A1638
G3084	SER	G2887	R2827	A2767	D2716	ALA	K2297	+	ARG	GLU	+	C1647
P3085	S2950	R2888	E2828	F2768	ALA	SER	V2298	+	SER	GLU	+	L1669
+	+	K2889	Q2829	D2769	ALA	TYR	V2299	+	LEU	GLU	+	L1694
V3088	L2960	K2890	E2830	K2770	TYR	SER	N2324	+	LEU	GLU	+	L1698
M3106	R2965	K2891	GLU	T2771	SER	LYS	Q2315	+	GLU	GLU	+	R1727
N3109	W2966	Q2892	GLU	Q2772	LYS	ALA	L2519	+	THR	GLU	+	L1731
L3110	K2967	E2893	THR	N2773	GLU	ALA	H2520	+	VAL	GLU	+	V1736
R3111	D2968	L2894	GLU	N2774	LYS	LYS	D2523	+	ARG	GLU	+	P1740
LEU	T2969	E2895	LYS	W2775	LYS	ALA	V2524	+	ALA	GLU	+	R1743
GLY	S2970	A2896	LYS	W2776	LYS	ALA	G2525	+	LYS	GLU	+	P1749
LYS	Q2971	A2896	LYS	Y2777	ALA	THR	G2526	+	LYS	GLU	+	PRO
VAL	F2972	K2897	THR	Y2777	THR	THR	V2527	+	LYS	GLU	+	GLY
+	L2974	G2898	ARG	G2778	VAL	VAL	P2528	+	GLU	GLU	+	ARG
GLN	E2978	G2899	LYS	E2779	ASP	ASP	N2349	+	ALA	GLU	+	GLY
ALA	ARG	G2900	ILE	N2780	ALA	GLU	N2351	+	LYS	GLU	+	GLY
THR	THR	T2901	SER	V2781	GLY	GLY	V2352	+	PRO	GLU	+	GLY
GLN	GLN	H2902	THR	D2782	ASN	ASN	V2353	+	GLU	ALA	+	GLY
VAL	SER	P2903	ALA	E2783	GLY	GLY	V2354	+	GLU	GLU	+	GLY
VAL	GLY	L2904	GLN	E2784	PHE	PHE	R2355	+	GLU	GLU	+	GLY
LYS	LYS	L2905	THR	E2785	ASP	ASP	L2368	+	GLU	GLU	+	GLY
+	VAL	L2906	TVR	L2786	P2737	P2737	+	+	GLU	GLU	+	GLY
+	GLU	P2907	ASP	K2786	R2738	R2738	+	+	GLU	GLU	+	GLY
+	LYS	Y2908	ARG	T2787	+	+	+	+	GLU	GLU	+	GLY
+	+	D2909	ARG	H2788	+	+	+	+	GLU	GLU	+	GLY
+	+	T2910	GLY	P2789	+	+	+	+	GLU	GLU	+	GLY
+	+	L2911	GLY	M2790	+	+	+	+	GLU	GLU	+	GLY
+	+	T2912	Y2855	L2791	+	+	+	+	GLU	GLU	+	GLY
+	+	A2913	P2857	R2792	+	+	+	+	GLU	GLU	+	GLY
+	+	K2914	Q2858	P2793	+	+	+	+	GLU	GLU	+	GLY
+	+	E2915	+	Y2794	+	+	+	+	GLU	GLU	+	GLY
+	+	K2916	+	K2795	+	+	+	+	GLU	GLU	+	GLY
+	+	A2917	+	T2796	+	+	+	+	GLU	GLU	+	GLY
+	+	R2918	+	F2797	+	+	+	+	GLU	GLU	+	GLY
+	+	+	+	S2798	+	+	+	+	GLU	GLU	+	GLY





• Molecule 1: Ryanodine receptor 1

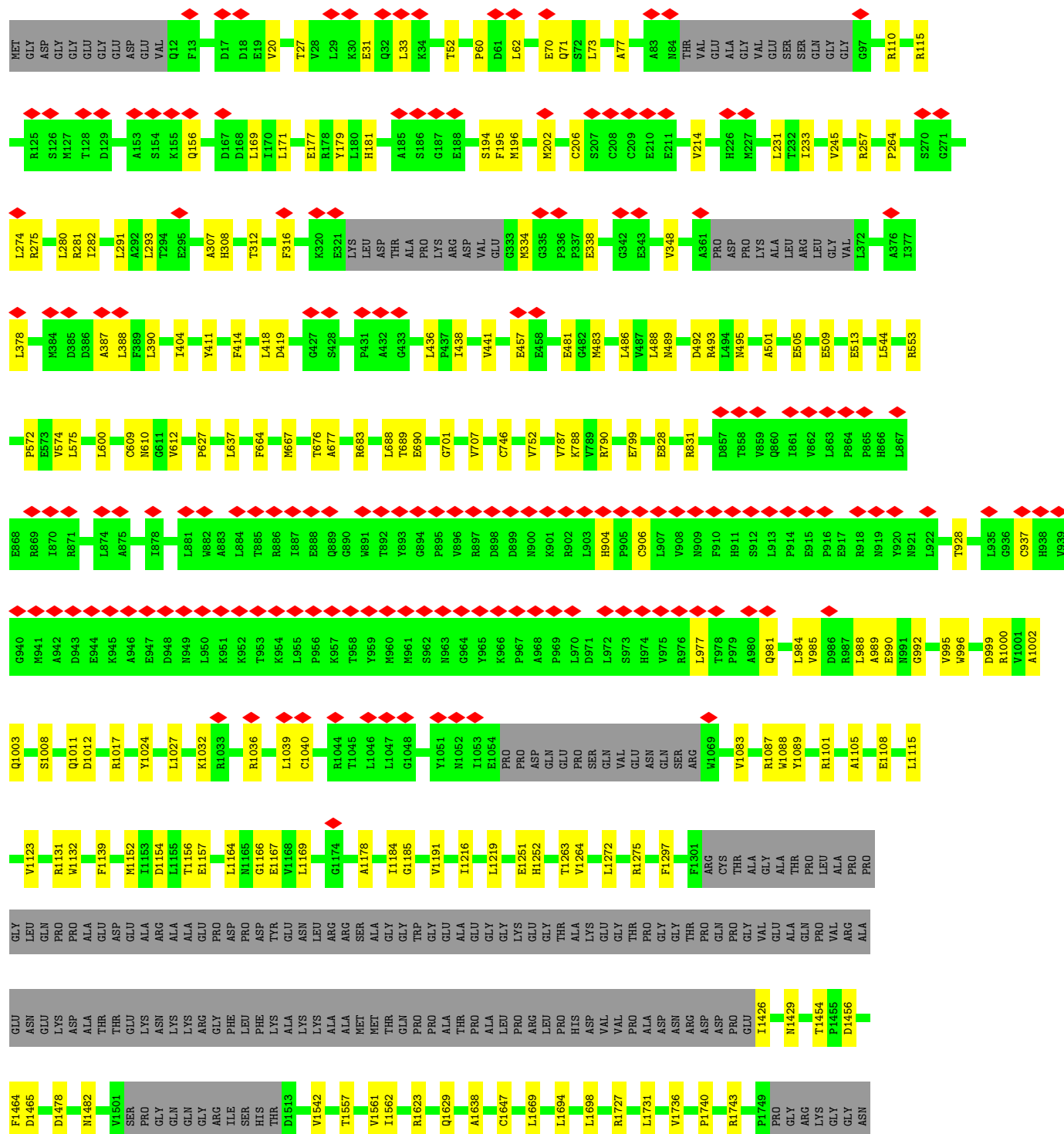


V1501	SER	V1765	ALA	GLU	K2013	V2098	M2228	VAL	I2603	N2744	I2804	G2864	Q2924	F3010
PRO	GLY	P1773	ALA	GLU	ASP	M2101	F2251	ARG	Q2620	V2745	Y2805	V2865	E2925	T3011
GLN	GLY	L1786	ALA	GLY	ASP	D2109	Y2256	ARG	R2624	I2746	R2806	T2866	I2926	F3017
GLY	ARG	ALA	ALA	GLY	GLU	D2109	L2257	ARG	R2625	I2747	N2807	L2867	L2927	T3020
ARG	ARG	ALA	ALA	GLY	GLU	S2113	L2258	ARG	L2626	E2748	P2808	S2868	K2928	P3021
ILE	SER	ALA	ALA	VAL	ASP	L2116	G2262	HIS	V2627	K2750	K2810	E2870	L2930	K3036
HIS	HIS	ALA	ALA	VAL	ALA	D2117	I2262	PHE	D2629	L2751	E2811	L2871	Q2931	M3038
THR	THR	ALA	ALA	VAL	ALA	V2117	GLY	GLY	P2631	D2752	S2812	Q2872	Q2932	L3046
D1513	D1513	ALA	ALA	VAL	ALA	M2120	LEU	GLU	E2635	S2753	L2813	A2873	M2933	
V1542	V1542	P1795	P1795	ALA	GLN	F2121	MET	PRO	K2638	F2754	K2814	M2874	G2934	
E1543	E1543	E1805	E1805	ALA	LEU	S2122	GLN	PRO	M2639	I2755	A2815	A2875	V2935	V3050
P1544	P1544	E1808	E1808	GLY	GLY	L2124	G2269	GLU	P2640	M2756	M2816	E2876	R3051	R3052
T1567	T1567	L1815	L1815	GLY	GLU	H2125	S2270	GLU	L2643	K2757	L2817	Q2877	V2937	H3052
V1561	V1561	L1819	L1819	LYS	GLU	R2126	T2271	E2449	L2644	F2758	A2818	L2878	T2938	F3057
I1562	I1562	V1819	V1819	GLU	GLU	Q2127	D2274	R2452	R2650	A2759	M2819	A2879	R2939	D3060
R1623	R1623	V1841	V1841	LEU	PRO	Y2128	A2276	L2478	C2651	E2760	E2820	E2880	GLY	A3061
Q1629	Q1629	E1867	E1867	GLU	GLU	D2151	V2280	GLY	E2670	T2762	T2822	Y2882	LEU	P3062
A1638	A1638	T1872	T1872	THR	THR	M2152	L2286	LYS	L2678	H2763	L2823	H2883	ASP	N3066
C1647	C1647	L1925	L1925	SER	SER	M2153	E2292	GLY	L2679	E2764	E2824	N2884	GLU	C3067
L1669	L1669	L1926	L1926	ARG	ARG	L2159	Q2283	ALA	M2698	K2765	K2825	T2885	LEU	L3068
L1694	L1694	L1927	L1927	LEU	LEU	Q2161	D2294	L2485	D2716	K2766	A2826	W2886	THR	A3077
R1727	R1727	Q1928	Q1928	ARG	ARG	R2162	E2296	K2499	ALA	A2767	R2827	Q2887	SER	R3078
L1731	L1731	V1935	V1935	LEU	LEU	S2164	K2297	V2503	ALA	F2768	E2828	R2888	GLY	T3079
V1736	V1736	M1939	M1939	ARG	ARG	L2165	V2298	Q2515	TRP	K2770	Q2829	K2889	LEU	V3080
P1740	P1740	L1943	L1943	THR	THR	P2172	N3324	L2519	SER	I2771	E2830	K2890	L2960	G3084
R1743	R1743	L1969	L1969	MET	MET	E2175	P3395	H2520	THR	Q2772	GLU	K2891	R2965	G3085
P1749	P1749	L1980	L1980	ALA	ALA	N2176	C3326	D2523	GLY	M2773	GLU	K2892	W2966	V3088
PRO	PRO	MET	MET	VAL	VAL	L2177	R2330	V2524	LYS	N2774	THR	E2893	M2967	M3106
GLY	GLY	ARG	ARG	LEU	LEU	M2178	F2334	L2627	GLY	W2775	LYS	L2894	D2968	N3109
ARG	ARG	THR	THR	LYS	LYS	K2189	D2333	L2627	ALA	S2776	THR	E2895	Q2970	L3110
LYS	LYS	ASP	ASP	GLU	GLU	M2196	E2348	M2530	VAL	Y2777	ARG	G2898	F2972	R3111
GLY	GLY	LEU	LEU	THR	THR	R2199	N2349	M2530	ASP	Q2778	LYS	G2899	I2974	LEU
ASP	ASP	GLU	GLU	ARG	ARG	M2203	A2350	M2530	ALA	E2779	ILE	G2899	E2978	LYS
GLU	GLU	THR	THR	LYS	LYS	V2212	V2352	F2541	GLY	N2780	SER	G2900	ALA	VAL
R1994	R1994	GLU	GLU	LYS	LYS	G2216	V2353	T2544	GLY	V2781	THR	H2901	VAL	GLN
S2000	S2000	LEU	LEU	ALA	ALA	GLY	R2355	A2547	ASN	D2782	GLN	H2902	SER	ARG
L2003	L2003	PRO	PRO	GLU	GLU	THR	R2355	R2575	ASP	E2784	THR	L2904	GLY	THR
L2009	L2009	LYS	LYS	GLU	GLU	GLY	L2368	K2575	ASP	L2785	TYR	L2905	VAL	ARG
		ASP	ASP	LYS	LYS	GLU	D2389	A2598	P2737	K2786	PRO	V2906	VAL	ARG
		GLU	GLU	LYS	LYS	GLU	P2395	Q2599	R2738	Y2787	GLU	P2907	GLY	LYS
									P2739	H2788	GLY	Y2908	LYS	
									V2740	T2789	Y2855	D2909	L3003	L3003
									E2741	M2790	N2856	T2910	P3004	P3004
									T2742	L2791	P2857	L2911	I3006	I3006
									L2743	A2792	Q2858	T2912	N3007	N3007
										R2796	P2859	A2913		
										Y2794	P2860	K2914		
										K2795	D2861	E2915		
										T2796	L2862	K2916		
										T2797	S2863	A2917		
										S2798		R2918		
										E2799		D2919		
										K2800		R2920		
										K2801		E2921		
										K2802		A2922		
										E2803		A2923		



