



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 05:10 AM UTC

PDB ID : 8RRT / pdb_00008rrt
EMDB ID : EMD-19464
Title : Structure of rabbit RyR1 reconstituted into lipid liposomes in open state in complex with FKBP and Nb9657
Authors : Li, C.; Efremov, R.G.
Deposited on : 2024-01-23
Resolution : 4.60 Å(reported)

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

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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:

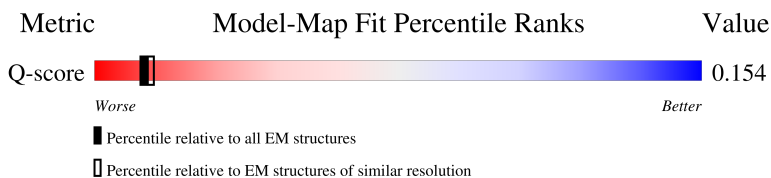
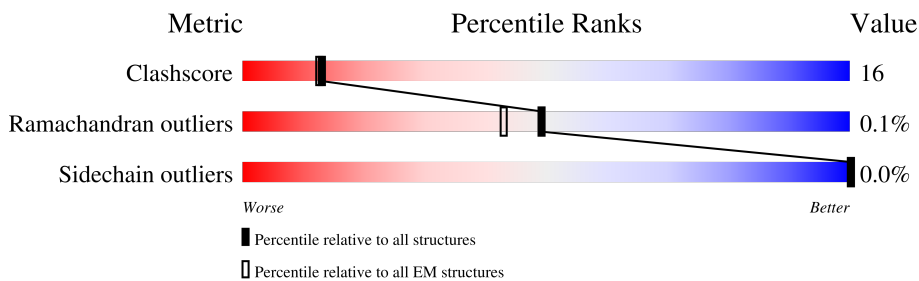
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 i

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

The reported resolution of this entry is 4.60 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	2407 (4.10 - 5.10)

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	B	5027	
1	E	5027	
1	G	5027	
1	J	5027	

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Mol	Chain	Length	Quality of chain
2	A	107	 65% 35%
2	D	107	 64% 36%
2	H	107	 63% 37%
2	I	107	 63% 37%
3	C	137	 51% 41% 8%
3	F	137	 50% 42% 8%
3	K	137	 52% 40% 8%
3	M	137	 55% 36% 8%

2 Entry composition i

There are 7 unique types of molecules in this entry. The entry contains 143740 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
			Total	C	N	O	S		
1	B	4319	34103	21737	5881	6261	224	1	0
1	E	4319	34103	21737	5881	6261	224	1	0
1	G	4319	34103	21737	5881	6261	224	1	0
1	J	4319	34103	21737	5881	6261	224	1	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	A	107	818	516	144	154	4	0	0
2	D	107	818	516	144	154	4	0	0
2	H	107	818	516	144	154	4	0	0
2	I	107	818	516	144	154	4	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	100	ASP	GLY	conflict	UNP Q8HYX6
D	100	ASP	GLY	conflict	UNP Q8HYX6
H	100	ASP	GLY	conflict	UNP Q8HYX6
I	100	ASP	GLY	conflict	UNP Q8HYX6

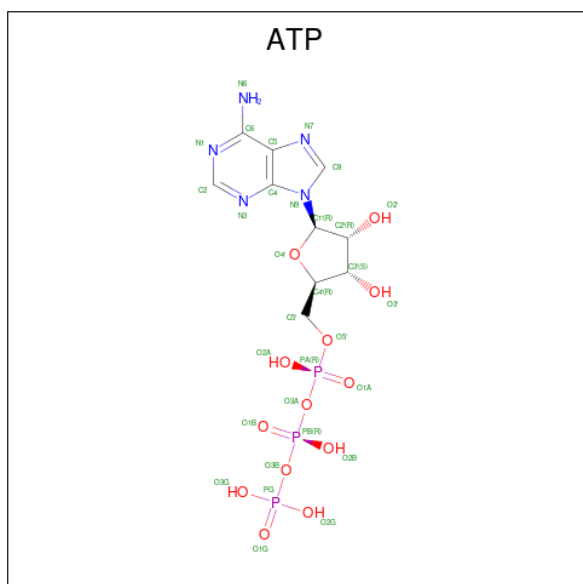
- Molecule 3 is a protein called Nanobody 9657.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	126	Total 967	C 597	N 170	O 195	S 5	0	0
3	F	126	Total 967	C 597	N 170	O 195	S 5	0	0
3	K	126	Total 967	C 597	N 170	O 195	S 5	0	0
3	M	126	Total 967	C 597	N 170	O 195	S 5	0	0

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
4	B	1	Total 1	Zn 1	0
4	E	1	Total 1	Zn 1	0
4	G	1	Total 1	Zn 1	0
4	J	1	Total 1	Zn 1	0

- Molecule 5 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃) (labeled as "Ligand of Interest" by depositor).



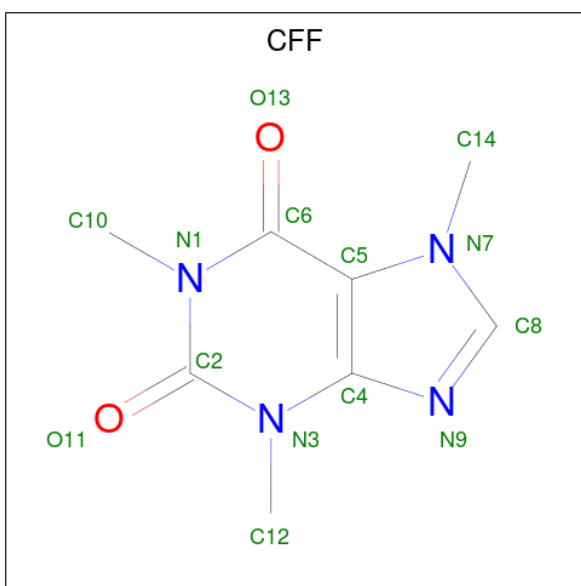
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
5	B	1	Total 31	C 10	N 5	O 13	P 3	0

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Mol	Chain	Residues	Atoms				AltConf	
			Total	C	N	O		P
5	E	1	Total 31	C 10	N 5	O 13	P 3	0
5	G	1	Total 31	C 10	N 5	O 13	P 3	0
5	J	1	Total 31	C 10	N 5	O 13	P 3	0

- Molecule 6 is CAFFEINE (CCD ID: CFF) (formula: $C_8H_{10}N_4O_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
6	B	1	Total 14	C 8	N 4	O 2	0
6	E	1	Total 14	C 8	N 4	O 2	0
6	G	1	Total 14	C 8	N 4	O 2	0
6	J	1	Total 14	C 8	N 4	O 2	0

- Molecule 7 is CALCIUM ION (CCD ID: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
			Total	Ca	
7	B	1	Total 1	Ca 1	0

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Mol	Chain	Residues	Atoms		AltConf
7	E	1	Total 1	Ca 1	0
7	G	1	Total 1	Ca 1	0
7	J	1	Total 1	Ca 1	0

H3734	ARG	ARG	ARG	ALA	ASN	GLY	GLU	ALA	GLU	GLU	S3747	S3752	E3755	K3756	E3757	M3758	E3759	K3760	Q3761	Y3765	Q3766	S3768	R3769	H3770	H3771	T3772	R3773	G3774	A3775	A3776	M3778	M3783	L3800	I3804	E3811	V3812	Q3813	Q3814	K3815	M3816	F3828	I3832	Q3833	A3834	I3835	M3836	Q3837	L3728	M3729	A3730				
H3445	D3531	L3532	L3533	M3534	L3535	A3536	K3537	L3538	R3539	Y3540	A3541	K3542	K3543	E3547	E3548	V3549	R3550	F3551	L3552	S3553	S3568	W3571	Q3572	M3573	A3574	L3575	Y3576	R3577	R3582	I3592	V3593	R3594	R3595	V3596	Q3597	H3605	L3606	F3612	TYR	LYS	SER	LYS	LYS	ALA	VAL	TRP	HIS	LYS	LEU	SER	LYS	GLN		
L3354	E3337	E3338	L3246	I3357	V3161	Q3162	V3163	R3093	F3094	S3164	C3165	Y3263	T3264	E3265	M3266	F3267	H3268	V3269	I3270	L3274	M3275	M3276	Y3280	L3281	F3282	L3315	L3316	G3317	R3318	L3319	L3320	R3321	L3322	V3324	H3325	N3326	L3327	A3332	T3333	M3334	K3335	R3337	L3338	A3339	F3340	R3341	M3342	Q3343	P3344	L3345	V3346	E3352	L3353	Y3444
L3354	H3357	I3359	P3360	T3361	I3362	L3365	L3366	K3367	K3371	K3384	A3385	E3386	A3387	E3388	E3391	V3394	R3395	F3398	S3399	V3400	L3401	C3402	R3403	D3404	R3405	Y3406	Y3409	I3413	R3414	Y3415	V3416	D3417	R3418	R3419	R3420	W3423	E3433	R3436	M3437	A3438	G3439	P3440	I3441	F3442	I3443	Y3444	L3514	K3515	L3516	M3517	L3518	P3519	M3524	Q3530
K3482	F2998	A2999	K3000	I3001	L3002	Q2931	M2932	M2933	G2934	N2935	Q2936	Y2937	T2938	R2939	N3011	N3012	L3018	S3019	T3020	P3021	A3031	S3032	K3033	E3034	E3035	K3036	E3037	L3042	K3045	L3046	A3047	K3048	L3049	R3051	H3052	R3053	V3054	F3057	D3060	V3065	H3069	I3070	R3073	S3074	L3075	A3076	A3077	R3078	Y3079	V3080	M3081			
L2826	L2927	K2928	F2929	L2930	Q2931	M2932	M2933	G2934	N2935	Q2936	Y2937	T2938	R2939	N3011	N3012	L3018	S3019	T3020	P3021	A3031	S3032	K3033	E3034	E3035	K3036	E3037	L3042	K3045	L3046	A3047	K3048	L3049	R3051	H3052	R3053	V3054	F3057	D3060	V3065	H3069	I3070	R3073	S3074	L3075	A3076	A3077	R3078	Y3079	V3080	M3081				
L2826	L2927	K2928	F2929	L2930	Q2931	M2932	M2933	G2934	N2935	Q2936	Y2937	T2938	R2939	N3011	N3012	L3018	S3019	T3020	P3021	A3031	S3032	K3033	E3034	E3035	K3036	E3037	L3042	K3045	L3046	A3047	K3048	L3049	R3051	H3052	R3053	V3054	F3057	D3060	V3065	H3069	I3070	R3073	S3074	L3075	A3076	A3077	R3078	Y3079	V3080	M3081				
K3082	F2998	A2999	K3000	I3001	L3002	Q2931	M2932	M2933	G2934	N2935	Q2936	Y2937	T2938	R2939	N3011	N3012	L3018	S3019	T3020	P3021	A3031	S3032	K3033	E3034	E3035	K3036	E3037	L3042	K3045	L3046	A3047	K3048	L3049	R3051	H3052	R3053	V3054	F3057	D3060	V3065	H3069	I3070	R3073	S3074	L3075	A3076	A3077	R3078	Y3079	V3080	M3081			
F3152	G3153	V3156	I3157	V3161	Q3162	V3163	R3093	F3094	S3164	C3165	Y3263	T3264	E3265	M3266	F3267	H3268	V3269	I3270	L3274	M3275	M3276	Y3280	L3281	F3282	L3315	L3316	G3317	R3318	L3319	L3320	R3321	L3322	V3324	H3325	N3326	L3327	A3332	T3333	M3334	K3335	R3337	L3338	A3339	F3340	R3341	M3342	Q3343	P3344	L3345	V3346	E3352	L3353	Y3444	
L3354	H3357	I3359	P3360	T3361	I3362	L3365	L3366	K3367	K3371	K3384	A3385	E3386	A3387	E3388	E3391	V3394	R3395	F3398	S3399	V3400	L3401	C3402	R3403	D3404	R3405	Y3406	Y3409	I3413	R3414	Y3415	V3416	D3417	R3418	R3419	R3420	W3423	E3433	R3436	M3437	A3438	G3439	P3440	I3441	F3442	I3443	Y3444	L3514	K3515	L3516	M3517	L3518	P3519	M3524	Q3530
H3445	D3531	L3532	L3533	M3534	L3535	A3536	K3537	L3538	R3539	Y3540	A3541	K3542	K3543	E3547	E3548	V3549	R3550	F3551	L3552	S3553	S3568	W3571	Q3572	M3573	A3574	L3575	Y3576	R3577	R3582	I3592	V3593	R3594	R3595	V3596	Q3597	H3605	L3606	F3612	TYR	LYS	SER	LYS	LYS	ALA	VAL	TRP	HIS	LYS	LEU	SER	LYS	GLN		
ARG	ARG	ALA	VAL	VAL	ALA	CYS	PHE	ARG	ARG	T3639	P3640	L3641	L3644	L3644	P3645	R3648	K3658	L3662	L3663	T3664	E3670	D3671	R3672	M3673	R3674	G3675	D3676	A3677	K3679	Q3683	V3690	K3693	K3694	P3695	H3699	Q3700	L3701	V3702	E3718	D3719	Y3720	L3721	Y3722	M3723	A3724	L3728	M3729	A3730						
H3734	E3740	ASN	GLY	GLU	ALA	GLU	GLU	GLU	GLU	T3639	P3640	L3641	L3644	L3644	P3645	R3648	K3658	L3662	L3663	T3664	E3670	D3671	R3672	M3673	R3674	G3675	D3676	A3677	K3679	Q3683	V3690	K3693	K3694	P3695	H3699	Q3700	L3701	V3702	E3718	D3719	Y3720	L3721	Y3722	M3723	A3724	L3728	M3729	A3730						
H3734	E3740	ASN	GLY	GLU	ALA	GLU	GLU	GLU	GLU	T3639	P3640	L3641	L3644	L3644	P3645	R3648	K3658	L3662	L3663	T3664	E3670	D3671	R3672	M3673	R3674	G3675	D3676	A3677	K3679	Q3683	V3690	K3693	K3694	P3695	H3699	Q3700	L3701	V3702	E3718	D3719	Y3720	L3721	Y3722	M3723	A3724	L3728	M3729	A3730						
H3734	E3740	ASN	GLY	GLU	ALA	GLU	GLU	GLU	GLU	T3639	P3640	L3641	L3644	L3644	P3645	R3648	K3658	L3662	L3663	T3664	E3670	D3671	R3672	M3673	R3674	G3675	D3676	A3677	K3679	Q3683	V3690	K3693	K3694	P3695	H3699	Q3700	L3701	V3702	E3718	D3719	Y3720	L3721	Y3722	M3723	A3724	L3728	M3729	A3730						
H3734	E3740	ASN	GLY	GLU	ALA	GLU	GLU	GLU	GLU	T3639	P3640	L3641	L3644	L3644	P3645	R3648	K3658	L3662	L3663	T3664	E3670	D3671	R3672	M3673	R3674	G3675	D3676	A3677	K3679	Q3683	V3690	K3693	K3694	P3695	H3699	Q3700	L3701	V3702	E3718	D3719	Y3720	L3721	Y3722	M3723	A3724	L3728	M3729	A3730						
H3734	E3740	ASN	GLY	GLU	ALA	GLU	GLU	GLU	GLU	T3639	P3640	L3641	L3644	L3644	P3645	R3648	K3658	L3662	L3663	T3664	E3670	D3671	R3672	M3673	R3674	G3675	D3676	A3677	K3679	Q3683	V3690	K3693	K3694	P3695	H3699	Q3700	L3701	V3702	E3718	D3719	Y3720	L3721	Y3722	M3723	A3724	L3728	M3729	A3730						
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H3734	E3740	ASN	GLY	GLU	ALA	GLU	GLU	GLU	GLU	T3639	P3640	L3641	L3644	L3644	P3645	R3648	K3658	L3662	L3663	T3664	E3670	D3671	R3672	M3673	R3674	G3675	D3676	A3677	K3679	Q3683	V3690	K3693	K3694	P3695	H3699	Q3700	L3701	V3702	E3718	D3719	Y3720	L3721	Y3722	M3723	A3724	L3728	M3729	A3730						
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H3734	E3740	ASN	GLY	GLU	ALA	GLU	GLU	GLU	GLU	T3639	P3640	L3641	L3644	L3644	P3645	R3648	K3658	L3662	L3663	T3664	E3670	D3671	R3672	M3673	R3674	G3675	D3676	A3677	K3679	Q3683	V3690	K3693	K3694	P3695	H3699	Q3700	L3701	V3702	E3718	D3719	Y3720	L3721	Y3722	M3723	A3724	L3728	M3729	A3730						
H3734	E3740	ASN	GLY	GLU	ALA	GLU	GLU	GLU	GLU	T3639	P3640	L3641	L3644	L3644	P3645	R3648	K3658	L3662	L3663	T3664	E3670	D3671	R3672	M3673	R3674	G3675	D3676	A3677	K3679	Q3683	V3690	K3693	K3694	P3695	H3699	Q3700	L3701	V3702	E3718	D3719	Y3720	L3721	Y3722	M3723	A3724	L3728	M3729	A3730						
H3734	E3740	ASN	GLY	GLU	ALA	GLU	GLU	GLU	GLU	T3639	P3640	L3641	L3644	L3644	P3645	R3648	K3658	L3662	L3663	T3664	E3670	D3671	R3672	M3673	R3674	G3675	D3676	A3677	K3679	Q3683	V3690	K3693	K3694	P3695	H3699	Q3700	L3701	V3702	E3718	D3719	Y3720	L3721	Y3722	M3723	A3724	L3728	M3729	A3730						
H3734	E3740	ASN	GLY	GLU	ALA	GLU	GLU	GLU	GLU	T3639	P3640	L3641	L3644	L3644	P3645	R3648	K3658	L3662	L3663	T3664	E3670	D3671	R3672	M3673	R3674	G3675	D3676	A3677	K3679	Q3683	V3690	K3693	K3694	P3695	H3699	Q3700	L3701	V3702	E3718	D3719	Y3720	L3721	Y3722	M3723	A3724	L3728	M3729	A3730						
H3734	E3740	ASN	GLY	GLU	ALA	GLU	GLU	GLU	GLU	T3639	P3640	L3641	L3644	L3644	P3645	R3648	K3658	L3662	L3663	T3664	E3670	D3671	R3672	M3673	R3674	G3675	D3676	A3677	K3679	Q3683	V3690	K3693	K3694	P3695	H3699	Q3700	L3701	V3702	E3718	D3719	Y3720	L3721	Y3722	M3723	A3724	L3728	M3729	A3730						
H3734	E3740	ASN	GLY	GLU	ALA	GLU	GLU	GLU	GLU	T3639	P3640	L3641	L3644	L3644	P3645	R3648	K3658	L3662	L3663	T3664	E3670	D3671	R3672	M3673	R3674	G3675	D3676	A3677	K3679	Q3683	V3690	K3693	K3694	P3695	H3699	Q3700	L3701	V3702	E3718	D3719	Y3720	L3721	Y3722	M3723	A3724	L3728	M3729	A3730						
H3734	E3740	ASN	GLY	GLU	ALA	GLU	GLU	GLU	GLU</																																													

V3841	L3842	K3959	Q3960	Q4043	F4132	GLU	LEU	MET	GLY	ASP	GLU	ASP	V4580	L4652	T4766	Y4909	E5016	
L3842	N3845	Q3960	V3961	M4044	Q4133	ASP	THR	PRO	GLY	GLY	GLU	GLU	Y4580	V4653	W4767	Y4909	W5016	
N3845	F3962	F3962	F3962	D4046	E4134	GLY	ALA	ASP	PRO	ASP	GLU	GLU	K4581	V4654	W4767	R4913	W5019	
F3847	F3962	F3962	F3962	D4046	E4134	GLY	ARG	THR	PHE	ARG	ASN	ASN	V4582	F4655	L4771	V4914	D5020	
E3848	L3965	L3965	L3965	M4047	M4142	MET	ALA	SER	ARG	PRO	GLY	GLY	D4584	C4657	K4774	I4918	P5023	
Q3850	T3966	T3966	T3966	L4048	M4142	GLU	ALA	ASP	PRO	LYS	LYS	LYS	F4587	I4658	Y4775	I4918	S5037	
R3850	E3967	E3967	E3967	V4049	T4148	ALA	THR	ASP	GLY	GLY	GLU	GLU	P4587	I4659	Q4776	I4927		
N3870	Y3968	Y3968	Y3968	M4057	M4149	ALA	ALA	VAL	ALA	ALA	VAL	VAL	G4660	G4661	K4779	I4931		
K3873	Y3968	Y3968	Y3968	F4061	S4151	ALA	LEU	GLY	GLY	GLY	GLY	GLY	A4661	Y4661	V4782	I4931		
V3874	Y3968	Y3968	Y3968	F4062	S4151	ALA	LEU	GLY	GLY	GLY	GLY	GLY	K4664	K4664	L4783	L4935		
K3875	Y3968	Y3968	Y3968	D4063	E4152	ALA	LEU	GLN	GLY	GLY	GLY	GLY	K4665	V4666	L4783	L4935		
D3877	Y3968	Y3968	Y3968	M4064	Y4177	GLU	LEU	PRO	ASP	ASP	PRO	PRO	V4666	V4666	S4788	A4959		
F3880	Q3970	Q3970	Q3970	K4067	R4180	GLY	TRP	ALA	MET	GLY	GLY	GLY	S4788	P4667	M4796	E4942		
L3884	Q3970	Q3970	Q3970	F4077	R4180	ALA	VAL	GLY	GLY	GLY	GLY	GLY	I4670	I4670	M4796	E4942		
F3885	Q3977	Q3977	Q3977	D4078	M4184	ALA	VAL	GLY	GLY	THR	THR	THR	I4670	I4670	L4800	L4943		
R3886	Q3977	Q3977	Q3977	Y4079	R4192	ALA	ARG	ASP	ALA	PRO	LYS	LYS	R4673	R4673	H4803	Q4946		
F3887	Q3977	Q3977	Q3977	D4080	S4198	ALA	ALA	ALA	ALA	ALA	ALA	ALA	E4674	E4674	H4803	Q4946		
L3888	Q3986	Q3986	Q3986	Y4081	E4199	ALA	ALA	GLY	GLY	GLY	GLY	GLY	K4675	K4675	F4807	E4948		
Q3889	D3987	D3987	D3987	I4088	T4200	GLY	ALA	ALA	ALA	ALA	ALA	ALA	E4676	E4676	F4807	Q4949		
L3890	D3987	D3987	D3987	S4089	T4200	VAL	ALA	THR	THR	THR	THR	THR	A4678	A4678	K4821	K4951		
E3893	H3994	H3994	H3994	K4091	E4206	ALA	ALA	GLY	GLY	GLY	GLY	GLY	R4679	R4679	T4822	E4952		
Q3906	F3995	F3995	F3995	D4092	M4207	ALA	ALA	GLY	GLY	GLY	GLY	GLY	K4680	K4680	L4823	D4953		
T3912	F3996	F3996	F3996	F4093	M4207	ALA	ALA	GLY	GLY	GLY	GLY	GLY	C4693	C4693	T4825	E4955		
C3918	F3997	F3997	F3997	A4096	Q4209	ALA	ALA	GLY	GLY	GLY	GLY	GLY	D4696	D4696	T4826	T4956		
T3919	H3998	H3998	H3998	S4099	V4210	ALA	THR	ASP	ILE	LEU	LEU	LEU	A4697	A4697	L4827	K4957		
L3923	M3999	M3999	M3999	A4099	V4210	ALA	ALA	ASP	ALA	ALA	ALA	ALA	V4698	V4698	V4830	F4958		
L3926	M4000	M4000	M4000	F4103	E4229	ALA	ALA	GLY	GLY	GLY	GLY	GLY	K4698	K4698	V4830	F4959		
S3929	L4003	L4003	L4003	T4104	E4232	ALA	ALA	ASP	ASP	ASP	ASP	ASP	G4699	G4699	N4833	I4960		
Y3934	L4009	L4009	L4009	C4105	E4232	ALA	ALA	ASP	GLY	GLY	GLY	GLY	Q4700	Q4700	N4833	I4960		
Y3937	L4013	L4013	L4013	L4108	T4241	ALA	PHE	GLU	GLY	GLY	GLY	GLY	W4701	W4701	V4838	E4981		
D3941	E4015	E4015	E4015	L4112	F4243	ALA	GLY	VAL	VAL	VAL	VAL	VAL	D4702	D4702	V4838	E4982		
V3942	L4016	L4016	L4016	L4118	E4244	ALA	GLY	HIS	LEU	LEU	LEU	LEU	R4703	R4703	V4841	H4983		
I3943	D4018	D4018	D4018	S4115	M4245	ALA	LEU	GLY	LEU	LEU	LEU	LEU	L4704	L4704	V4841	Y4988		
E3944	L4019	L4019	L4019	D4118	M4245	ALA	LEU	GLY	VAL	VAL	VAL	VAL	F4719	F4719	F4856	F4991		
Q3946	K4021	K4021	K4021	M4122	E4253	ALA	LEU	GLY	VAL	VAL	VAL	VAL	D4725	D4725	F4856	L4992		
K3948	M4023	M4023	M4023	I4123	S4252	ALA	LEU	GLY	GLY	GLY	GLY	GLY	L4726	L4726	F4859	L4992		
R3949	V4024	V4024	V4024	N4124	E4253	ALA	VAL	GLY	GLY	GLY	GLY	GLY	D4728	D4728	R4860	I4996		
M3955	M4025	M4025	M4025	F4125	E4253	ALA	VAL	GLY	GLY	GLY	GLY	GLY	K4727	K4727	Y4863	I4997		
A3958	L4027	L4027	L4027	E4126	E4253	ALA	VAL	GLY	GLY	GLY	GLY	GLY	H4728	H4728	M4864	K4998		
	L4031	L4031	L4031	F4128	E4253	ALA	VAL	GLY	GLY	GLY	GLY	GLY	M4627	M4627	K4865	D4999		
	M4039	M4039	M4039	F4129	E4253	ALA	VAL	GLY	GLY	GLY	GLY	GLY	Y4630	Y4630	C4876	E5002		
	I4040	I4040	I4040	N4130	E4253	ALA	VAL	GLY	GLY	GLY	GLY	GLY	F4631	F4631	D4877	H5003		
	A3958	A3958	A3958	R4131	E4253	ALA	VAL	GLY	GLY	GLY	GLY	GLY	L4632	L4632	M4879	E5007		
													A4642	A4642	M4880	Y5009		
													L4646	L4646	M4743	Y5010		
													S4647	S4647	M4743	M5011		
													L4648	L4648	I4901	K5012		
													T4651	T4651	P4761	M5013		
															P4761	P4761	Y117	