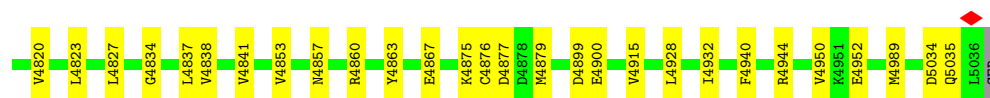


• Molecule 1: Ryanodine receptor 1

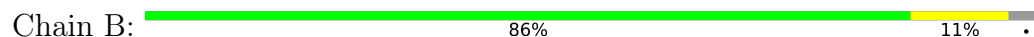




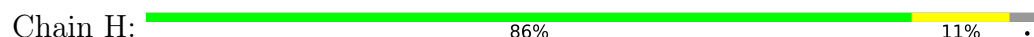




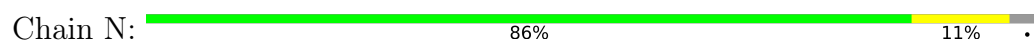
- Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1B



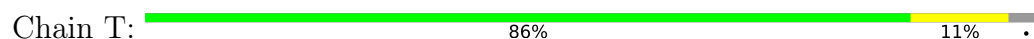
- Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1B



- Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1B



- Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1B



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	694588	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.866	Depositor
Minimum map value	0.000	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.022	Depositor
Recommended contour level	0.123	Depositor
Map size (Å)	491.52, 491.52, 491.52	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.96, 0.96, 0.96	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, 117, CFF, CA

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	0.37	2/32589 (0.0%)	0.55	7/44174 (0.0%)
1	G	0.37	2/32589 (0.0%)	0.55	7/44174 (0.0%)
1	M	0.37	2/32589 (0.0%)	0.55	7/44174 (0.0%)
1	S	0.37	2/32589 (0.0%)	0.55	7/44174 (0.0%)
2	B	0.18	0/827	0.38	0/1111
2	H	0.18	0/827	0.38	0/1111
2	N	0.18	0/827	0.38	0/1111
2	T	0.18	0/827	0.38	0/1111
All	All	0.36	8/133664 (0.0%)	0.54	28/181140 (0.0%)

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	4915	VAL	C-O	-5.97	1.17	1.24
1	G	4915	VAL	C-O	-5.97	1.17	1.24
1	M	4915	VAL	C-O	-5.97	1.17	1.24
1	S	4915	VAL	C-O	-5.97	1.17	1.24
1	A	4640	GLU	N-CA	5.53	1.50	1.46

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	4697	VAL	N-CA-C	-7.50	104.00	113.22
1	G	4697	VAL	N-CA-C	-7.50	104.00	113.22
1	M	4697	VAL	N-CA-C	-7.50	104.00	113.22
1	S	4697	VAL	N-CA-C	-7.50	104.00	113.22
1	A	4164	LEU	N-CA-C	-5.56	105.23	112.23

There are no chirality outliers.

There are no planarity outliers.

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	31873	0	31185	400	0
1	G	31873	0	31185	408	0
1	M	31873	0	31185	403	0
1	S	31873	0	31185	406	0
2	B	811	0	806	8	0
2	H	811	0	806	8	0
2	N	811	0	806	8	0
2	T	811	0	806	8	0
3	A	14	0	10	1	0
3	G	14	0	10	1	0
3	M	14	0	10	1	0
3	S	14	0	10	1	0
4	A	1	0	0	0	0
4	G	1	0	0	0	0
4	M	1	0	0	0	0
4	S	1	0	0	0	0
5	A	123	0	102	8	0
5	G	123	0	102	10	0
5	M	123	0	102	10	0
5	S	123	0	102	9	0
6	A	1	0	0	0	0
6	G	1	0	0	0	0
6	M	1	0	0	0	0
6	S	1	0	0	0	0
All	All	131292	0	128412	1642	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.

The worst 5 of 1642 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:4629:TYR:OH	1:S:4860:ARG:NH1	1.94	1.00
1:M:4860:ARG:NH1	1:S:4629:TYR:OH	1.94	0.99
1:G:4860:ARG:NH1	1:M:4629:TYR:OH	1.94	0.98

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4860:ARG:NH1	1:G:4629:TYR:OH	1.94	0.98
1:A:2626:LEU:HD22	1:A:2640:PRO:HB3	1.47	0.96

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	3992/5037 (79%)	3897 (98%)	94 (2%)	1 (0%)	100	100
1	G	3992/5037 (79%)	3897 (98%)	94 (2%)	1 (0%)	100	100
1	M	3992/5037 (79%)	3897 (98%)	94 (2%)	1 (0%)	100	100
1	S	3992/5037 (79%)	3897 (98%)	94 (2%)	1 (0%)	100	100
2	B	105/111 (95%)	100 (95%)	5 (5%)	0	100	100
2	H	105/111 (95%)	100 (95%)	5 (5%)	0	100	100
2	N	105/111 (95%)	100 (95%)	5 (5%)	0	100	100
2	T	105/111 (95%)	100 (95%)	5 (5%)	0	100	100
All	All	16388/20592 (80%)	15988 (98%)	396 (2%)	4 (0%)	100	100

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	3971	GLY
1	G	3971	GLY
1	M	3971	GLY
1	S	3971	GLY

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	3379/4276 (79%)	3379 (100%)	0	100	100
1	G	3379/4276 (79%)	3379 (100%)	0	100	100
1	M	3379/4276 (79%)	3379 (100%)	0	100	100
1	S	3379/4276 (79%)	3379 (100%)	0	100	100
2	B	86/91 (94%)	86 (100%)	0	100	100
2	H	86/91 (94%)	86 (100%)	0	100	100
2	N	86/91 (94%)	86 (100%)	0	100	100
2	T	86/91 (94%)	86 (100%)	0	100	100
All	All	13860/17468 (79%)	13860 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 152 such sidechains are listed below:

Mol	Chain	Res	Type
1	S	465	GLN
1	S	3667	HIS
1	S	1429	ASN
1	S	2441	HIS
1	S	4812	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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 24 ligands modelled in this entry, 8 are monoatomic - leaving 16 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	117	S	5104	-	44,44,44	0.79	1 (2%)	55,61,61	0.90	2 (3%)
5	117	G	5105	-	44,44,44	0.78	0	55,61,61	0.95	2 (3%)
3	CFF	A	5101	-	15,15,15	1.07	3 (20%)	23,23,23	2.22	9 (39%)
5	117	G	5103	-	44,44,44	0.78	1 (2%)	55,61,61	1.31	5 (9%)
5	117	M	5103	-	44,44,44	0.78	1 (2%)	55,61,61	1.31	5 (9%)
5	117	M	5105	-	44,44,44	0.78	0	55,61,61	0.95	2 (3%)
5	117	S	5105	-	44,44,44	0.78	0	55,61,61	0.95	2 (3%)
3	CFF	S	5101	-	15,15,15	1.07	3 (20%)	23,23,23	2.22	9 (39%)
5	117	A	5103	-	44,44,44	0.78	1 (2%)	55,61,61	1.31	5 (9%)
5	117	G	5104	-	44,44,44	0.79	1 (2%)	55,61,61	0.90	2 (3%)
5	117	M	5104	-	44,44,44	0.79	1 (2%)	55,61,61	0.90	2 (3%)
5	117	A	5105	-	44,44,44	0.78	0	55,61,61	0.95	2 (3%)
5	117	A	5104	-	44,44,44	0.79	1 (2%)	55,61,61	0.90	2 (3%)
5	117	S	5103	-	44,44,44	0.78	1 (2%)	55,61,61	1.31	5 (9%)
3	CFF	G	5101	-	15,15,15	1.07	3 (20%)	23,23,23	2.22	9 (39%)
3	CFF	M	5101	-	15,15,15	1.07	3 (20%)	23,23,23	2.22	9 (39%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	117	S	5104	-	-	0/33/33/33	0/4/4/4
5	117	G	5105	-	-	9/33/33/33	0/4/4/4
5	117	G	5103	-	-	6/33/33/33	0/4/4/4
5	117	M	5103	-	-	6/33/33/33	0/4/4/4
5	117	M	5105	-	-	9/33/33/33	0/4/4/4
3	CFF	A	5101	-	-	-	0/2/2/2
5	117	S	5105	-	-	9/33/33/33	0/4/4/4
3	CFF	S	5101	-	-	-	0/2/2/2
5	117	A	5103	-	-	6/33/33/33	0/4/4/4
5	117	G	5104	-	-	0/33/33/33	0/4/4/4
5	117	M	5104	-	-	0/33/33/33	0/4/4/4
5	117	A	5105	-	-	9/33/33/33	0/4/4/4
5	117	A	5104	-	-	0/33/33/33	0/4/4/4
5	117	S	5103	-	-	6/33/33/33	0/4/4/4
3	CFF	G	5101	-	-	-	0/2/2/2
3	CFF	M	5101	-	-	-	0/2/2/2

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	5101	CFF	C6-N1	-2.43	1.35	1.40
3	G	5101	CFF	C6-N1	-2.43	1.35	1.40
3	M	5101	CFF	C6-N1	-2.43	1.35	1.40
3	S	5101	CFF	C6-N1	-2.43	1.35	1.40
5	A	5103	117	C12-C10	-2.21	1.45	1.49

The worst 5 of 72 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	5103	117	C19-N2-C18	-6.06	116.69	127.45
5	G	5103	117	C19-N2-C18	-6.06	116.69	127.45
5	M	5103	117	C19-N2-C18	-6.06	116.69	127.45
5	S	5103	117	C19-N2-C18	-6.06	116.69	127.45
3	A	5101	CFF	N3-C4-N9	4.84	133.88	126.27

There are no chirality outliers.

5 of 60 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	5103	117	C9-C11-C18-O18
5	A	5105	117	O5-C5-C6-C7

Continued on next page...

Continued from previous page...