● Molecule 1: Ryanodine receptor 1



V11	Q12	F13	T16	V21	L22	L35	L49	A63	I64	L69	E70	Q71	S72	L73	R76	Q79	L82	A83	N84	THR	VAL	GLU	ALA	GLY	VAL	SER	SER	GLN	GLY	G97	H98	R99	T100	L101	L102	Y103	A106	I107	L108	H111	A112	H113	S114	R115	M116	Y117
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V1552	W1437	VAL	E1093	I1013	A934	T888	V599	E463	PRO	F223	L118
T1557	R1438	GLU	A1094	R1017	L935	T888	L600	E463	PRO	H224	L121
Q1559	V1439	ALA	V1095	M1018	G936	T861	D601	E338	PRO	D228	L131
N1560	G1442	PRO	G1098	P1019	C937	L861	R615	Y341	PRO	C230	L134
V1561	Q1443	VAL	E1099	R1020	H938	L863	R622	L345	PRO	L231	D134
V1562	E1444	ARG	M1100	L1021	M941	L866	L625	C346	PRO	T232	L137
Q1563	P1445	ALA	R1101	L1022	E947	L867	L626	H350	PRO	V245	E144
F1564	W1449	ASN	A1105	Y1024	L950	E968	L626	G354	PRO	Y247	W147
E1565	W1450	GLN	P1106	R1025	L950	F757	R629	L355	PRO	G249	W148
Q1569	P1455	PRO	P1107	L1026	K951	R758	R629	T388	PRO	G250	M150
I1572	H1458	ALA	E1114	L1027	K952	G761	L633	L480	PRO	V252	H151
M1573	M1476	THR	L1115	T1031	T953	V764	Q694	L488	PRO	E248	W147
P1574	G1477	ASP	G1116	M1035	K954	G766	Q694	N488	PRO	G249	W148
L1575	G1477	GLU	E1119	R1036	R954	G766	L637	Y359	PRO	G250	M150
L1581	W1483	ASN	E1123	D1037	L955	F782	L638	A360	PRO	V252	H151
R1584	H1484	LYS	F1124	C1040	Y959	S782	M639	K365	PRO	H255	E159
S1485	S1485	LYS	N1125	Q1041	M960	F783	I648	L369	PRO	A256	G160
S1486	S1486	ARG	G1126	A1042	S962	H502	G651	L372	PRO	R261	K162
L1487	L1487	PRO	H1127	V1043	G964	G786	G651	K373	PRO	R261	V163
K1488	L1487	PHE	H1127	Y965	L894	G786	T657	K374	PRO	R266	R164
C1489	C1488	LEU	R1128	K966	K788	K788	Q658	K375	PRO	L267	D167
M1494	C1489	PHE	G1129	P967	T885	K788	Q658	A376	PRO	S268	D168
M1494	M1494	TYR	Q1130	A968	R886	K788	Y659	I377	PRO	W269	L169
G1497	G1497	GLU	R1131	P969	I887	R789	Y663	L378	PRO	G271	V172
K1498	G1497	ASN	W1132	L970	H891	L792	Y663	G382	PRO	W276	S173
D1499	S1498	LYS	H1133	D971	T892	L793	F664	H383	PRO	G277	W174
F1500	F1500	ALA	L1134	S973	Y893	L793	F664	M384	PRO	R283	S175
S1501	F1501	ARG	P1138	L977	G894	G798	V688	L388	PRO	H284	E177
S1502	F1501	GLY	W1143	L902	R897	E799	D669	L388	PRO	R283	R178
G1503	P1503	GLY	W1148	L903	R902	F800	E670	F389	PRO	H284	Y179
G1504	P1503	TRP	V1148	H904	R904	P804	V671	L388	PRO	T284	L180
G1504	H1252	GLY	M1152	H904	P905	Y808	L675	R392	PRO	Q297	H181
G1504	H1252	ALA	I1153	P905	L906	L816	T676	C393	PRO	L182	L182
I1509	E1256	ALA	D1154	L988	L907	L816	L682	Q394	PRO	A311	L189
I1509	E1256	GLY	D1154	L988	L907	P817	L682	E397	PRO	A311	L189
D1513	M1260	LYS	L1155	A989	N908	R818	R683	I660	PRO	C315	F195
L1514	M1260	LYS	L1155	E990	N909	E819	V684	I660	PRO	F316	M196
C1518	C1269	GLY	T1159	Q1066	L913	R890	E700	S571	PRO	M202	M202
L1518	L1270	GLY	I1160	W1069	L913	L821	N705	F572	PRO	L323	L323
V1520	L1270	LEU	I1161	D1070	N994	H822	N705	E573	PRO	ASP	ASP
D1521	R1271	THR	I1161	R1071	N994	L823	D710	I577	PRO	THR	THR
L1522	R1271	THR	M1170	V1072	W995	L823	L711	I578	PRO	ALA	ALA
L1522	H1274	LYS	M1170	R1073	A997	L823	D710	I578	PRO	ALA	ALA
L1522	R1275	GLY	E1176	I1074	A997	L823	L711	I578	PRO	ALA	ALA
L1526	R1290	THR	F1177	F1075	R998	L823	G718	H582	PRO	ALA	ALA
M1527	R1290	THR	A1178	R1076	D999	L823	G718	H582	PRO	ALA	ALA
M1527	L1291	ALA	F1179	R1076	R998	L823	G718	H582	PRO	ALA	ALA
M1527	S1292	GLY	R1180	A1077	R998	L823	G718	H582	PRO	ALA	ALA
L1293	L1293	GLY	R1180	E1078	R998	L823	G718	H582	PRO	ALA	ALA
F1540	L1293	GLY	I1181	K1079	R998	L823	G718	H582	PRO	ALA	ALA
F1540	F1297	THR	I1182	S1080	R998	L823	G718	H582	PRO	ALA	ALA
F1540	F1297	THR	E1183	Y1081	S1086	L823	G718	H582	PRO	ALA	ALA
F1549	T1304	GLN	I1184	Y1081	S1086	L823	G718	H582	PRO	ALA	ALA
T1660	T1304	GLN	I1184	Y1081	S1086	L823	G718	H582	PRO	ALA	ALA
A1551	ALA	GLY	L1189	R1087	S1086	L823	G718	H582	PRO	ALA	ALA
A1551	ALA	GLY	L1189	R1087	S1086	L823	G718	H582	PRO	ALA	ALA
A1551	ALA	GLY	L1189	R1087	S1086	L823	G718	H582	PRO	ALA	ALA

A2141	GLU	R1508	LEU	M1260	I1180	W1069	H994	E917	I826
Y2142	GLU	I1509	PRO	C1269	I1161	D1070	Y995	E917	K827
T2143	GLU	Q1629	ARG	L1270	M1170	R1071	M996	E928	L828
I2144	GLU	D1513	LEU	R1271	E1170	V1072	A997	Y829	Y829
M2153	ALA	L1514	THR	H1274	E1176	R1073	R998	N921	N921
E2157	GLU	C1518	HIS	R1275	T1177	I1074	D999	L922	H838
R2163	GLY	L1519	ASP	H1276	A1178	F1075	R1000	Q923	L839
L2166	VAL	V1520	VAL	R1276	F1179	R1076	Q1003	M924	V840
I2167	GLU	L1521	VAL	R1276	F1179	R1076	S925	G926	P853
E2175	GLU	L1522	VAL	R1276	F1179	R1076	G926	G926	P853
M2178	GLU	L1522	PRO	R1290	E1181	E1078	M1005	C854	C854
I2179	GLU	L1522	ALA	L1291	E1181	K1079	M1005	P855	P855
I2182	PRO	L1526	ASP	S1292	I1182	S1080	S1066	K930	K930
V2190	GLU	M1527	GLY	L1293	E1183	Y1081	S1066	T931	T931
Q2193	LYS	L1527	THR	L1293	E1183	Y1081	S1066	L932	L932
H2194	LYS	F1540	GLN	F1297	I1184	R1087	S1008	L932	L932
L2197	GLU	F1540	GLN	F1297	I1184	R1087	S1008	L933	L933
M2198	GLU	F1540	GLN	F1297	I1184	R1087	S1008	L933	L933
G2202	GLU	F1549	PRO	T1304	L1189	E1093	D1012	A934	A934
M2203	GLU	P1550	GLY	T1304	V1191	E1093	I1013	A934	A934
H2204	GLU	A1551	VAL	GLY	C1192	A1094	I1013	L935	L935
E2205	GLU	S1552	GLU	ALA	S1193	V1095	R1017	G936	G936
T2206	GLU	H1665	ALA	THR	L1194	G1098	M1018	C937	C937
V2207	GLU	T1666	ALA	THR	G1195	E1099	P1019	H938	H938
M2208	GLU	L1667	GLN	PRO	P1196	E1099	R1020	M941	M941
E2209	GLU	R1668	PRO	LEU	V1199	M1100	L1021	E947	E947
V2210	GLU	I1669	VAL	ALA	V1199	R1101	P1022	L850	L850
M2211	GLU	Y1670	ARG	PRO	G1200	A1105	Y1024	L850	L850
N2212	GLU	L1676	ALA	PRO	H1201	R1106	R1025	K951	K951
N2213	GLU	L1676	ASN	GLY	H1201	R1106	R1025	K952	K952
V2214	GLU	M1679	GLU	LEU	V1208	P1107	L1026	T953	T953
L2215	GLU	E1565	LYS	GLN	V1208	E1114	L1027	K954	K954
G2216	GLU	H1683	ASP	PRO	A1215	L1115	T1031	L955	L955
GLY	LEU	Q1569	THR	ALA	L1219	G1116	T1031	L955	L955
M2120	GLY	I1572	THR	ASP	L1219	E1119	M1035	Y959	Y959
F2121	GLU	M1573	GLU	GLU	Q1220	E1119	R1036	M960	M960
S2122	THR	P1574	LYS	ALA	E1221	V1123	D1037	W882	W882
L2123	GLU	L1575	ASN	ARG	G1222	F1124	A883	S962	S962
R2126	GLU	S1576	LYS	ALA	F1223	M1125	G1040	N963	N963
Q2127	GLU	A1577	ARG	ALA	E1224	H1125	Q1041	G964	G964
Y2110	GLU	L1581	LYS	ALA	I1228	G1126	Q1041	Y965	Y965
V2111	GLU	L1581	ARG	ALA	L1228	H1127	A1042	K966	K966
Q2112	GLU	L1581	ARG	ALA	M1229	R1128	V1043	K966	K966
L2214	ASP	L1581	PHE	ASP	N1229	G1129	R1044	P967	P967
L2215	GLU	R1584	LEU	PRO	R1232	Q1130	T1045	A968	A968
G2216	GLU	Y1712	PHE	ASP	R1232	Q1130	L1046	P969	P969
M2120	GLU	Y1712	LYS	TYR	T1235	W1132	L1047	L970	L970
F2121	GLU	I1716	ALA	GLU	K1240	H1133	Y1051	D971	D971
S2122	THR	I1716	LYS	ASN	S1241	L1134	P1055	W896	W896
L2123	GLU	E1721	LYS	ARG	L1242	P1138	P1055	L972	L972
R2126	GLU	A1722	ALA	ARG	P1243	P1138	P1055	L972	L972
Q2127	PRO	C1724	MET	SER	Q1244	W143	ASP	L977	L977
Y2128	GLU	G1497	THR	ALA	G1244	W143	GLN	L977	L977
L2131	GLU	G1498	GLY	ALA	F1245	W143	GLN	A980	A980
L2134	GLU	F1500	THR	ALA	P1249	V1148	PRD	Q951	Q951
L2138	GLU	V1501	GLN	GLY	V1248	V1148	PRD	Q951	Q951
Y2238	GLU	S1502	PRO	GLY	P1249	M1152	SER	P905	P905
		G1504	PRO	GLY	H1282	M1152	GLN	V985	V985
		R1623	ALA	GLU	H1282	M1152	GLN	V985	V985
		L1623	THR	ALA	E1256	D1154	VAL	L988	L988
		L1623	THR	ALA	E1256	L1155	GLU	A989	A989
		L1623	THR	ALA	E1256	L1155	GLU	E990	E990
		L1623	THR	ALA	E1256	L1155	GLU	A989	A989
		L1623	THR	ALA	E1256	L1155	GLU	E990	E990
		L1623	THR	ALA	E1256	L1155	GLU	A989	A989
		L1623	THR	ALA	E1256	L1155	GLU	E990	E990
		L1623	THR	ALA	E1256	L1155	GLU	A989	A989
		L1623	THR	ALA	E1256	L1155	GLU	E990	E990
		L1623	THR	ALA	E1256	L1155	GLU	A989	A989
		L1623	THR	ALA	E1256	L1155	GLU	E990	E990
		L1623	THR	ALA	E1256	L1155	GLU	A989	A989
		L1623	THR	ALA	E1256	L1155	GLU	E990	E990
		L1623	THR	ALA	E1256	L1155	GLU	A989	A989
		L1623	THR	ALA	E1256	L1155	GLU	E990	E990
		L1623	THR	ALA	E1256	L1155	GLU	A989	A989
		L1623	THR	ALA	E1256	L1155	GLU	E990	E990
		L1623	THR	ALA	E1256	L1155	GLU	A989	A989
		L1623	THR	ALA	E1256	L1155	GLU	E990	E990
		L1623	THR	ALA	E1256	L1155	GLU	A989	A989
		L1623	THR	ALA	E1256	L1155	GLU	E990	E990
		L1623	THR	ALA	E1256	L1155	GLU	A989	A989
		L1623	THR	ALA	E1256	L1155	GLU	E990	E990
		L1623	THR	ALA	E1256	L1155	GLU	A989	A989
		L1623	THR	ALA	E1256	L1155	GLU	E990	E990
		L1623	THR	ALA	E1256	L1155	GLU	A989	A989
		L1623	THR	ALA	E1256	L1155	GLU	E990	E990
		L1623	THR	ALA	E1256	L1155	GLU	A989	A989
		L1623	THR	ALA	E1256	L1155	GLU	E990	E990
		L1623	THR	ALA	E1256	L1155	GLU	A989	A989
		L1623	THR	ALA	E1256	L1155	GLU	E990	E990
		L1623	THR	ALA	E1256	L1155	GLU	A989	A989
		L1623	THR	ALA	E1256	L1155	GLU	E990	E990
		L1623	THR	ALA	E1256	L1155	GLU	A989	A989
		L1623	THR	ALA	E1256	L1155	GLU	E990	E990
		L1623	THR	ALA	E1256	L1155	GLU	A989	A989
		L1623	THR	ALA	E1256	L1155	GLU	E990	E990
		L1623	THR	ALA	E1256	L1155	GLU	A989	A989
		L1623	THR	ALA	E1256	L1155	GLU	E990	E990
		L1623	THR	ALA	E1256	L1155	GLU	A989	A989
		L1623	THR	ALA	E1256	L1155	GLU	E990	E990
		L1623	THR	ALA	E1256	L1155	GLU	A989	A989
		L1623	THR	ALA	E1256	L1155	GLU	E990	E990
		L1623	THR	ALA	E1256	L1155	GLU	A989	A989
		L1623	THR	ALA	E1256	L1155	GLU	E990	E990
		L1623	THR	ALA	E1256	L1155	GLU	A989	A989
		L1623	THR	ALA	E1256	L1155	GLU	E990	E990
		L1623	THR	ALA	E1256	L1155	GLU	A989	A989
		L1623	THR	ALA	E1256	L1155	GLU	E990	E990
		L1623	THR	ALA	E1256	L1155	GLU	A989	A989
		L1623	THR	ALA	E1256	L1155	GLU	E990	E990
		L1623	THR	ALA	E1256	L1155	GLU	A989	A989
		L1623	THR	ALA	E1256	L1155	GLU	E990	E990
		L1623	THR	ALA	E1256	L1155	GLU	A989	A989
		L1623	THR	ALA	E1256	L1155	GLU	E990	E990
		L1623	THR	ALA	E1256	L1155	GLU	A989	A989
		L1623	THR	ALA	E1256	L1155	GLU	E990	E990
		L1623	THR	ALA	E1256	L1155	GLU	A989	A989
		L1623	THR	ALA	E1256	L1155	GLU	E990	E990
		L1623	THR	ALA	E1256	L1155	GLU	A989	A989
		L1623	THR	ALA	E1256	L1155	GLU	E990	E990
		L1623	THR	ALA	E1256	L1155	GLU	A989	A989
		L1623	THR	ALA	E1256	L1155	GLU	E990	E990
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		L1623	THR	ALA	E1256	L1155	GLU	E990	E990
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		L1623	THR	ALA	E1256	L1155	GLU	E990	E990
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		L1623	THR	ALA	E1256	L1155	GLU	E990	E990
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		L1623	THR	ALA	E1256	L1155	GLU	E990	E990
		L1623	THR	ALA	E1256	L1155	GLU	A989	A989
		L1623	THR	ALA	E1256	L1155	GLU	E990	E990
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		L1623	THR	ALA	E1256	L1155	GLU	E990	E990
		L1623	THR	ALA	E1256	L1155	GLU	A989	A989
		L1623	THR	ALA	E1256	L1155	GLU	E990	E990
		L1623	THR	ALA	E1256	L1155	GLU	A989	A989
		L1623	THR	ALA	E1256	L1155	GLU	E990	E990
		L1623	THR	ALA	E1256	L1155	GLU	A989	A989
		L1623	THR	ALA	E1256	L1155	GLU	E990	E990