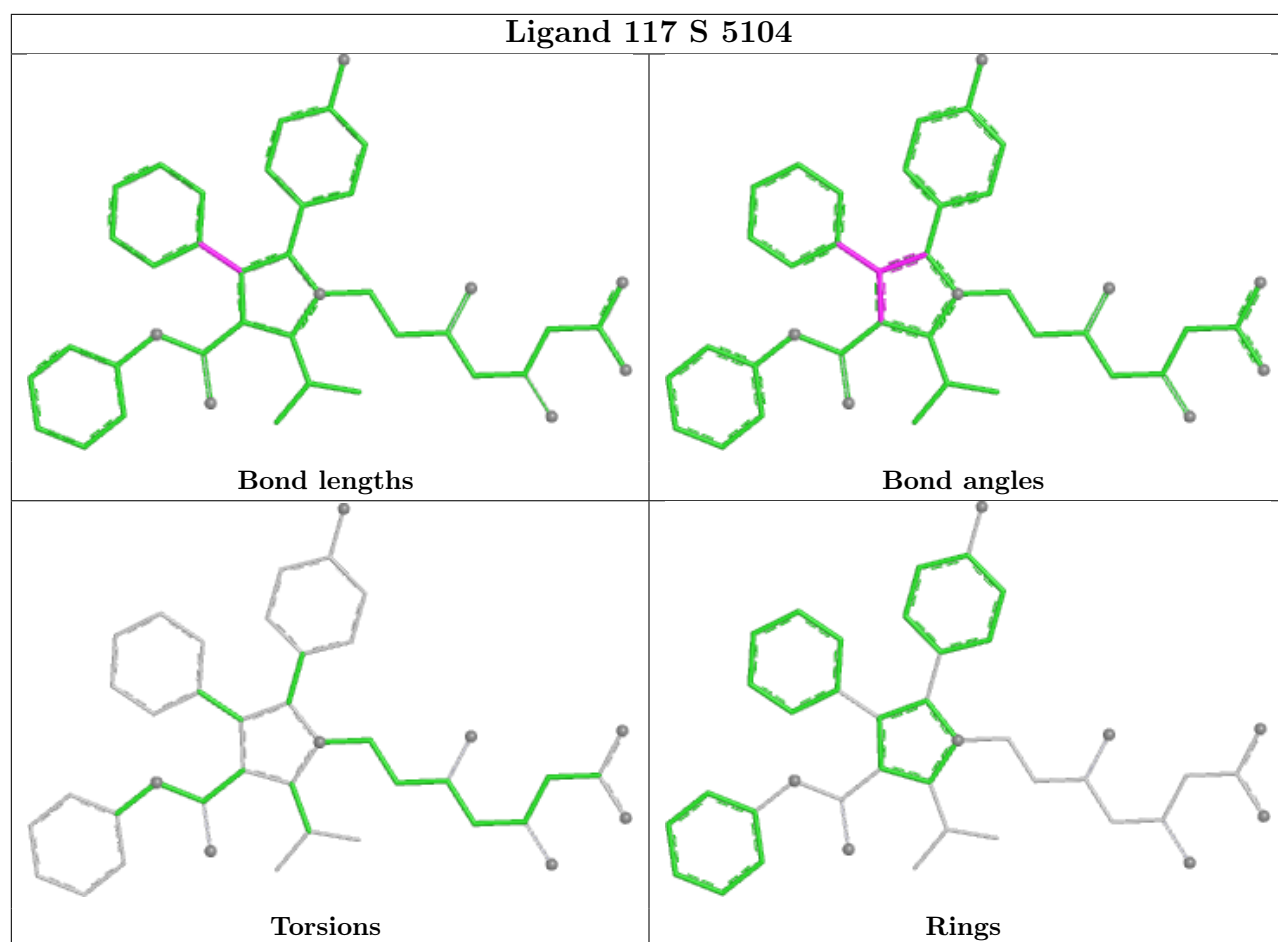
Mol	Chain	Res	Type	Atoms
5	A	5105	117	C9-C11-C18-N2
5	G	5103	117	C9-C11-C18-O18
5	G	5105	117	O5-C5-C6-C7

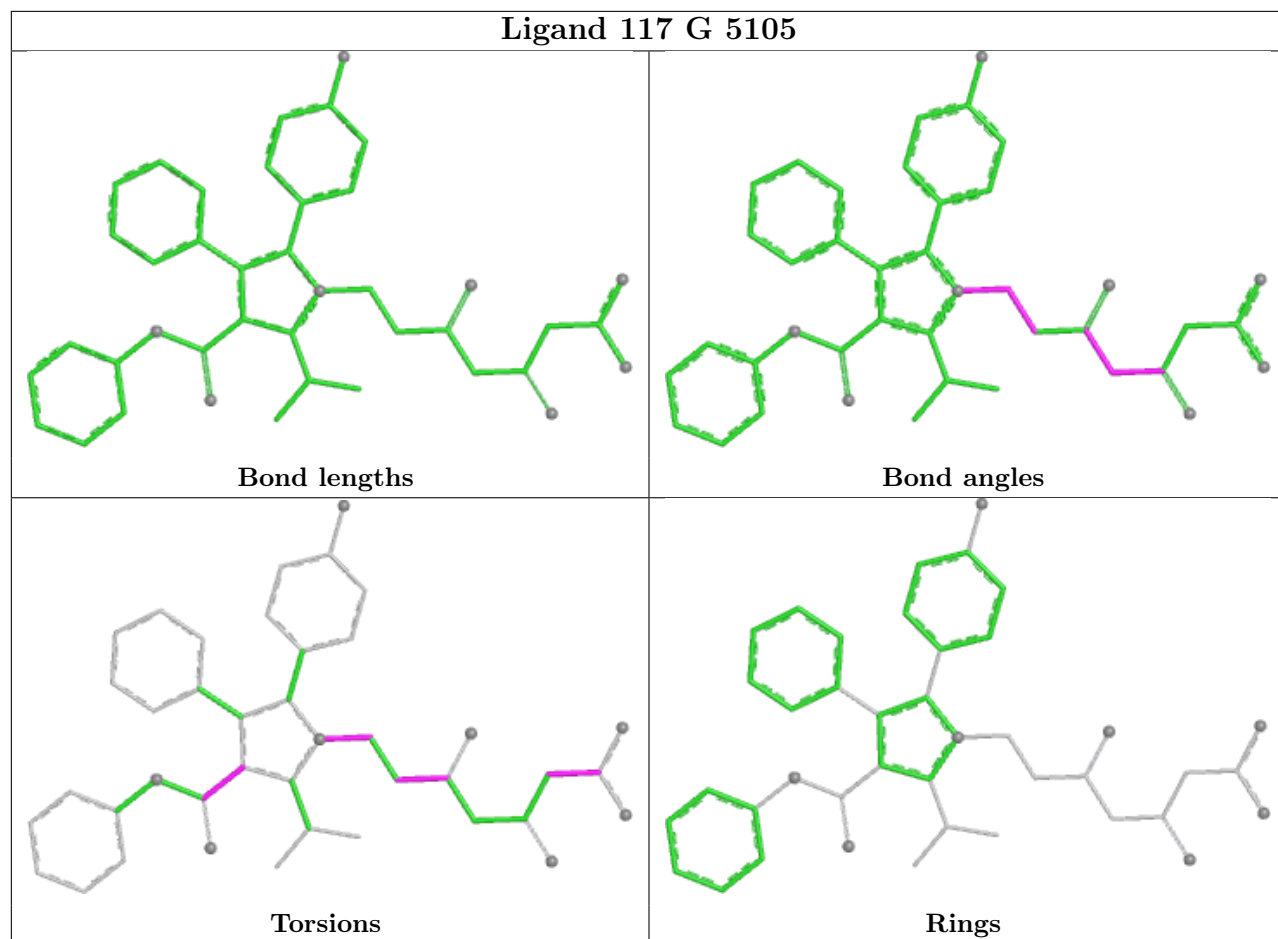
There are no ring outliers.

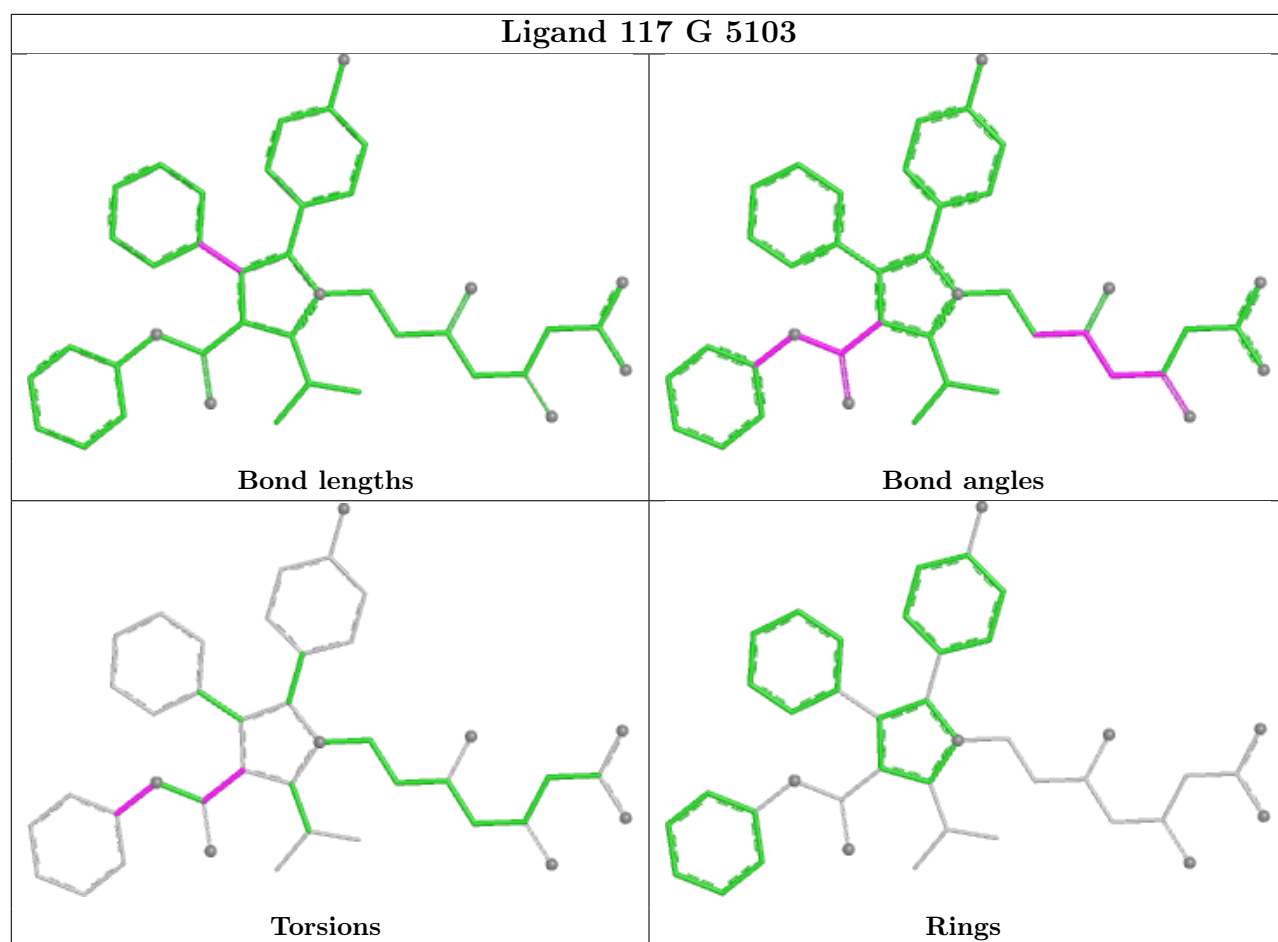
16 monomers are involved in 41 short contacts:

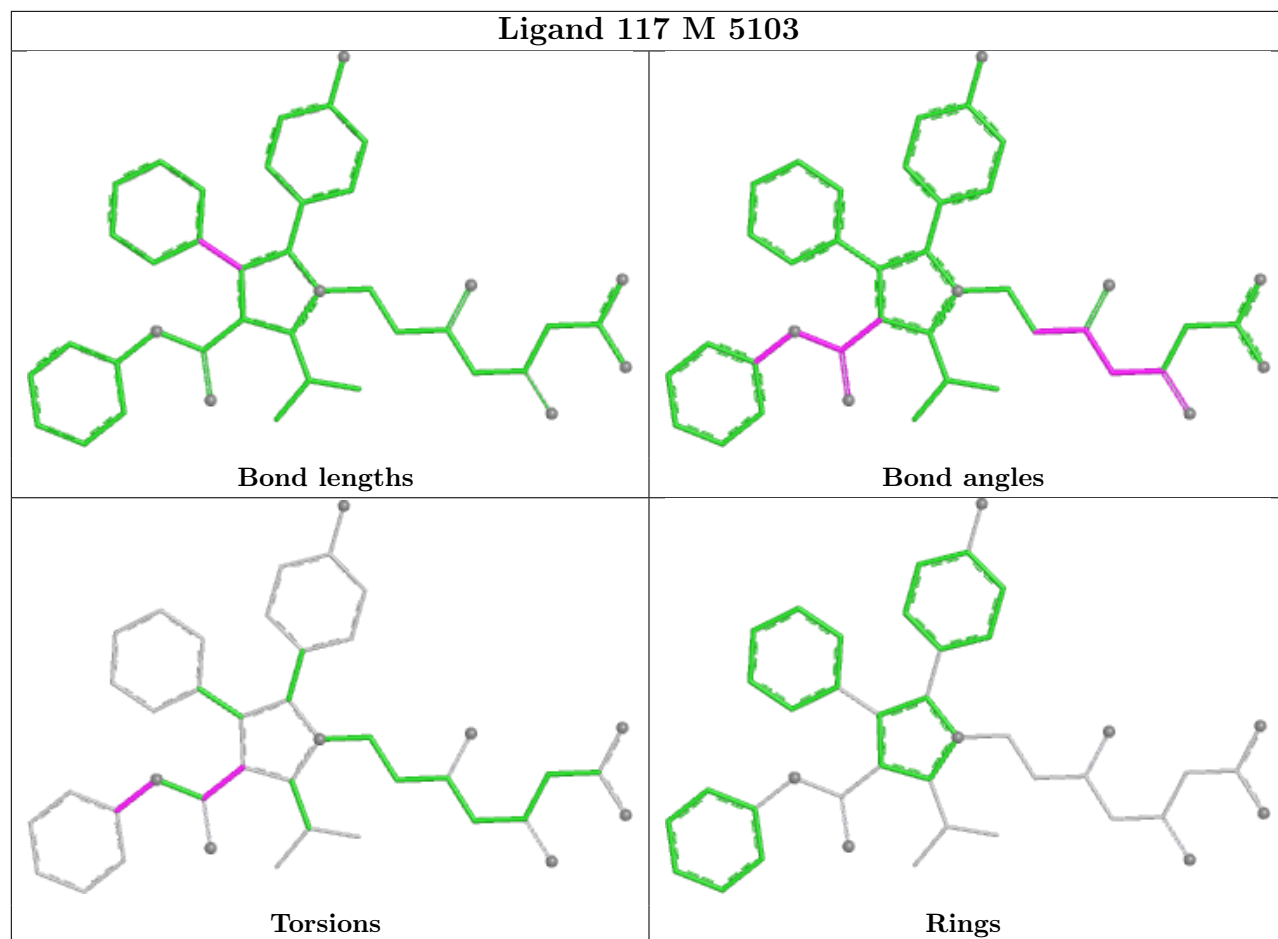
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	S	5104	117	3	0
5	G	5105	117	5	0
3	A	5101	CFF	1	0
5	G	5103	117	4	0
5	M	5103	117	4	0
5	M	5105	117	5	0
5	S	5105	117	4	0
3	S	5101	CFF	1	0
5	A	5103	117	4	0
5	G	5104	117	3	0
5	M	5104	117	3	0
5	A	5105	117	3	0
5	A	5104	117	3	0
5	S	5103	117	4	0
3	G	5101	CFF	1	0
3	M	5101	CFF	1	0

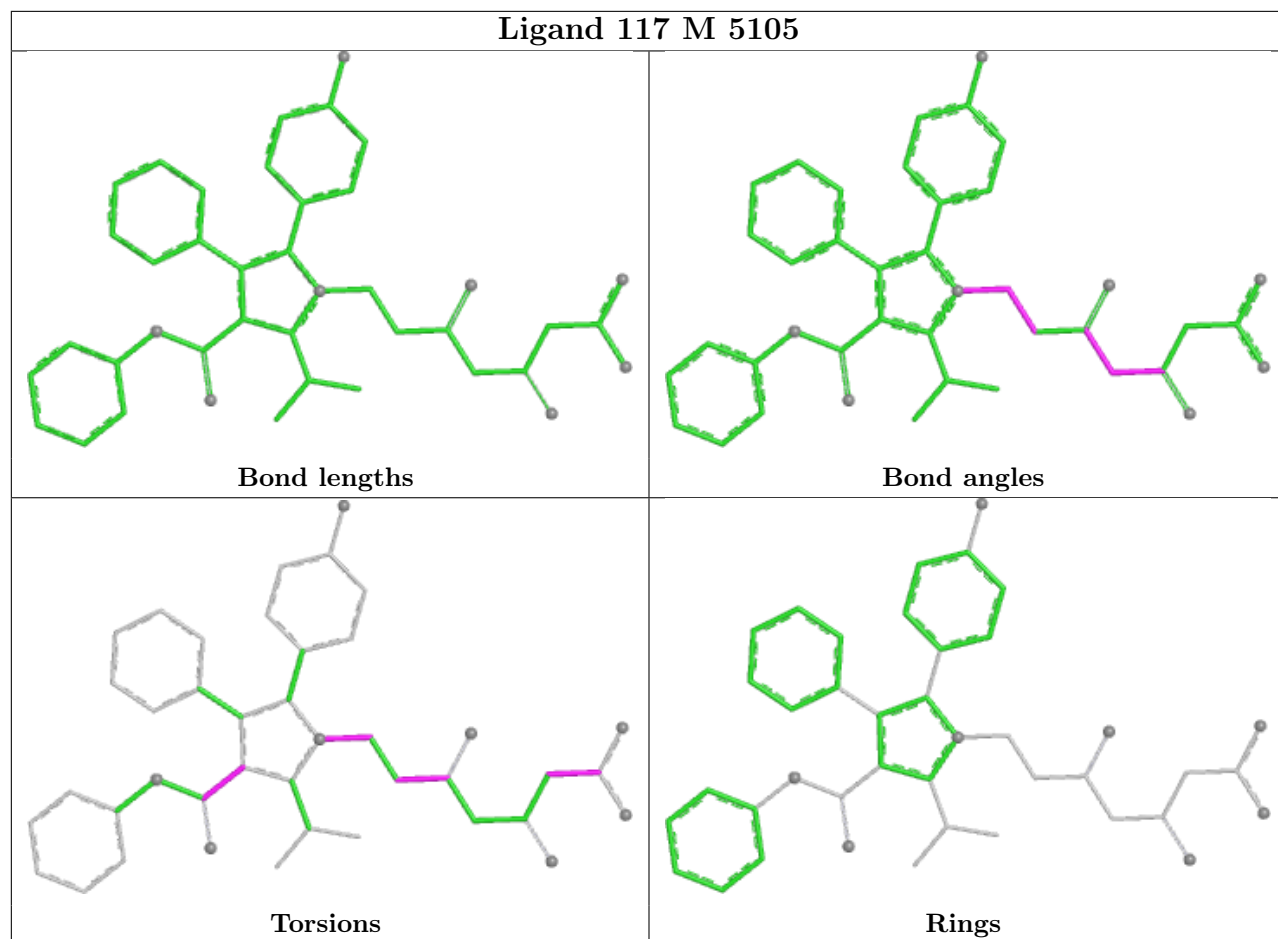
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

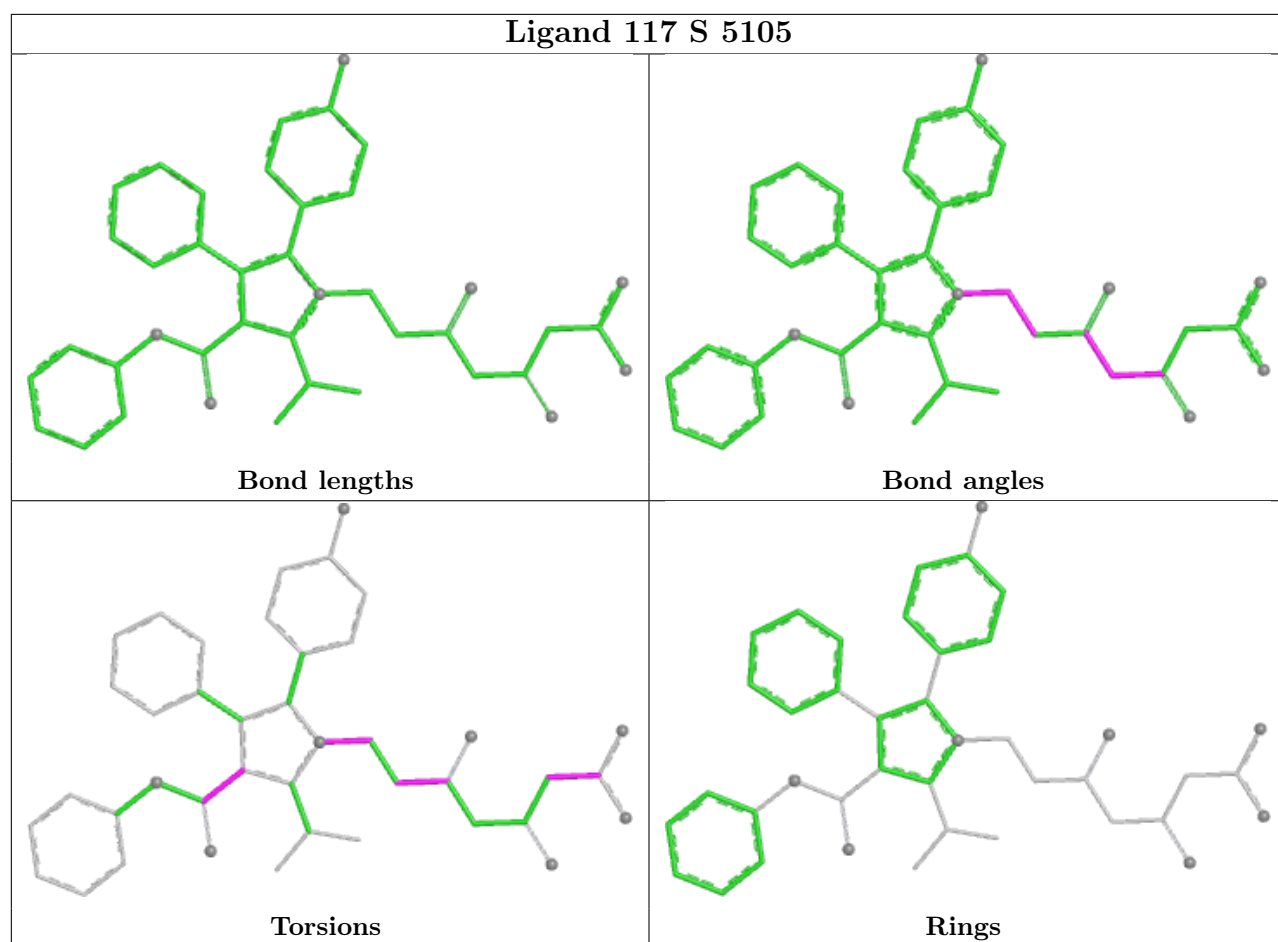


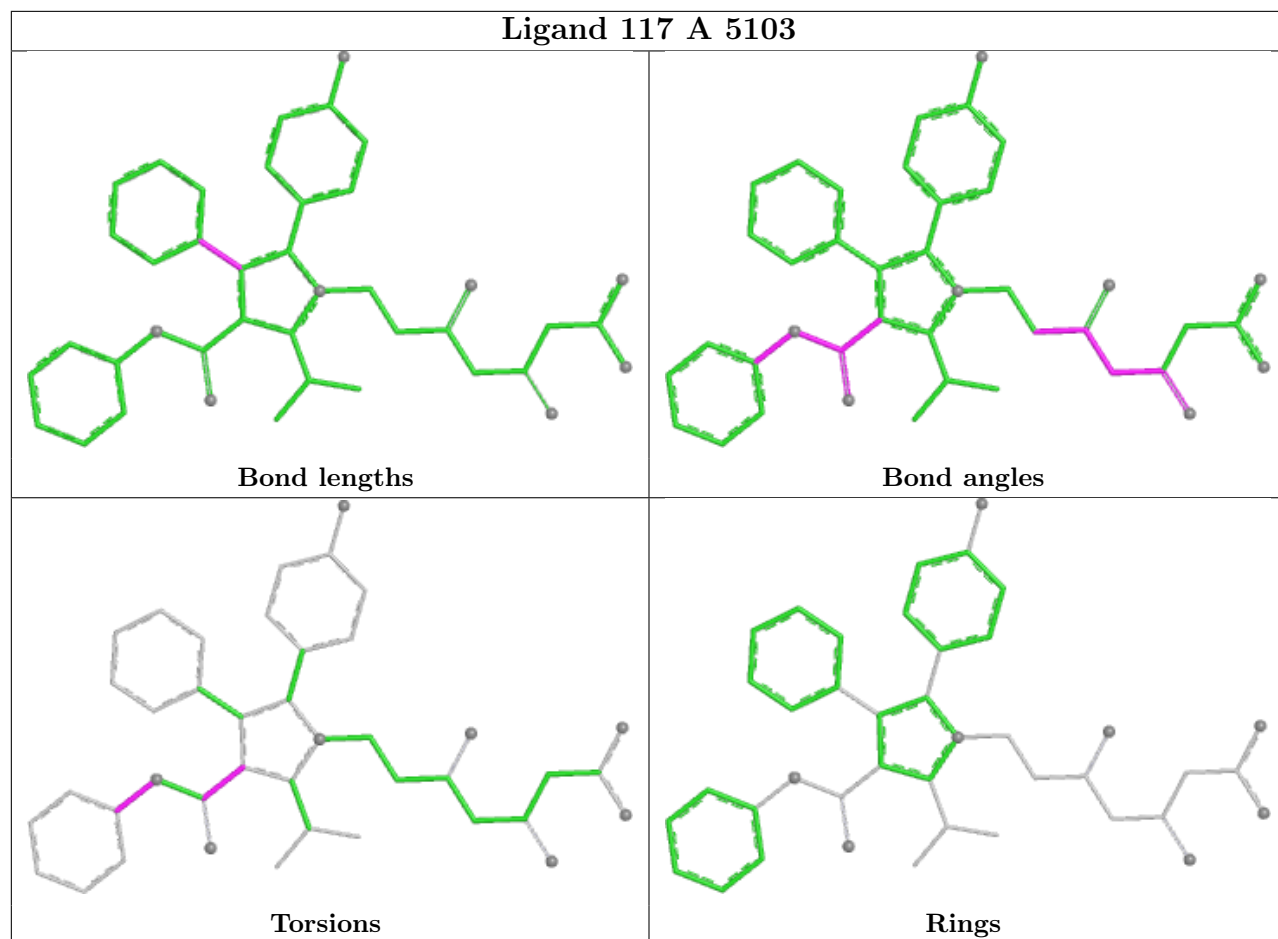


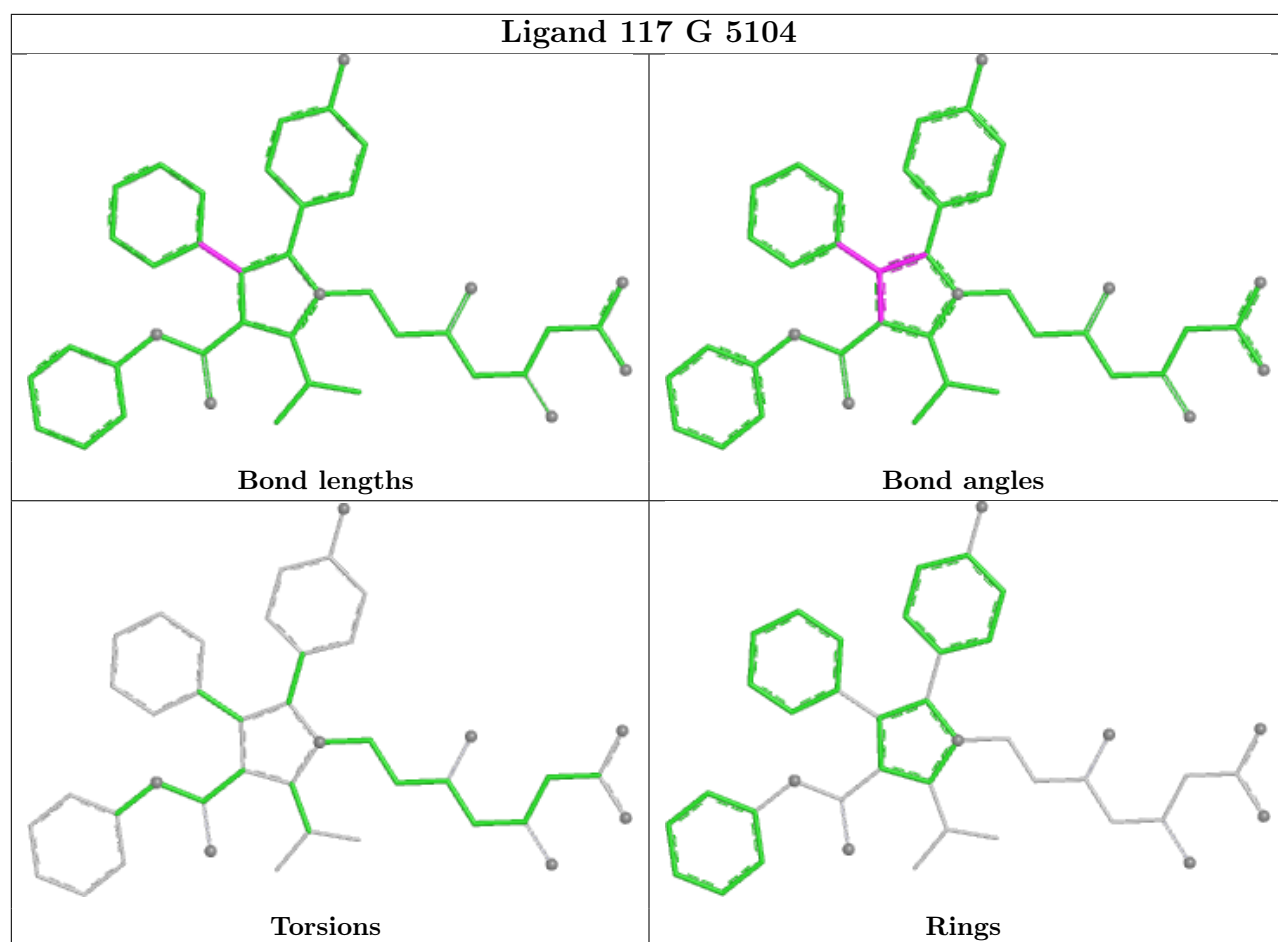


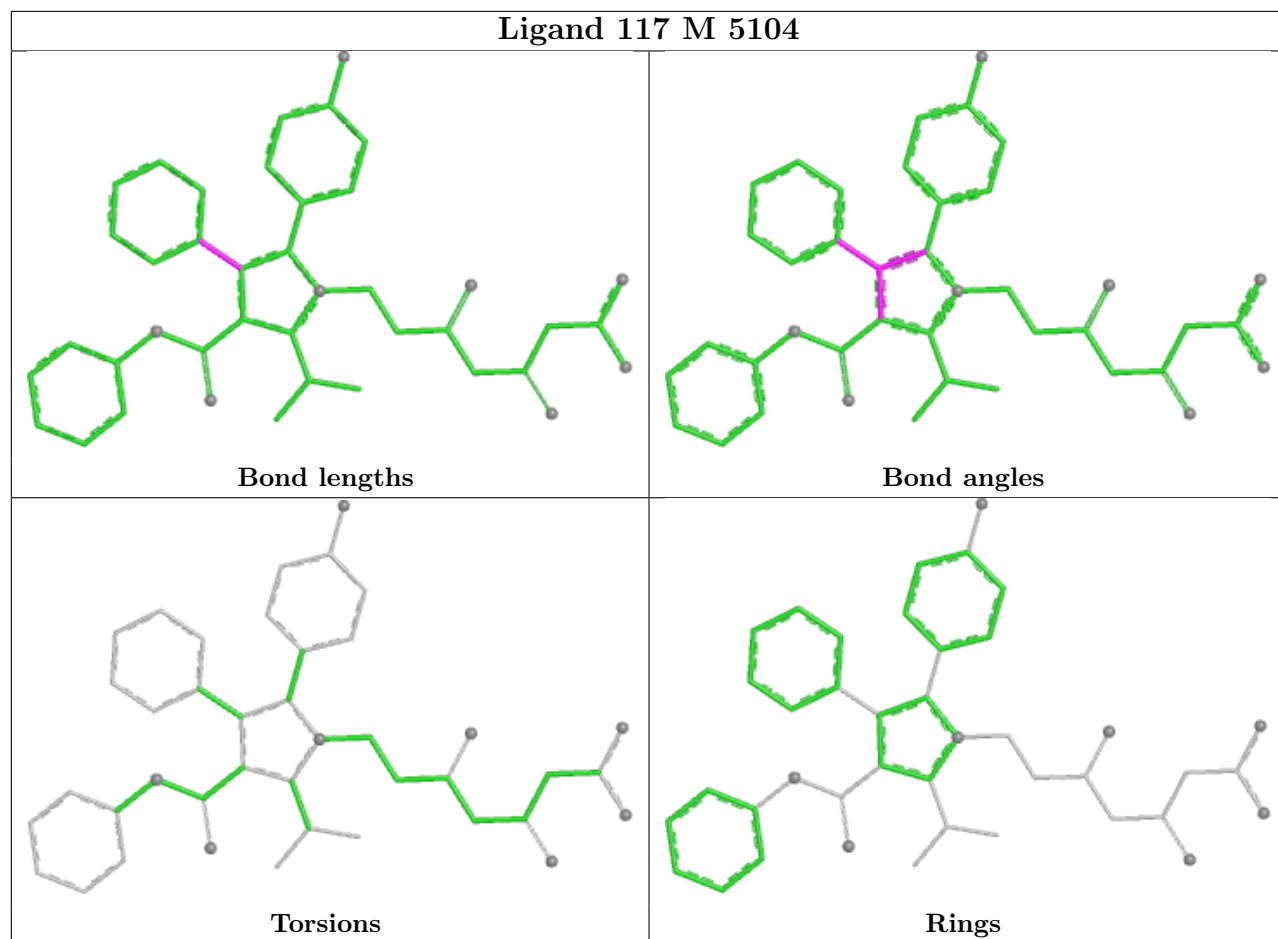




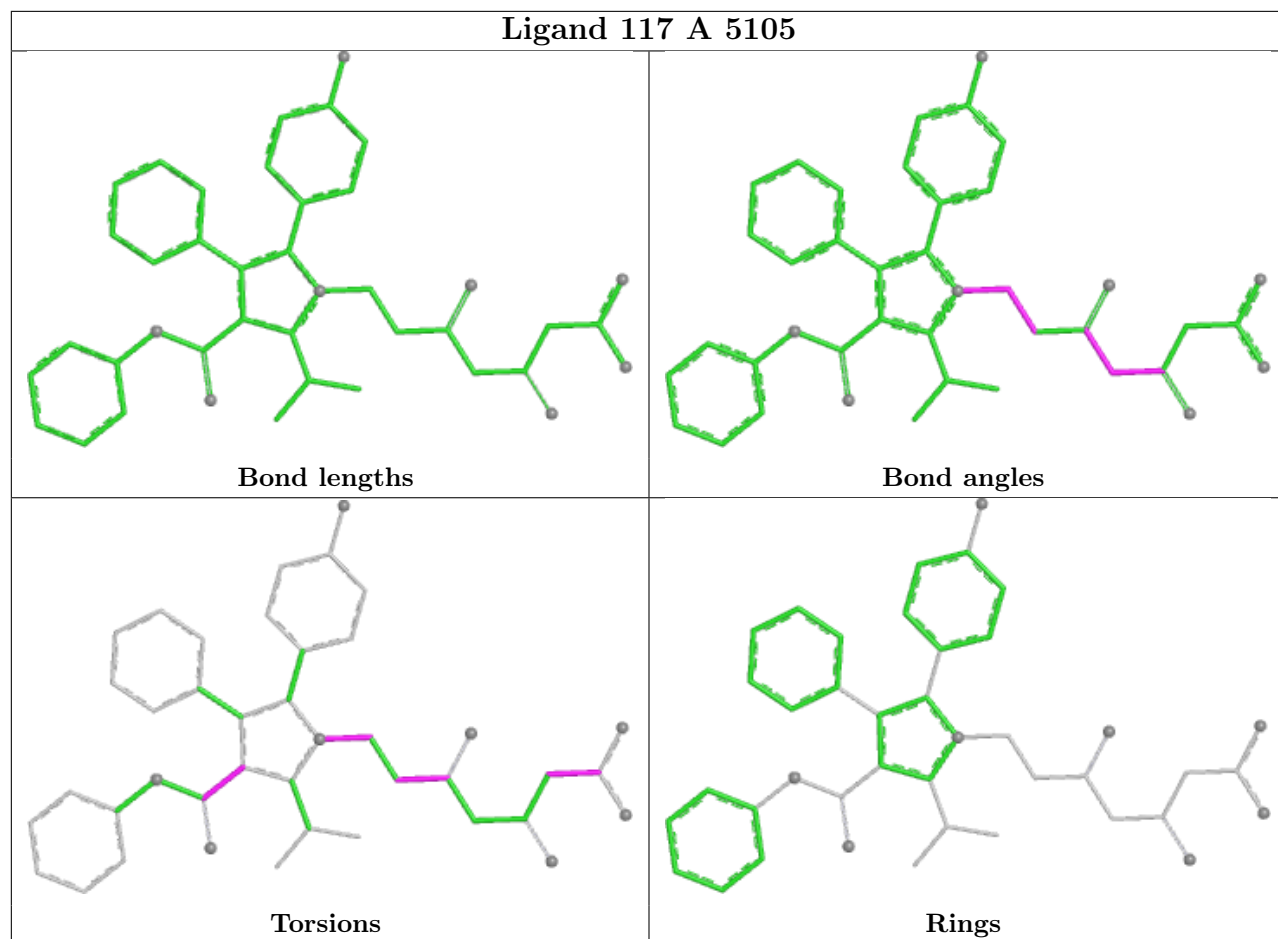


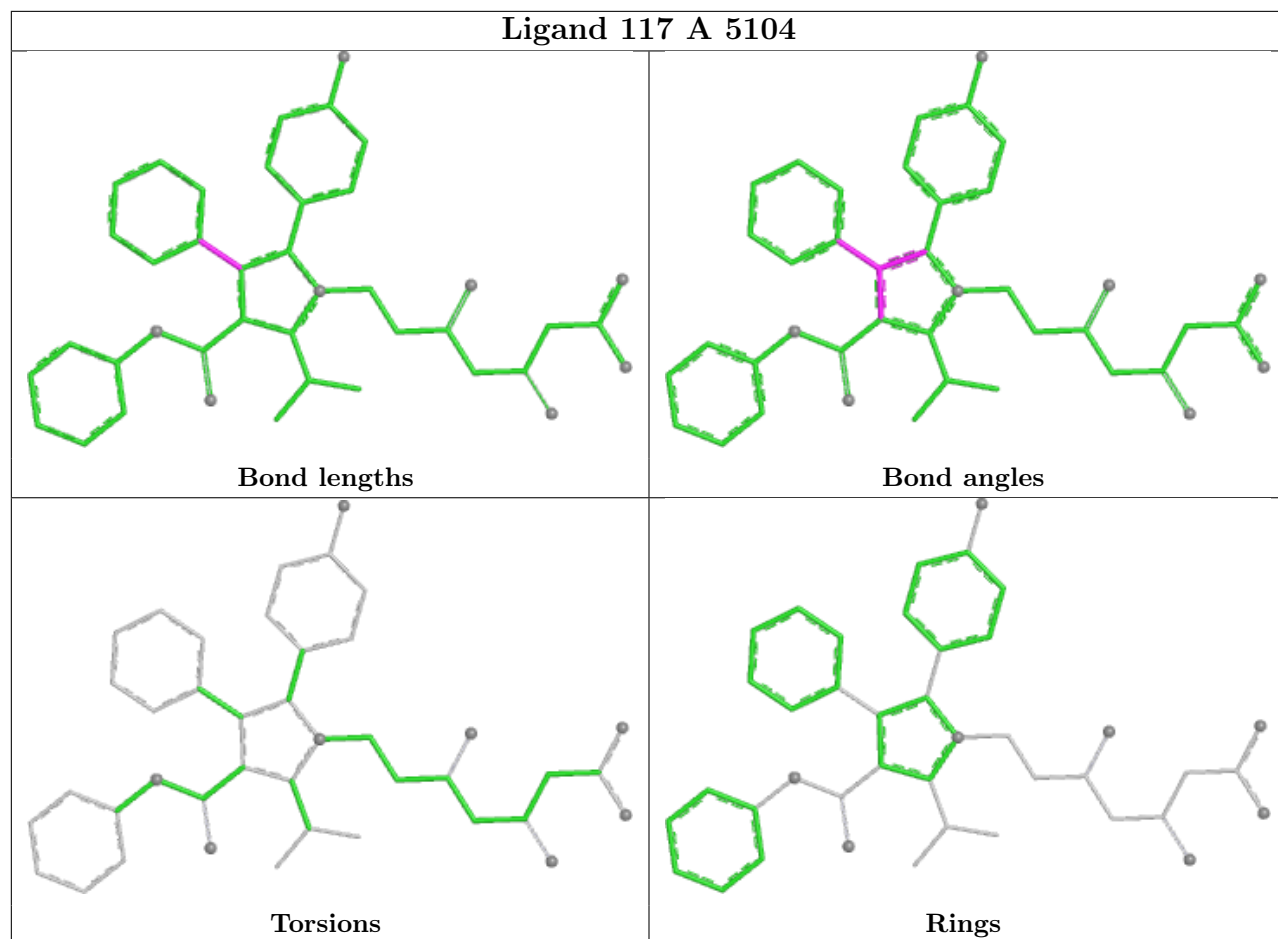


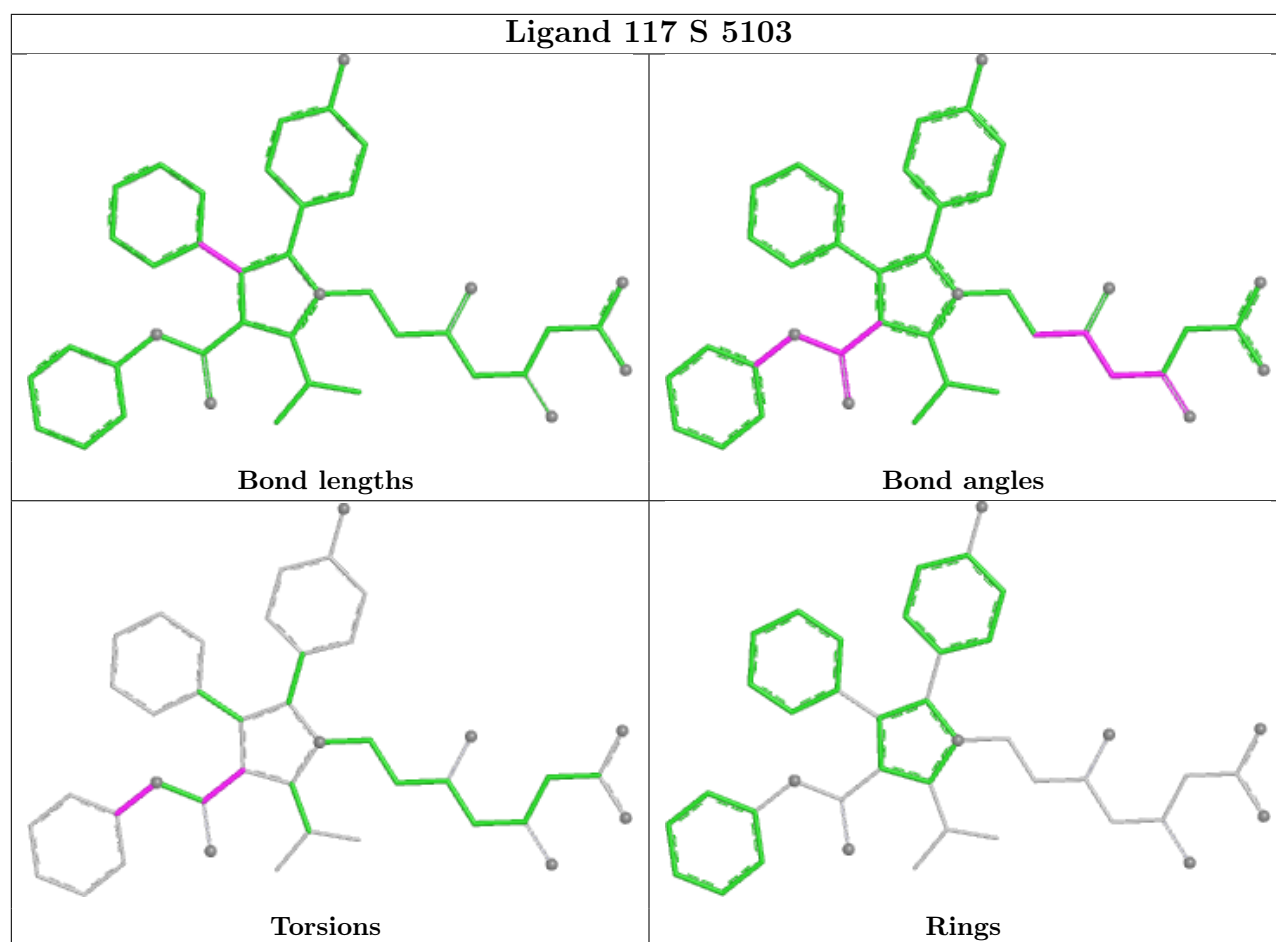




Ligand 117 A 5105







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.

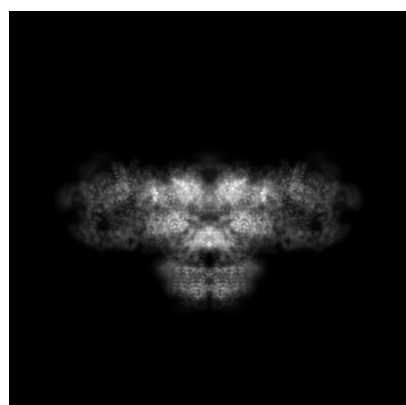
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-70589. These allow visual inspection of the internal detail of the map and identification of artifacts.

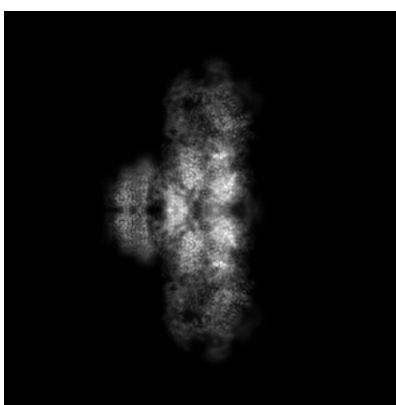
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