F3398	F3400	F3401	F3402	F3403	F3404	F3405	Y3409	I3413	I3414	I3415	V3417	N3418	N3419	N3420	W3423	E3433	R3436	M3437	V3438	E3439	E3440	E3441	F3442	I3443	W3445	N3450	F3451	N3457	F3458	V3459	V3460	Q3461	I3464	K3475	SER	LYS	MET	ALA	ALA	GLY	ASP	ALA	GLN	SER	GLY	GLY						
E3192	C3193	L3194	A3195	R3196	L3197	A3198	M3201	P3202	V3203	A3204	F3205	L3206	E3207	P3208	V3218	K3222	S3223	P3224	R3225	E3226	R3227	A3228	I3229	L3232	P3233	V3236	E3237	E3238	L3246	L3249	M3250	I3253	A3261	R3262	Y3263	T3264	E3265	M3266	P3267	H3268	I3270	L3274	L3275	L3276	L3277	L3278	L3279	L3280	L3281	P3282		
L3315	L3316	G3317	N3318	L3319	L3320	R3321	L3322	V3323	N3324	N3325	N3326	L3327	A3332	L3333	N3334	N3335	K3336	R3337	L3338	A3339	F3341	A3342	Q3343	P3344	I3345	V3346	A3349	L3353	L3354	H3357	F3358	L3359	P3360	T3361	L3362	L3365	K3366	K3367	K3371	L3384	K3384	E3386	A3387	E3388	A3391	V3394	R3395	L3396	P3397	P3398		
VAL	SER	GLN	ALA	ARG	THR	GLN	VAL	GLY	GLY	Q3127	T3130	T3131	T3132	A3135	L3136	V3139	T3142	L3143	F3144	Q3145	H3146	I3147	H3150	H3151	F3152	G3153	V3156	I3157	V3161	Q3162	R3163	S3164	C3165	V3166	R3167	T3168	L3172	E3173	M3174	D3175	I3176	N3180	L3181	P3182	K3185	L3186	R3187	P3188	LYS			
M2884	T2885	W2886	G2887	R2888	Q2892	E2893	L2894	E2895	A2896	G2898	G2899	G2900	T2901	H2902	F2903	L2904	L2905	V2906	P2907	Y2908	D2909	L2910	E2915	Q2924	E2925	L2926	L2927	K2928	F2929	L2930	Q2931	M2932	N2933	G2934	Y2935	A2936	V2937	T2938	P2939	GLY	LEU	LYS	ASP	MET	GLU	L2946	S2950	P2954	F2957	G2958		
Q2961	Q2962	L2963	L2964	R2965	W2966	N2967	D2968	S2970	F2973	K2974	A2975	E2978	A2979	V2980	V2981	V2986	S2989	E2992	Q2993	E2994	R2996	F2997	F2998	A2999	K3000	L3001	L3002	P3004	L3005	L3006	N3007	R3008	S3009	F3010	T3011	N3012	L3018	S3019	T3020	P3021	A3031	S3032	N3033	K3034	E3035	K3036	E3037	L3042				
K3045	L3046	A3047	R3048	L3049	V3050	R3051	K3052	R3053	V3054	F3057	D3060	V3065	N3066	C3067	L3068	H3073	S3074	L3075	D3076	A3077	R3078	T3079	V3080	M3081	K3082	P3085	E3086	K3089	L3092	R3093	S3094	F3095	F3096	E3097	S3098	A3099	S3100	E3101	D3102	I3103	E3104	M3106	V3107	R3111	LEU	GLY	LYS					
VAL	SER	GLN	ALA	ARG	THR	GLN	VAL	GLY	GLY	Q3127	T3130	T3131	T3132	A3135	L3136	V3139	T3142	L3143	F3144	Q3145	H3146	I3147	H3150	H3151	F3152	G3153	V3156	I3157	V3161	Q3162	R3163	S3164	C3165	V3166	R3167	T3168	L3172	E3173	M3174	D3175	I3176	N3180	L3181	P3182	K3185	L3186	R3187	P3188	LYS			
E3192	C3193	L3194	A3195	R3196	L3197	A3198	M3201	P3202	V3203	A3204	F3205	L3206	E3207	P3208	V3218	K3222	S3223	P3224	R3225	E3226	R3227	A3228	I3229	L3232	P3233	V3236	E3237	E3238	L3246	L3249	M3250	I3253	A3261	R3262	Y3263	T3264	E3265	M3266	P3267	H3268	I3270	L3274	L3275	L3276	L3277	L3278	L3279	L3280	L3281	P3282		
L3315	L3316	G3317	N3318	L3319	L3320	R3321	L3322	V3323	N3324	N3325	N3326	L3327	A3332	L3333	N3334	N3335	K3336	R3337	L3338	A3339	F3341	A3342	Q3343	P3344	I3345	V3346	A3349	L3353	L3354	H3357	F3358	L3359	P3360	T3361	L3362	L3365	K3366	K3367	K3371	L3384	K3384	E3386	A3387	E3388	A3391	V3394	R3395	L3396	P3397	P3398		
F3398	S3399	V3400	L3401	C3402	R3403	D3404	L3405	Y3409	I3413	I3414	I3415	V3417	N3418	N3419	N3420	W3423	E3433	R3436	M3437	V3438	E3439	E3440	E3441	F3442	I3443	W3445	N3450	F3451	N3457	F3458	V3459	V3460	Q3461	I3464	K3475	SER	LYS	MET	ALA	ALA	GLY	ASP	ALA	GLN	SER	GLY	GLY					
I2242	Q2247	F2251	Y2256	L2257	L2263	G2264	L2265	G2266	S2270	T2271	P2272	L2273	S2279	L2286	R2286	Q2293	E2296	C2305	L2306	C2310	L2313	Y2318	L2321	R2324	P2325	E2329	R2330	D2333	F2334	L2335	R2336	V2352	V2353	R2354	R2355	L2356	L2357	L2358	R2359	E2362	C2363	F2364										
G2365	L2368	R2369	G2372	L2376	I2380	E2381	L2382	L2383	K2384	R2385	P2395	VAL	ARG	ARG	ASP	ARG	ARG	ARG	ARG	ARG	ARG	ARG	HIS	PHE	GLY	GLU	GLU	PRO	PRO	GLU	GLU	N2414	L2418	G2419	H2420	A2421	I2422	M2423	L2429	I2450	D2431	R2435	E2439	M2440	H2441	L2442	I2443	K2447	G2448	E2449	A2450	L2451
R2452	I2453	R2454	R2458	L2463	I2469	L2472	L2475	L2479	K2489	M2490	S2491	F2494	V2495	P2496	D2497	H2498	K2499	M2502	F2505	L2506	D2507	L2508	V2509	Y2510	L2511	L2512	Q2515	D2516	F2517	L2518	L2519	L2522	F2526	F2541	L2550	L2550	V2558	L2559	L2562	T2563	K2564	C2565	T2572	P2573								
H2574	R2575	V2579	D2580	S2581	M2582	L2583	H2584	V2585	R2591	G2592	R2593	S2594	L2595	A2598	Q2599	R2600	D2601	L2603	E2604	D2605	C2606	L2607	D2608	A2609	L2610	I2614	R2615	P2616	S2617	M2618	L2619	Q2620	H2621	L2622	L2623	R2624	R2625	L2626	V2627	F2628	D2629	V2630	P2631	L2633	F2636	M2639	P2640	L2641				
K2642	L2643	L2644	T2645	H2646	S2647	Y2648	C2651	W2652	K2653	V2654	Y2655	C2656	W2661	S2668	E2671	L2672	H2673	L2674	K2677	L2678	L2682	F2683	D2684	H2688	K2689	K2690	D2692	Q2693	E2694	L2695	Y2696	R2697	M2698	C2702	I2706	L2710	P2711	D2716	L2725	ALA	THR	VAL	ASP	ALA	ALA	GLU						
GLY	M2734	P2739	T2742	I2746	L2747	P2748	E2749	K2750	L2751	F2754	L2755	A2759	E2760	E2764	K2765	W2766	A2767	F2768	D2769	K2770	L2771	D2772	N2773	E2779	E2783	E2784	L2785	Q2786	T2787	H2788	P2789	M2790	L2791	R2792	P2793	F2797	S2798	E2799	K2800	D2801	K2802	R2806	K2810	L2813	K2814	A2815	M2816					
L2817	A2818	W2819	E2820	W2821	T2822	L2823	R2827	E2830	GLU	GLU	THR	LYS	LYS	LYS	THR	ARG	L2905	V2906	P2907	Y2908	D2909	L2910	E2915	Q2924	E2925	L2926	L2927	K2928	F2929	L2930	Q2931	M2932	N2933	G2934	Y2935	A2936	V2937	T2938	P2939	GLY	LEU	LYS	ASP	MET	GLU	L2946	S2950	P2954	F2957	G2958		
M2884	T2885	W2886	G2887	R2888	Q2892	E2893	L2894	E2895	A2896	G2898	G2899	G2900	T2901	H2902	F2903	L2904	L2905	V2906	P2907	Y2908	D2909	L2910	E2915	Q2924	E2925	L2926	L2927	K2928	F2929	L2930	Q2931	M2932	N2933	G2934	Y2935	A2936	V2937	T2938	P2939	GLY	LEU	LYS	ASP	MET	GLU	L2946	S2950	P2954	F2957	G2958		
Q2961	Q2962	L2963	L2964	R2965	W2966	N2967	D2968	S2970	F2973	K2974	A2975	E2978	A2979	V2980	V2981	V2986	S2989	E2992	Q2993	E2994	R2996	F2997	F2998	A2999	K3000	L3001	L3002	P3004	L3005	L3006	N3007	R3008	S3009	F3010	T3011	N3012	L3018	S3019	T3020	P3021	A3031	S3032	N3033	K3034	E3035	K3036	E3037	L3042				
K3045	L3046	A3047	R3048	L3049	V3050	R3051	K3052	R3053	V3054	F3057	D3060	V3065	N3066	C3067	L3068	H3073	S3074	L3075	D3076	A3077	R3078	T3079	V3080	M3081	K3082	P3085	E3086	K3089	L3092	R3093	S3094	F3095	F3096	E3097	S3098	A3099	S3100	E3101	D3102	I3103	E3104	M3106	V3107	R3111	LEU	GLY	LYS					
VAL	SER	GLN	ALA	ARG	THR	GLN	VAL	GLY	GLY	Q3127	T3130	T3131	T3132	A3135	L3136	V3139	T3142	L3143	F3144	Q3145	H3146	I3147	H3150	H3151	F3152	G3153	V3156	I3157	V3161	Q3162	R3163	S3164	C3165	V3166	R3167	T3168	L3172	E3173	M3174	D3175	I3176	N3180	L3181	P3182	K3185	L3186	R3187	P3188	LYS			
E3192	C3193	L3194	A3195	R3196	L3197	A3198	M3201	P3202	V3203	A3204	F3205	L3206	E3207	P3208	V3218	K3222	S3223	P3224	R3225	E3226	R3227	A3228	I3229	L3232	P3233	V3236	E3237	E3238	L3246	L3249	M3250	I3253	A3261	R3262	Y3263	T3264	E3265	M3266	P3267	H3268	I3270	L3274	L3275	L3276	L3277	L3278	L3279	L3280	L3281	P3282		
L3315	L3316	G3317	N3318	L3319	L3320	R3321	L3322	V3323	N3324	N3325	N3326	L3327	A3332	L3333	N3334	N3335	K3336	R3337	L3338	A3339	F3341	A3342	Q3343	P3344	I3345	V3346	A3349	L3353	L3354	H3357	F3358	L3359	P3360	T3361	L3362	L3365	K3366	K3367	K3371	L3384	K3384	E3386	A3387	E3388	A3391	V3394	R3395	L3396	P3397	P3398		
F3398	S3399	V3400	L3401	C3402	R3403	D3404	L3405	Y3409	I3413	I3414	I3415	V3417	N3418	N3419	N3420	W3423	E3433	R3436	M3437	V3438	E3439	E3440	E3441	F3442	I3443	W3445	N3450	F3451	N3457	F3458	V3459	V3460	Q3461	I3464	K3475	SER	LYS	MET	ALA	ALA	GLY	ASP	ALA	GLN	SER	GLY	GLY					

V4830	G4699	SER	G4699	GLY	ALA	ARG	ALA	D4092	V3995	L3890	H3771	R3672	M3573	SER
V4833	Q4700	GLY	ALA	F4093	F3996	LEU	LEU	F4093	F3996	E3893	T3772	M3673	A3574	ASP
V4838	D4702	GLY	ASP	A4096	H3998	TRP	ALA	A4096	H3998	A3977	G3774	L3674	L3575	GLN
V4841	R4703	GLY	ASP	M4097	M3999	GLY	ALA	M4097	M3999	Q3906	A3775	D3676	Y3576	GLU
F4856	L4704	ALA	ASP	D4098	M4000	SER	ALA	D4098	M4000	T3912	A3776	R3679	R3577	THR
F4859	F4719	GLY	GLY	S4099	L4003	PHE	ALA	S4099	L4003	C3918	M3778	K3682	R3582	LYS
R4860	L4725	GLY	VAL	F4103	Q4009	GLY	ALA	F4103	Q4009	T3919	M3793	Q3683	I3592	LYS
V4863	D4726	ASP	ALA	T4104	L4013	GLY	LEU	T4104	L4013	V3690	R3594	R3690	V3593	ARG
V4864	K4727	ASP	HIS	G4105	K4014	LEU	GLY	G4105	K4014	L3923	L3800	V3690	R3594	ARG
V4865	H4728	GLY	VAL	M4108	E4015	VAL	LEU	M4108	E4015	L3926	I3804	K3693	R3595	GLY
V4866	E4735	GLY	ALA	L4112	L4016	GLY	SER	L4112	L4016	L3926	I3804	K3694	R3597	ASP
V4867	R4736	GLY	PRO	S4115	D4017	GLY	THR	S4115	D4017	Y3934	E3811	P3695	Q3597	ARG
V4868	I4737	GLY	PRO	D4118	D4021	VAL	ARG	D4118	D4021	Y3934	E3811	P3695	Q3597	ARG
V4869	A4738	GLY	LYS	M4122	M4023	THR	VAL	M4122	M4023	V3942	E3812	R3688	H3605	TYR
V4870	E4739	GLY	LYS	I4123	V4024	THR	VAL	I4123	V4024	V3943	R3812	H3699	L3606	LYS
V4871	H4740	GLY	VAL	F4125	F4025	THR	ARG	F4125	F4025	E3944	Q3813	Q3700	L3509	LYS
V4872	L4741	GLY	VAL	M4125	M4026	THR	ARG	M4125	M4026	E3945	Q3814	Q3701	I3510	LYS
V4873	M4743	GLY	VAL	E4126	L4027	THR	ARG	E4126	L4027	Q3946	M3815	V3702	Y3511	LYS
V4874	P4760	GLY	ALA	E4127	L4031	THR	ARG	E4127	L4031	G3947	I3832	M3723	H3605	TYR
V4875	P4761	GLY	ASP	F4128	L4031	THR	ARG	F4128	L4031	R3949	Q3833	M3724	L3606	LYS
V4876	T4766	GLY	ASP	A4129	M4039	THR	PRO	A4129	M4039	E3944	A3834	E3718	L3510	LYS
V4877	W4767	GLY	PRO	M4130	I4040	THR	ASP	M4130	I4040	M3955	R3820	D3719	K3514	LYS
V4878	I4771	GLY	PHE	R4131	I4040	THR	ASP	R4131	I4040	M3955	R3820	D3719	K3514	LYS
V4879	V4772	GLY	ARG	F4132	M4044	THR	GLY	F4132	M4044	A3988	Q3833	E3718	K3514	LYS
V4880	D4773	GLY	ARG	Q4133	K3989	THR	GLY	Q4133	K3989	M3955	R3820	D3719	K3514	LYS
V4881	K4774	GLY	LYS	E4134	V4045	THR	ALA	E4134	V4045	Q3960	V3841	E3718	K3514	LYS
V4882	Y4775	GLY	GLY	F4135	M4046	THR	ALA	F4135	M4046	F3962	L3842	E3718	K3514	LYS
V4883	Q4776	GLY	VAL	M4142	L4048	THR	ALA	M4142	L4048	L3965	L3842	E3718	K3514	LYS
V4884	K4779	ASP	PRO	T4148	V4049	THR	ALA	T4148	V4049	E3967	M3845	E3718	K3514	LYS
V4885	V4782	ASP	ALA	M4149	M4057	THR	ALA	M4149	M4057	E3967	M3845	E3718	K3514	LYS
V4886	I4783	GLY	ALA	L4150	F4061	THR	LEU	L4150	F4061	Y3968	F3847	E3718	K3514	LYS
V4887	S4788	SER	PRO	S4151	F4062	THR	LEU	S4151	F4062	Y3968	F3847	E3718	K3514	LYS
V4888	M4796	ALA	PRO	E4152	D4063	THR	VAL	E4152	D4063	Q3970	Q3850	E3718	K3514	LYS
V4889	L4800	ASP	PRO	Y4177	M4064	THR	VAL	Y4177	M4064	C3973	M3870	S3752	L3542	ARG
V4890	H4803	GLY	LYS	M4184	K4067	THR	ALA	M4184	K4067	T3974	K3873	E3755	E3547	ARG
V4891	F4807	GLY	ALA	R4192	V4072	THR	ALA	R4192	V4072	N3976	V3874	K3756	E3548	ARG
V4892	K4821	SER	PRO	S4199	F4077	THR	ALA	S4199	F4077	Q3977	M3875	E3757	V3549	ARG
V4893	D4822	SER	PRO	T4200	Q4078	THR	ALA	T4200	Q4078	Q3977	M3875	E3757	V3549	ARG
V4894	L4823	GLY	ALA	M4201	D4079	THR	VAL	M4201	D4079	Q3978	A3876	M3758	R3550	ARG
V4895	R4824	GLY	LYS	M4207	V4081	THR	ALA	M4207	V4081	Q3978	A3876	M3758	R3550	ARG
V4896	T4825	SER	PRO	F4288	I4088	THR	ALA	F4288	I4088	M3986	D3877	E3789	E3551	ARG
V4897	I4826	GLY	GLY	Q4209	S4089	THR	ALA	Q4209	S4089	D3987	F3880	K3760	F3552	ARG
V4898	L4827	GLY	ALA	Y4210	K4091	THR	ALA	Y4210	K4091	H3994	F3880	Q3761	L3553	ARG
V4899	H4827	GLY	LYS			ALA	LEU							
V4900	T4766	GLY	ASP			ALA	LEU							
V4901	W4767	GLY	PRO			ALA	LEU							
V4902	I4771	GLY	PHE			ALA	LEU							
V4903	V4772	GLY	ARG			ALA	LEU							
V4904	D4773	GLY	ARG			ALA	LEU							
V4905	K4774	GLY	LYS			ALA	LEU							
V4906	Y4775	GLY	GLY			ALA	LEU							
V4907	Q4776	GLY	VAL			ALA	LEU							
V4908	K4779	ASP	PRO			ALA	LEU							
V4909	V4782	ASP	ALA			ALA	LEU							
V4910	I4783	GLY	ALA			ALA	LEU							
V4911	S4788	SER	PRO			ALA	LEU							
V4912	M4796	ALA	PRO			ALA	LEU							
V4913	L4800	ASP	PRO			ALA	LEU							
V4914	H4803	GLY	LYS			ALA	LEU							
V4915	F4807	GLY	ALA			ALA	LEU							
V4916	K4821	SER	PRO			ALA	LEU							
V4917	D4822	SER	PRO			ALA	LEU							
V4918	L4823	GLY	ALA			ALA	LEU							
V4919	R4824	GLY	LYS			ALA	LEU							
V4920	T4825	SER	PRO			ALA	LEU							
V4921	I4826	GLY	GLY			ALA	LEU							
V4922	L4827	GLY	ALA			ALA	LEU							
V4923	H4827	GLY	LYS			ALA	LEU							