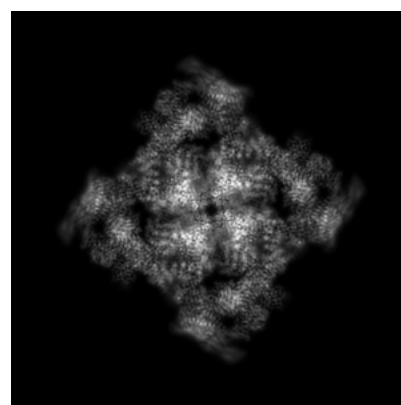
6.1.1 Primary map



X



Y



Z

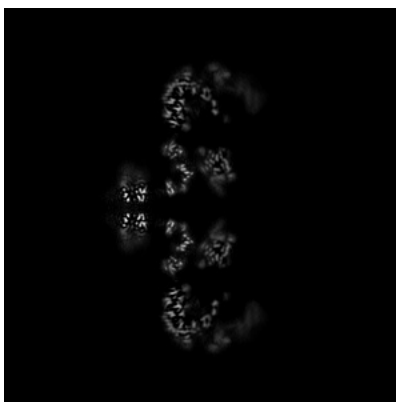
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

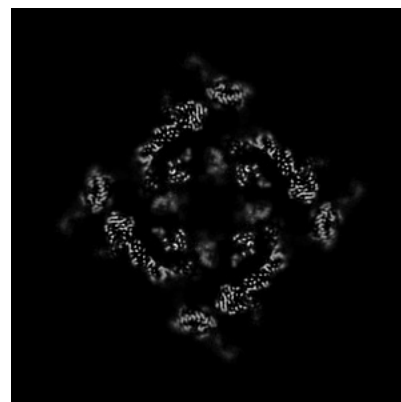
6.2.1 Primary map



X Index: 256



Y Index: 256



Z Index: 256

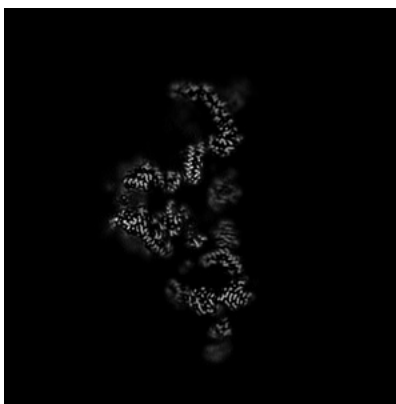
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

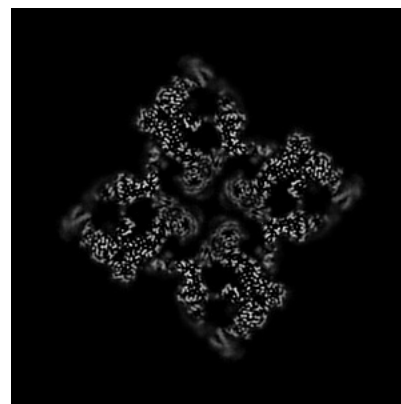
6.3.1 Primary map



X Index: 227



Y Index: 227

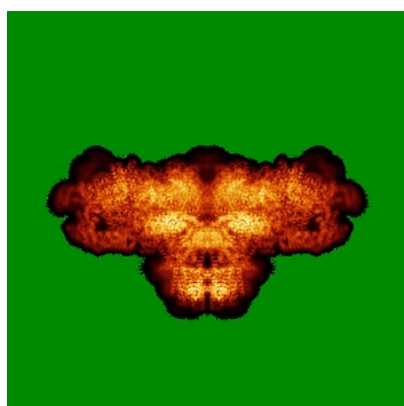


Z Index: 282

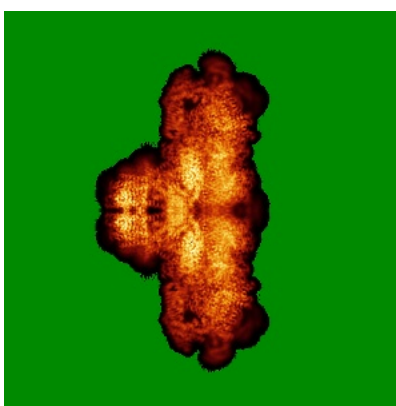
The images above show the largest variance slices of the map in three orthogonal directions.