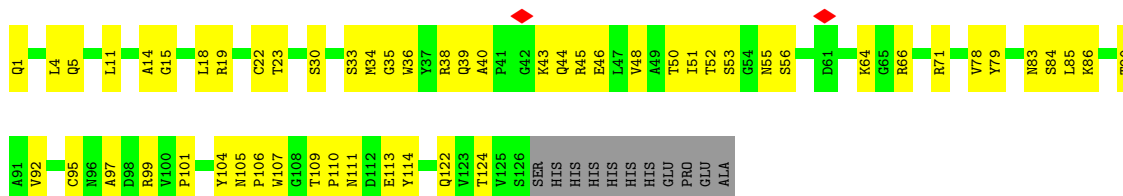


● Molecule 1: Ryanodine receptor 1

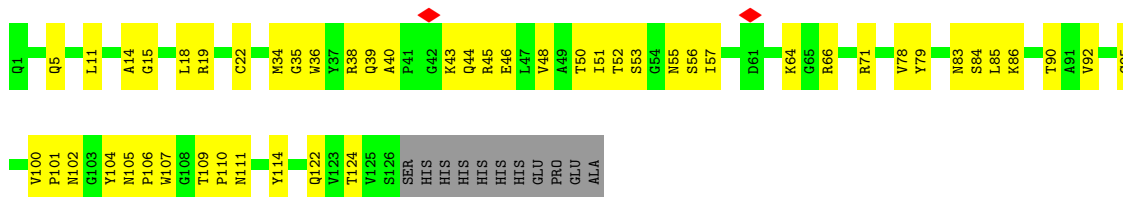


V11	Q12	F13	T16	V21	L22	L35	L49	A63	I64	A63	I64	THR	VAL	GLU	ALA	GLY	VAL	GLU	SER	SER	GLN	GLY	G97	H98	R99	T100	L101	L102	Y103	A106	I107	L108	H111	A112	H113	S114	R115	M116	Y117											
L118	L121	L131	D134	L137	E144	L147	W148	T149	M150	H151	E159	G160	K162	V163	R164	D167	D168	L169	V172	S173	V174	S175	S176	E177	R178	A376	Y179	L180	H181	L182	L189	F195	M196	M202	I205	C206	S207	C208	E210	E210	Y213	V214	G217	H218						
V219	F223	H224	D228	E229	C230	T232	A235	V245	Y246	Y247	E248	G249	C250	A251	V252	H255	A256	R257	R261	R266	S268	W269	S270	G271	H273	W276	G277	R283	H284	T294	Q297	A311	C315	F316	K322	L323	A400	A401	THR	ALA	PRO	LYS	ARG							
ASP	VAL	GLY	MET	PRO	PRO	E338	Y341	L345	C346	H350	G354	L355	T358	Y359	A360	D363	P364	K365	C366	L369	L372	K373	K374	K375	A376	I377	L378	G382	H383	M384	L388	F389	R392	C393	Q394	E397	S398	Q399	A400	A401	R402	M403	F414							
P437	I438	E439	A440	V441	Y451	L459	E462	E463	L468	R469	S470	L471	R472	M473	R474	Q479	E480	W487	L488	M489	I491	R493	T499	H502	S514	I518	L525	L526	L529	C537	A538	L539	F540	S541	V547	V548	L551	I560	S571	P572										
E573	V574	I577	I578	H582	I586	L590	N596	H597	K598	L600	D601	R615	T622	L625	L626	R629	L633	Q634	L637	I638	N639	I648	G651	T657	Q658	Y659	Y663	F664	E665	V668	D669	E670	V671	L675	V676	L682	R683	V684	E700											
W705	D710	L711	G718	W722	A727	R728	L737	L738	A739	P740	E741	C747	L748	P753	S754	I755	S756	F757	R758	G761	V764	Q765	G766	L773	V781	S782	F783	G786	V787	K788	V789	R790	L791	L793	G798	E799	F800	L803	P804	Y808	L816									
P817	R818	E819	L823	Y829	H838	V840	P853	G854	P855	T858	I861	V862	L863	H866	L867	R869	I870	R871	L874	A875	E876	M877	I878	H879	E880	L881	P882	A883	L884	T885	R886	I887	W891	T892	Y893	G894	R897	R902	L903	H904	P905	C906	L907	N909						
L913	E917	Y920	N921	L922	Q923	M924	K930	T931	L932	A934	L935	G936	C937	H938	M941	E947	L950	K951	K952	K954	L955	Y959	M960	M961	S962	N963	G964	Y965	K966	P967	A968	P969	L970	D971	L972	S973	L977	A980	Q981	V985	L988	E990								
H993	N994	Y995	W996	A997	R998	R1000	Q1003	L839	G1004	S1005	M1005	S1006	Y1007	S1008	I1013	R1017	M1018	P1019	R1020	L1021	V1022	Y1024	R1025	L1026	L1027	T1031	M1035	R1036	D1037	G1040	Q1041	A1042	V1043	R1044	T1045	L1046	L1047	Y1051	P1055	ASP	GLN	GLU	PRO	PRO	SER	GLN	VAL	GLU	M1085	Q1066
W1069	D1070	V1071	R1072	R1073	F1075	L1076	A1077	K1078	E1079	S1080	Y1081	R1087	E1093	A1094	V1095	G1098	E1099	M1100	R1101	A1105	R1106	P1107	E1114	L1115	G1116	E1119	V1123	F1124	N1125	G1126	H1127	R1128	G1129	Q1130	H1131	W1132	H1133	L1134	P1138	W1143	V1148	M1152	T1153	D1154	L1155	T1159				
I1160	I1161	M1170	E1176	T1177	A1178	F1179	E1180	E1181	I1182	E1183	I1184	L1189	P1190	C1192	S1193	L1194	P1196	V1199	G1200	H1201	V1208	A1215	L1219	Q1220	E1221	G1222	F1223	E1224	T1228	N1229	H1229	R1232	T1235	K1240	L1242	P1243	Q1244	F1245	V1248	P1249	H1252	E1256								
M1260	C1269	L1270	R1271	H1274	R1275	R1290	L1291	S1292	L1293	F1297	T1304	ALA	GLY	ALA	THR	PRO	LEU	ALA	PRO	PRO	ALA	GLU	GLN	PRO	ALA	GLU	ASP	GLU	ALA	ARG	ALA	ALA	GLU	LEU	ARG	ARG	SER	ALA	GLY	GLY	TRP	GLY	GLU	ALA	GLU	GLY				

V3995	F3996	H3771	R3672	R3582	ASP	S3399	L3316	C3193	L3046	R2988	H2819
H3772	R3673	I3772	M3673	R3582	GLN	V3400	G3317	L3194	A3047	R2988	E2820
I3773	I3674	R3773	I3674	R3582	ARG	L3401	M3318	A3195	A3048	Q2892	E2821
G3774	D3675	I3592	D3675	I3592	GLU	C3402	I3319	R3196	R3049	Q2892	T2822
A3775	D3676	R3593	D3676	R3593	THR	R3403	L3320	L3197	L3049	L2894	T2822
A3776	A3776	R3594	A3776	R3594	LYS	D3404	R3321	A3198	R3051	E2895	I2823
E3777	R3679	R3595	R3679	R3595	LYS	L3405	I3322	A3199	H3052	E2897	R2827
M3778	Q3683	V3596	Q3683	V3596	LYS	M3201	L3323	M3201	F2973	A2896	R2827
M3793	Q3683	Q3597	Q3683	Q3597	ARG	P3202	V3324	P3202	K2897	E2830	E2830
L3600	V3690	Y3604	V3690	Y3604	ARG	V3203	N3325	A3204	A2975	G2898	GLU
L3604	H3605	H3605	H3605	H3605	GLY	A3204	N3326	A3204	G2976	G2899	GLU
K3693	K3694	R3414	K3693	R3414	ASP	R3414	L3327	A3205	T2901	ARG	ARG
K3694	K3694	Y3415	K3694	Y3415	ARG	Y3415	L3327	F3206	T2901	THR	THR
F3695	F3695	V3416	F3695	V3416	TYR	V3416	A3332	E3207	H2902	GLU	GLU
E3612	E3612	D3417	E3612	D3417	ASP	D3417	T3333	P3208	V2980	L2904	LYS
L3514	L3514	N3418	L3514	N3418	LYS	N3418	W3334	V3218	L2904	LYS	LYS
K3515	K3515	R3419	K3515	R3419	LYS	R3419	M3335	V3218	L2905	LYS	LYS
A3516	A3516	R3420	A3516	R3420	ALA	R3420	K3336	K3222	L2906	ARG	ARG
M3517	M3517	L3511	M3517	L3511	LYS	L3511	R3337	K3222	P2907	LYS	LYS
L3518	L3518	S3504	L3518	S3504	LYS	S3504	L3338	K3222	Y2908	ILE	ILE
P3519	P3519	L3514	P3519	L3514	LYS	L3514	A3339	P3224	D2909	SER	SER
M3524	M3524	K3515	M3524	K3515	LYS	K3515	F3340	R3224	T2910	GLN	GLN
Q3530	Q3530	R3516	Q3530	R3516	ALA	R3516	F3341	E3226	T2911	GLN	GLN
D3531	D3531	VAL	D3531	VAL	VAL	VAL	A3342	R3227	THR	THR	THR
L3532	L3532	R3436	L3532	R3436	THR	R3436	Q3343	R3227	ALA	ALA	ALA
L3533	L3533	M3437	L3533	M3437	HIS	M3437	Q3344	A3228	GLN	GLN	GLN
M3534	M3534	Y3438	M3534	Y3438	LYS	Y3438	P3344	I3229	THR	THR	THR
A3535	A3535	G3439	A3535	G3439	LEU	G3439	V3345	L3232	T2924	TYR	TYR
ALA	ALA	E3440	ALA	E3440	LEU	E3440	V3346	P3233	A2925	ASP	ASP
VAL	VAL	I3441	VAL	I3441	SER	I3441	A3349	R3233	M3081	PRO	PRO
VAL	VAL	L3441	VAL	L3441	LYS	L3441	F3442	V3236	K3082	ARG	ARG
ALA	ALA	S3443	ALA	S3443	GLN	S3443	E3352	E3237	F2928	GLU	GLU
PHE	PHE	R3444	PHE	R3444	ARG	R3444	L3353	E3238	P2929	GLY	GLY
ARG	ARG	M3445	ARG	M3445	ARG	M3445	L3354	E3238	L2930	Y2855	Y2855
MET	MET	N3450	MET	N3450	ARG	N3450	F3357	L3246	Q2931	M2856	M2856
P3640	P3640	F3451	P3640	F3451	ALA	F3451	H3357	L3246	M2932	P2857	P2857
L3641	L3641	R3457	L3641	R3457	VAL	R3457	F3358	L3249	Q2933	P2857	P2857
L3644	L3644	F3458	L3644	F3458	VAL	F3458	I3359	I3253	C2934	P2858	P2858
P3645	P3645	V3459	P3645	V3459	ALA	V3459	F3360	A3261	Y2935	P2859	P2859
R3648	R3648	GLU	R3648	GLU	CYS	GLU	I3362	C3165	A2936	P2860	P2860
K3658	K3658	ARG	K3658	ARG	PHE	ARG	L3365	Y3166	T2938	J2861	J2861
E3755	E3755	MET	E3755	MET	MET	MET	R3366	R3262	R3097	L2862	L2862
K3756	K3756	ARG	K3756	ARG	ARG	ARG	K3367	Y3263	E3097	S2863	S2863
E3757	E3757	P3640	E3757	P3640	ASP	P3640	K3367	T3264	GLY	S2863	S2863
M3758	M3758	L3641	M3758	L3641	LYS	L3641	R3367	E3265	LEU	T2866	T2866
E3759	E3759	L3644	E3759	L3644	LYS	L3644	K3371	M3266	LYS	L2866	L2866
K3760	K3760	L3645	K3760	L3645	ASP	L3645	R3371	P3267	ASP	L2867	L2867
Q3761	Q3761	P3645	Q3761	P3645	GLY	P3645	K3371	H3268	ASP	S2868	S2868
F3880	F3880	L3648	F3880	L3648	LYS	L3648	K3384	V3269	GLU	S2868	S2868
L3884	L3884	R3648	L3884	R3648	LYS	R3648	A3385	I3270	A2874	A2874	A2874
F3885	F3885	K3658	F3885	K3658	ALA	K3658	E3386	L3274	S2950	A2874	A2874
R3886	R3886	K3658	R3886	K3658	GLY	R3886	A3387	P3275	R2950	L2878	L2878
F3887	F3887	M3571	F3887	M3571	ASP	M3571	E3388	M3276	R2954	L2878	L2878
L3888	L3888	I3662	L3888	I3662	ALA	I3662	E3391	Y3280	F2957	E2880	E2880
L3889	L3889	K3572	L3889	K3572	GLN	K3572	E3391	L3281	G2958	E2880	E2880
L3770	L3770	A3574	L3770	A3574	SER	A3574	V3394	L2881	L2946	E2881	E2881
E3670	E3670	R3664	E3670	R3664	GLY	R3664	R3395	P3282	L3042	E2881	E2881
R3677	R3677	G3677	R3677	G3677	GLY	G3677	F3398	L3315	Q2961	E2882	E2882
S3768	S3768	L3770	S3768	L3770	GLY	L3770	F3398	L3315	Q2962	E2882	E2882
R3769	R3769	L3770	R3769	L3770	SER	L3770	F3398	L3315	L2963	E2882	E2882
L3770	L3770	L3770	L3770	L3770	SER	L3770	F3398	L3315	L2964	E2882	E2882



• Molecule 3: Nanobody 9657



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	26815	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	JEOL CRYO ARM 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	5.503	Depositor
Minimum map value	-0.105	Depositor
Average map value	0.053	Depositor
Map value standard deviation	0.121	Depositor
Recommended contour level	0.2	Depositor
Map size (\AA)	504.0, 504.0, 504.0	wwPDB
Map dimensions	336, 336, 336	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.5, 1.5, 1.5	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: CFF, ATP, CA, 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	B	0.13	0/34879	0.35	1/47280 (0.0%)
1	E	0.13	0/34879	0.34	1/47280 (0.0%)
1	G	0.13	0/34879	0.35	1/47280 (0.0%)
1	J	0.13	0/34879	0.35	1/47280 (0.0%)
2	A	0.21	0/834	0.47	0/1123
2	D	0.21	0/834	0.47	0/1123
2	H	0.21	0/834	0.47	0/1123
2	I	0.21	0/834	0.48	0/1123
3	C	0.18	0/987	0.49	0/1340
3	F	0.18	0/987	0.49	0/1340
3	K	0.17	0/987	0.49	0/1340
3	M	0.17	0/987	0.47	0/1340
All	All	0.14	0/146800	0.35	4/198972 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	1503	PRO	N-CA-CB	7.25	110.09	103.20
1	J	1503	PRO	N-CA-CB	7.23	110.07	103.20
1	G	1503	PRO	N-CA-CB	7.20	110.04	103.20
1	B	1503	PRO	N-CA-CB	7.17	110.01	103.20

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	B	34103	0	33491	1103	0
1	E	34103	0	33491	1106	0
1	G	34103	0	33491	1110	0
1	J	34103	0	33491	1112	0
2	A	818	0	824	26	0
2	D	818	0	824	30	0
2	H	818	0	824	33	0
2	I	818	0	824	31	0
3	C	967	0	916	50	0
3	F	967	0	916	51	0
3	K	967	0	916	49	0
3	M	967	0	916	46	0
4	B	1	0	0	0	0
4	E	1	0	0	0	0
4	G	1	0	0	0	0
4	J	1	0	0	0	0
5	B	31	0	12	2	0
5	E	31	0	12	1	0
5	G	31	0	12	1	0
5	J	31	0	12	2	0
6	B	14	0	10	1	0
6	E	14	0	10	1	0
6	G	14	0	10	1	0
6	J	14	0	10	1	0
7	B	1	0	0	0	0
7	E	1	0	0	0	0
7	G	1	0	0	0	0
7	J	1	0	0	0	0
All	All	143740	0	141012	4657	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 16.