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

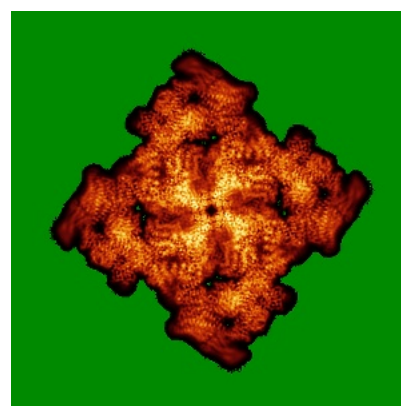
6.4.1 Primary map



X



Y

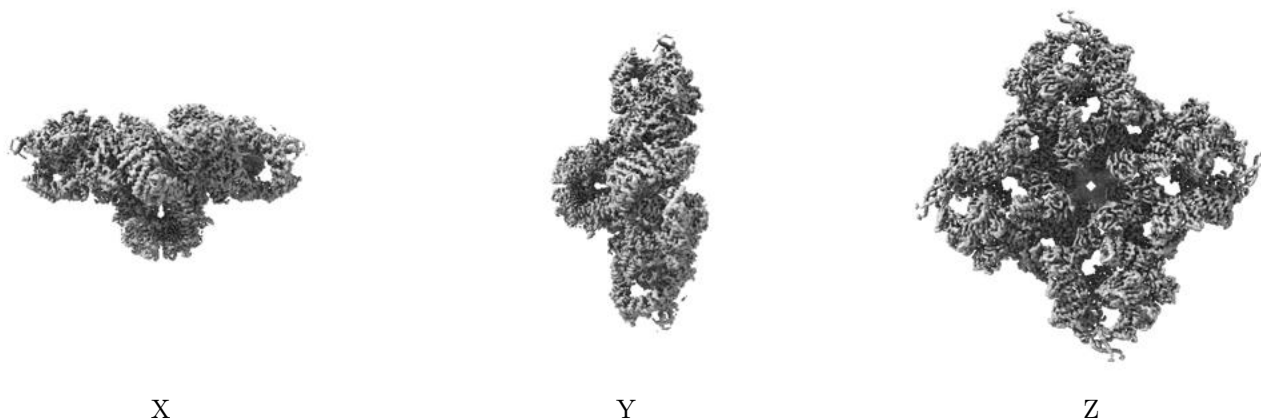


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.123. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

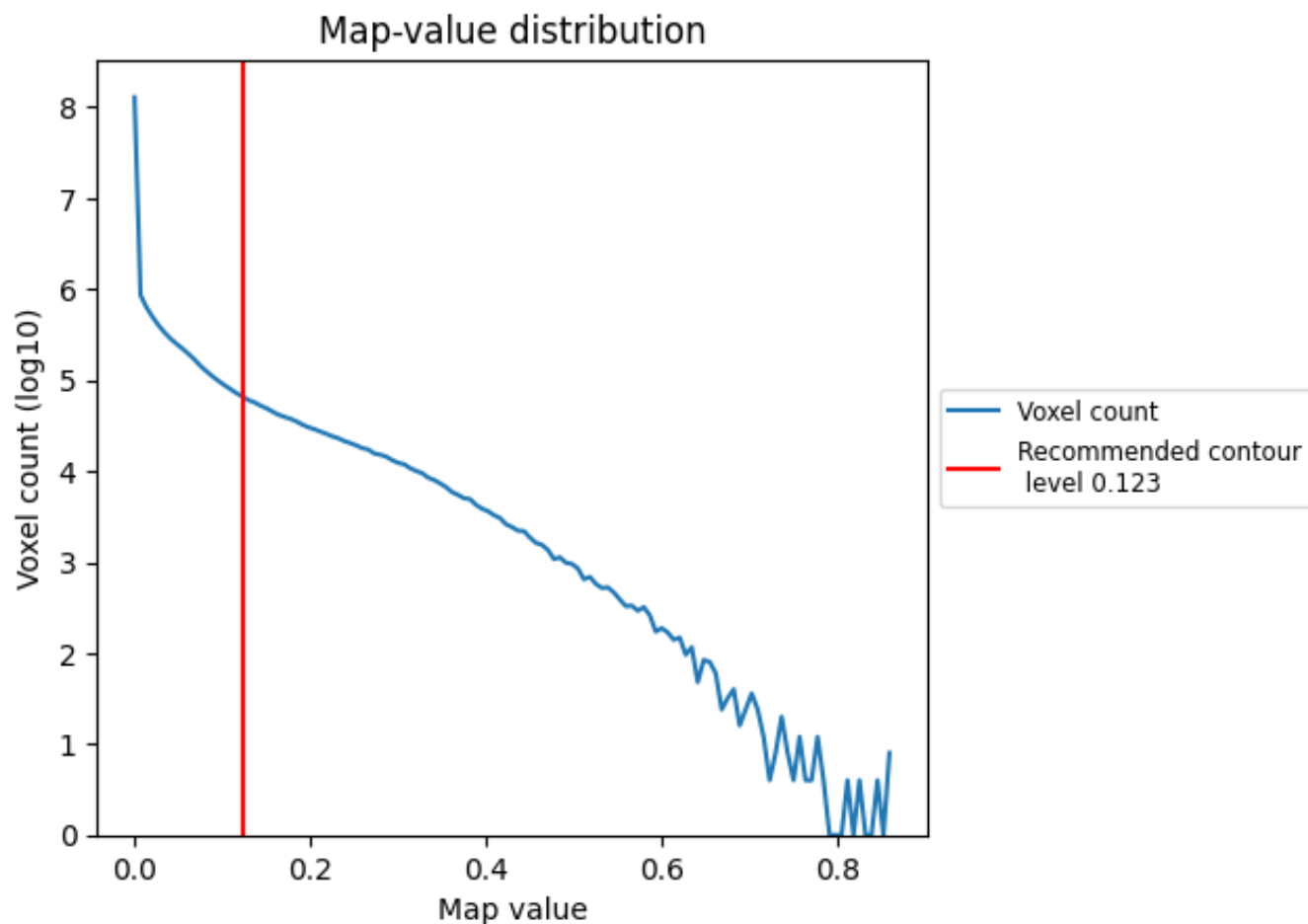
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

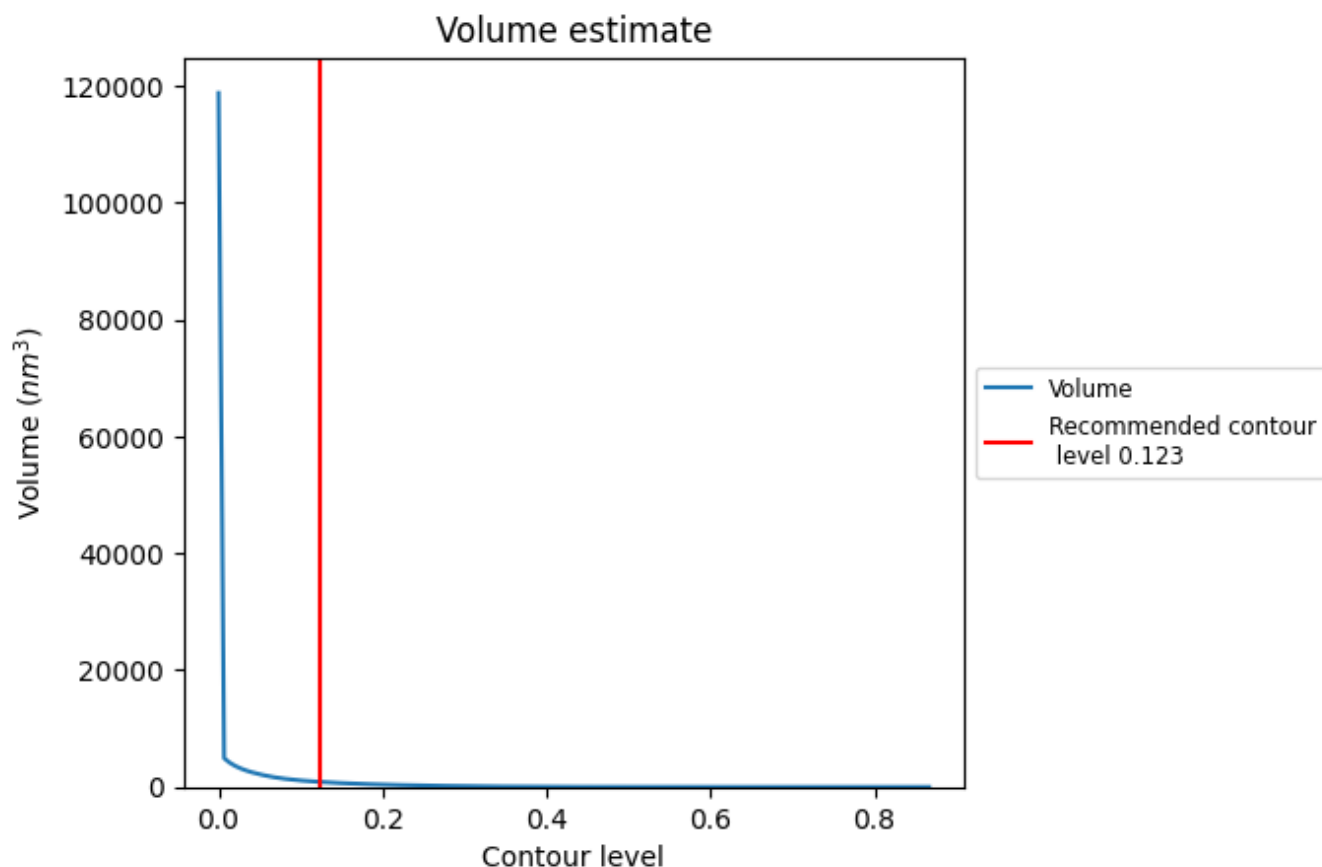
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

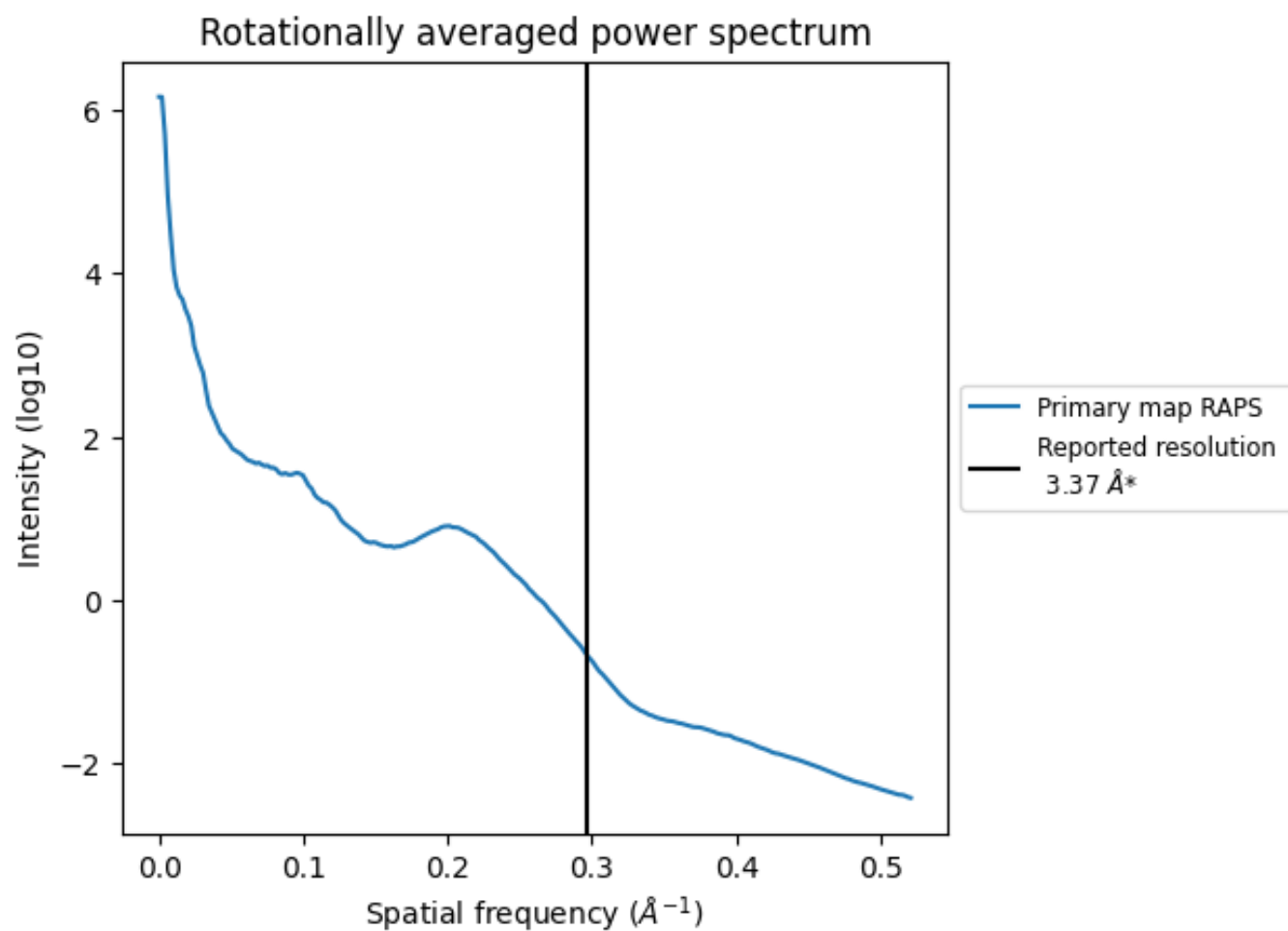
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 869 nm³; this corresponds to an approximate mass of 785 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 0.297 Å⁻¹

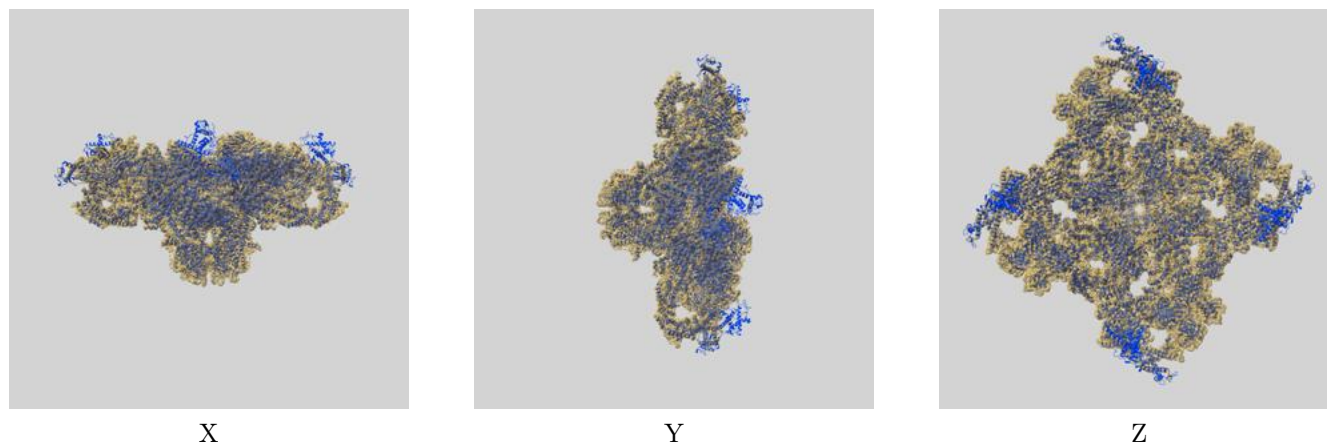
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

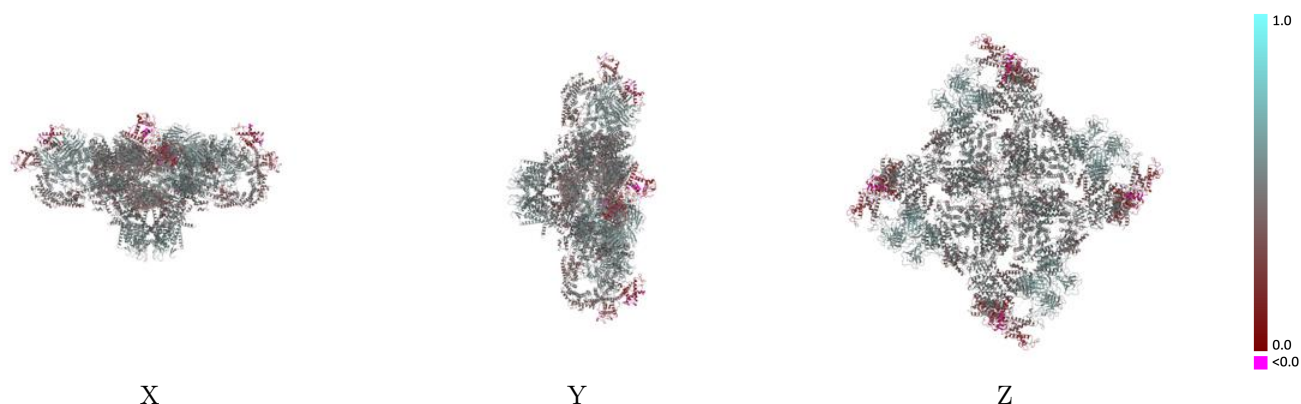
This section contains information regarding the fit between EMDB map EMD-70589 and PDB model 9OL4. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



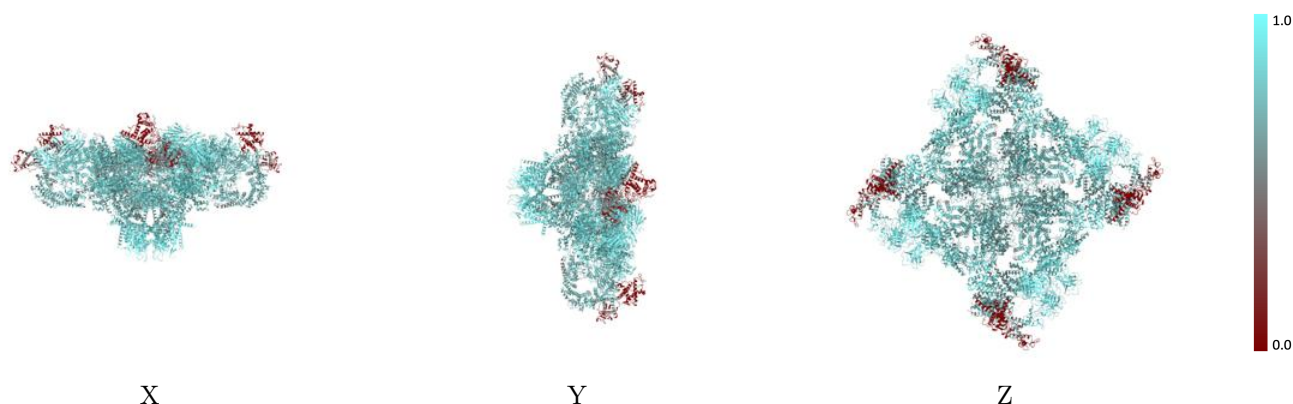
The images above show the 3D surface view of the map at the recommended contour level 0.123 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



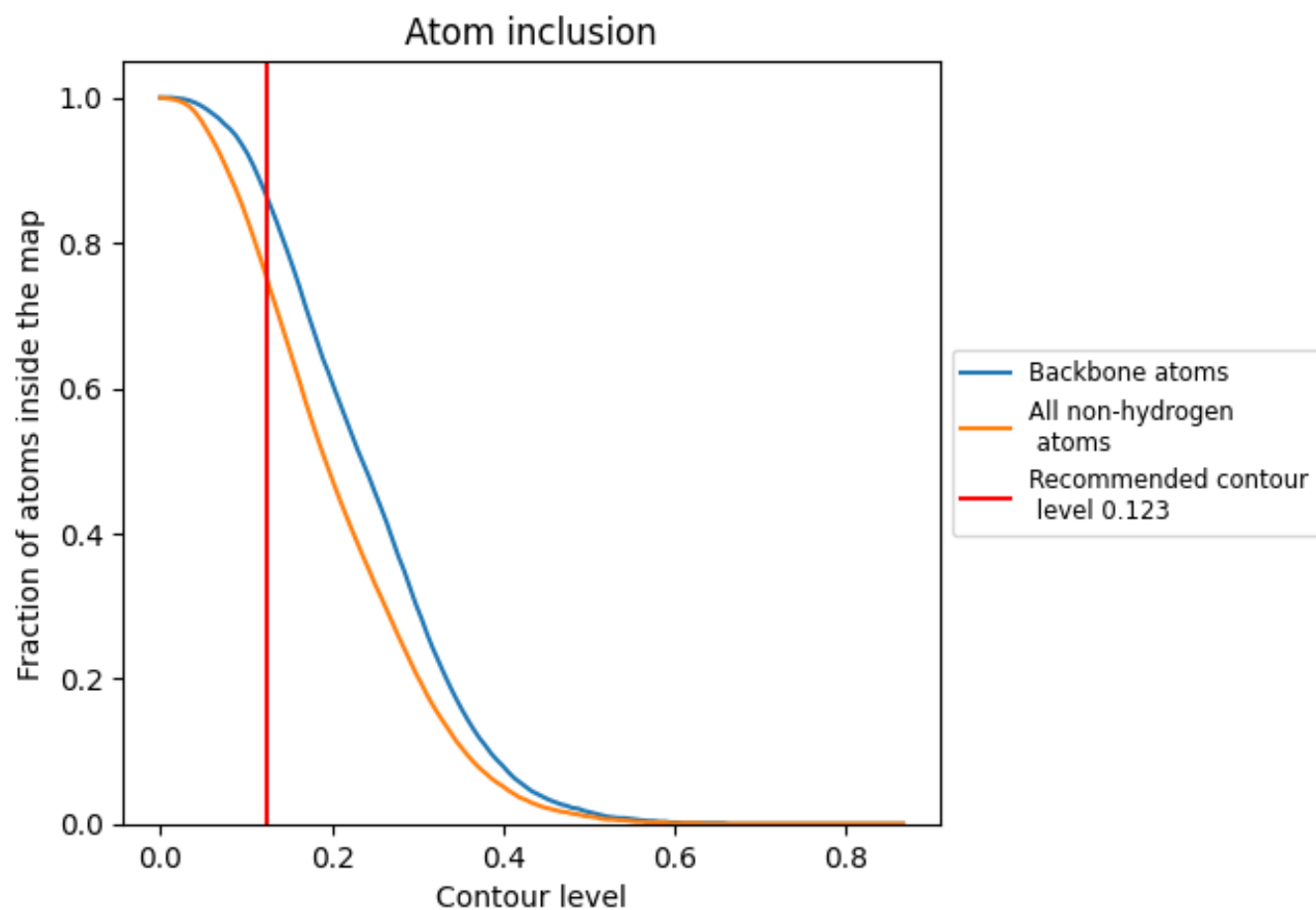
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.123).

9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 76% 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 (0.123) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7560	0.4620
A	0.7530	0.4600
B	0.8570	0.5390
G	0.7530	0.4600
H	0.8570	0.5390
M	0.7530	0.4600
N	0.8570	0.5410
S	0.7530	0.4610
T	0.8570	0.5400

1.0

0.0

<0.0