The worst 5 of 4657 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:G:2874:MET:HE3	1:G:2937:VAL:HG11	1.54	0.88
1:J:2874:MET:HE3	1:J:2937:VAL:HG11	1.54	0.88
1:E:2874:MET:HE3	1:E:2937:VAL:HG11	1.54	0.87
1:B:2874:MET:HE3	1:B:2937:VAL:HG11	1.54	0.86
1:B:3261:ALA:HB3	1:B:3266:MET:HE1	1.58	0.86

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	B	4280/5027 (85%)	4189 (98%)	89 (2%)	2 (0%)	100	100
1	E	4280/5027 (85%)	4190 (98%)	88 (2%)	2 (0%)	100	100
1	G	4280/5027 (85%)	4190 (98%)	88 (2%)	2 (0%)	100	100
1	J	4280/5027 (85%)	4190 (98%)	88 (2%)	2 (0%)	100	100
2	A	105/107 (98%)	96 (91%)	8 (8%)	1 (1%)	12	47
2	D	105/107 (98%)	96 (91%)	8 (8%)	1 (1%)	12	47
2	H	105/107 (98%)	96 (91%)	8 (8%)	1 (1%)	12	47
2	I	105/107 (98%)	96 (91%)	8 (8%)	1 (1%)	12	47
3	C	124/137 (90%)	113 (91%)	11 (9%)	0	100	100
3	F	124/137 (90%)	113 (91%)	11 (9%)	0	100	100
3	K	124/137 (90%)	113 (91%)	11 (9%)	0	100	100
3	M	124/137 (90%)	111 (90%)	13 (10%)	0	100	100
All	All	18036/21084 (86%)	17593 (98%)	431 (2%)	12 (0%)	49	83

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	86	GLY

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	D	86	GLY
2	H	86	GLY
2	I	86	GLY
1	B	2909	ASP

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	B	3659/4270 (86%)	3659 (100%)	0	100	100
1	E	3659/4270 (86%)	3659 (100%)	0	100	100
1	G	3659/4270 (86%)	3659 (100%)	0	100	100
1	J	3659/4270 (86%)	3658 (100%)	1 (0%)	100	100
2	A	88/88 (100%)	88 (100%)	0	100	100
2	D	88/88 (100%)	88 (100%)	0	100	100
2	H	88/88 (100%)	88 (100%)	0	100	100
2	I	88/88 (100%)	88 (100%)	0	100	100
3	C	104/114 (91%)	104 (100%)	0	100	100
3	F	104/114 (91%)	104 (100%)	0	100	100
3	K	104/114 (91%)	104 (100%)	0	100	100
3	M	104/114 (91%)	104 (100%)	0	100	100
All	All	15404/17888 (86%)	15403 (100%)	1 (0%)	100	100

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

Mol	Chain	Res	Type
1	J	372	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 160 such sidechains are listed below:

Mol	Chain	Res	Type
1	J	904	HIS
1	J	4946	GLN
1	J	1691	GLN
1	J	3149	GLN
3	F	5	GLN

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](#)

Of 16 ligands modelled in this entry, 8 are monoatomic - leaving 8 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	ATP	J	5102	-	32,33,33	0.25	0	48,52,52	0.31	0
5	ATP	E	5102	-	32,33,33	0.26	0	48,52,52	0.31	0
5	ATP	B	5102	-	32,33,33	0.26	0	48,52,52	0.31	0
6	CFF	B	5103	-	15,15,15	0.49	0	23,23,23	0.71	1 (4%)
6	CFF	J	5103	-	15,15,15	0.49	0	23,23,23	0.70	1 (4%)
6	CFF	E	5103	-	15,15,15	0.49	0	23,23,23	0.71	1 (4%)
5	ATP	G	5102	-	32,33,33	0.25	0	48,52,52	0.31	0
6	CFF	G	5103	-	15,15,15	0.50	0	23,23,23	0.71	1 (4%)

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	ATP	J	5102	-	-	5/22/38/38	0/3/3/3
5	ATP	E	5102	-	-	5/22/38/38	0/3/3/3
5	ATP	B	5102	-	-	5/22/38/38	0/3/3/3
6	CFF	B	5103	-	-	-	0/2/2/2
6	CFF	J	5103	-	-	-	0/2/2/2
6	CFF	E	5103	-	-	-	0/2/2/2
5	ATP	G	5102	-	-	5/22/38/38	0/3/3/3
6	CFF	G	5103	-	-	-	0/2/2/2

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	G	5103	CFF	C12-N3-C2	2.25	121.26	117.33
6	E	5103	CFF	C12-N3-C2	2.25	121.25	117.33
6	B	5103	CFF	C12-N3-C2	2.24	121.23	117.33
6	J	5103	CFF	C12-N3-C2	2.23	121.21	117.33

There are no chirality outliers.

5 of 20 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	5102	ATP	C5'-O5'-PA-O1A
5	B	5102	ATP	C5'-O5'-PA-O2A
5	B	5102	ATP	C5'-O5'-PA-O3A
5	E	5102	ATP	C5'-O5'-PA-O1A
5	E	5102	ATP	C5'-O5'-PA-O2A

There are no ring outliers.

8 monomers are involved in 10 short contacts:

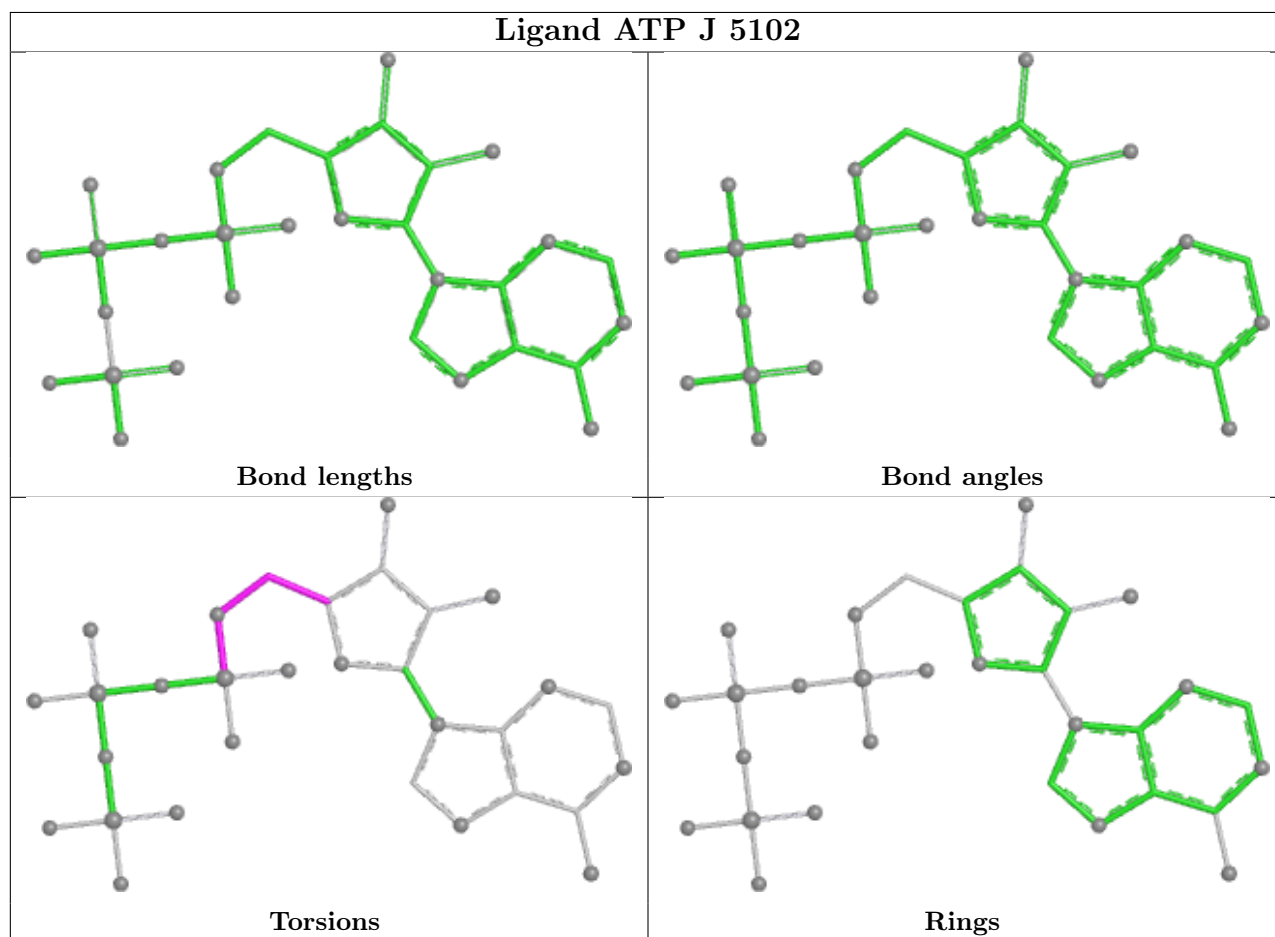
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	J	5102	ATP	2	0
5	E	5102	ATP	1	0
5	B	5102	ATP	2	0
6	B	5103	CFF	1	0

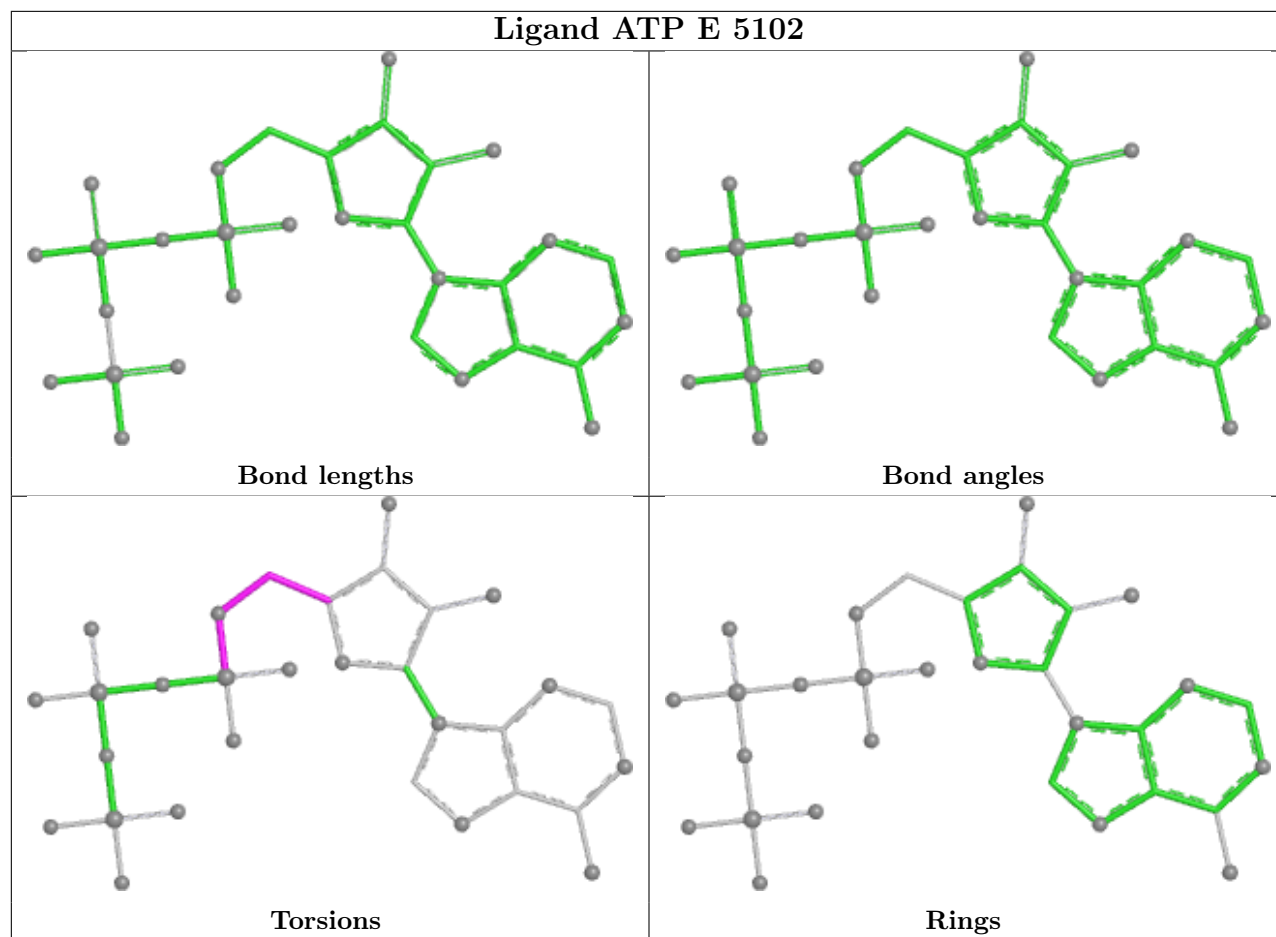
Continued on next page...

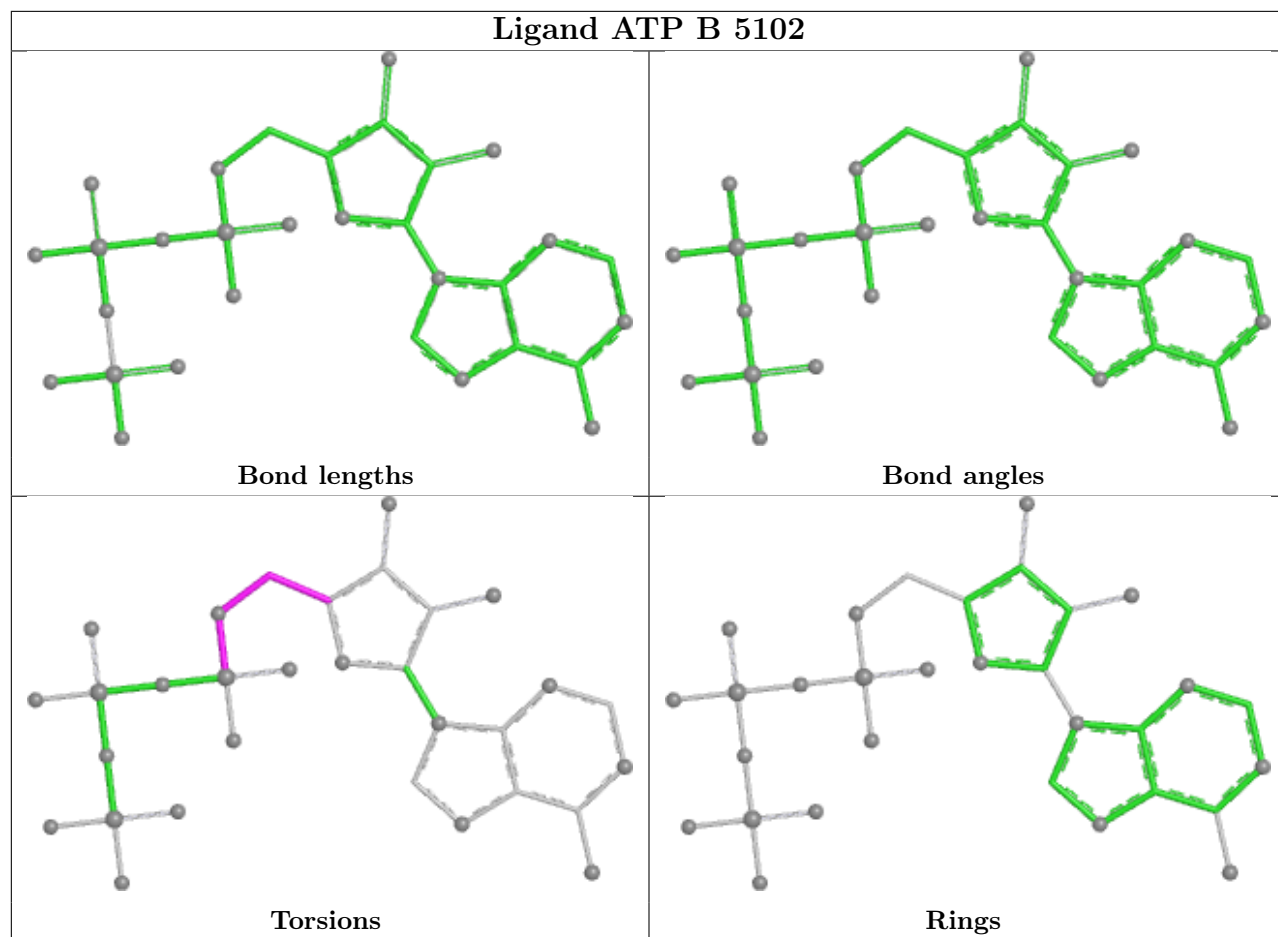
Continued from previous page...

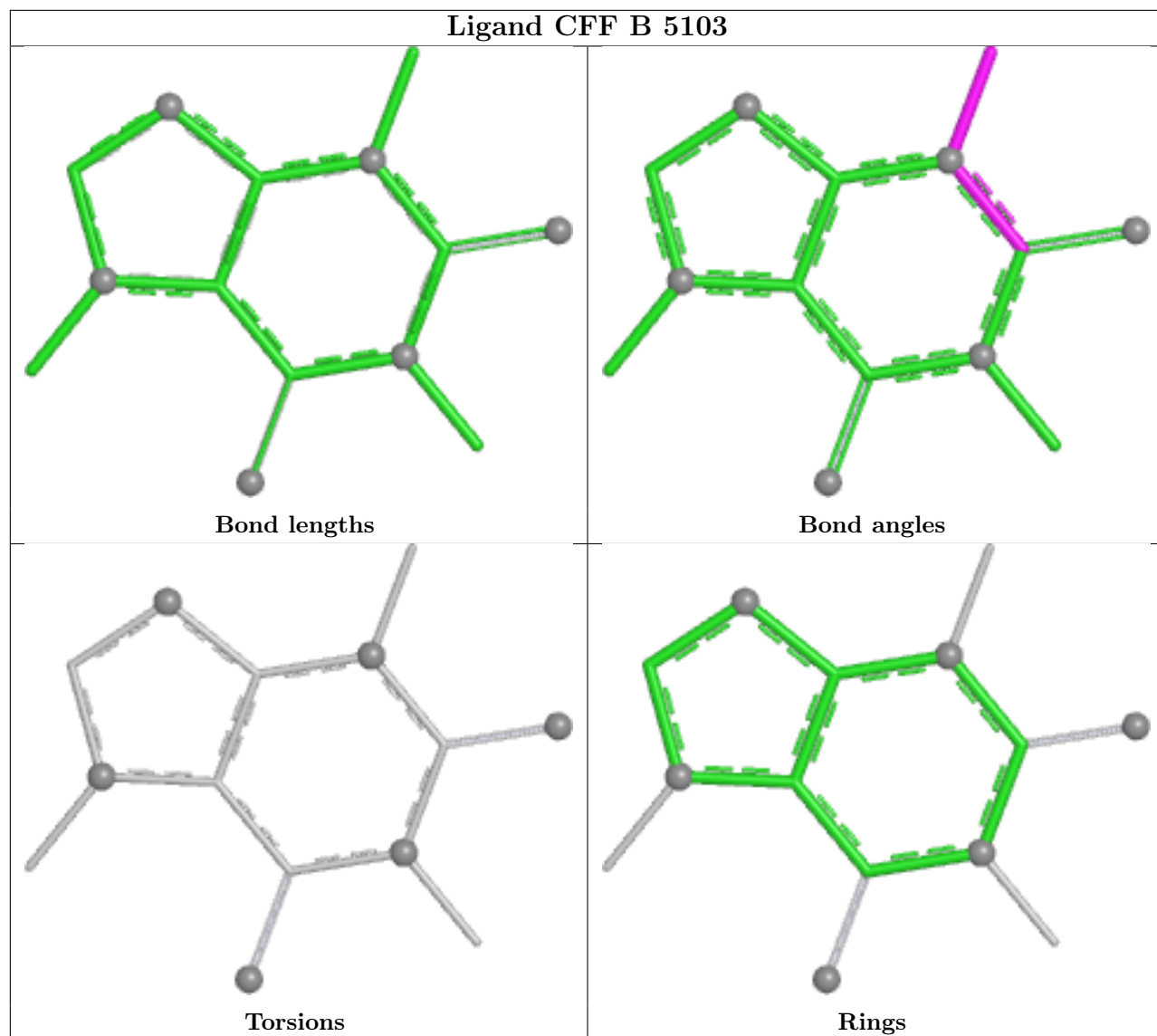
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	J	5103	CFF	1	0
6	E	5103	CFF	1	0
5	G	5102	ATP	1	0
6	G	5103	CFF	1	0

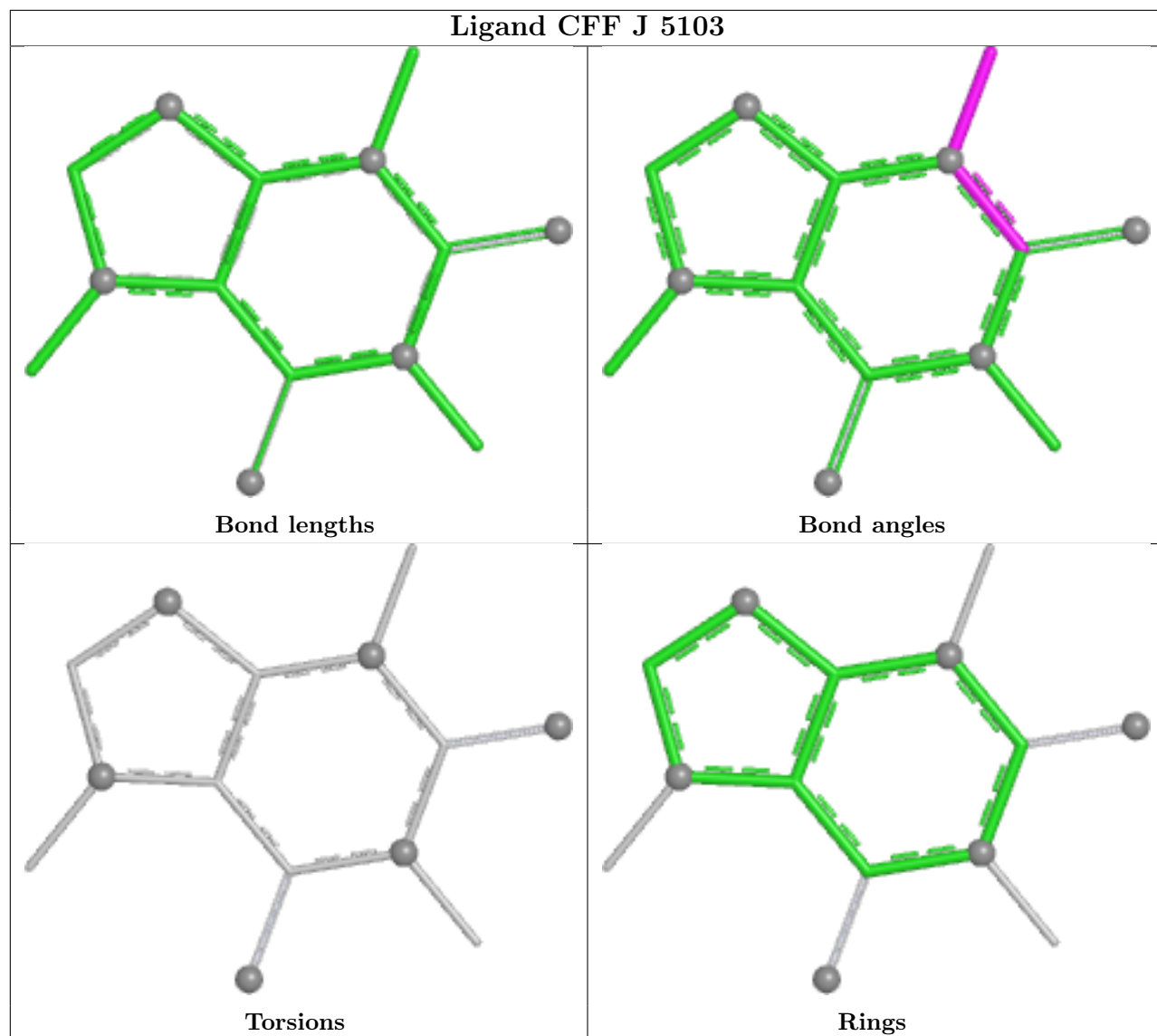
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

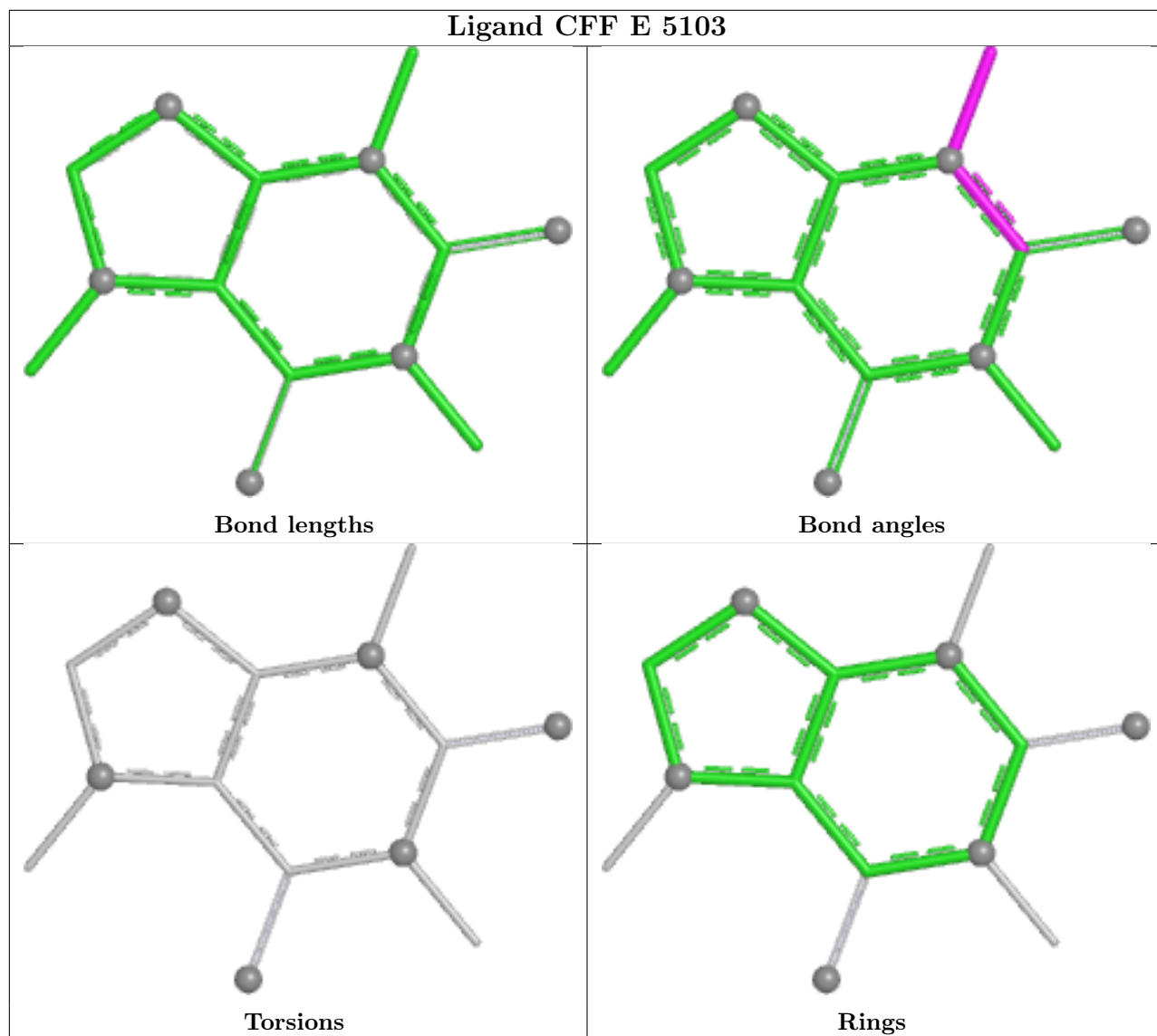


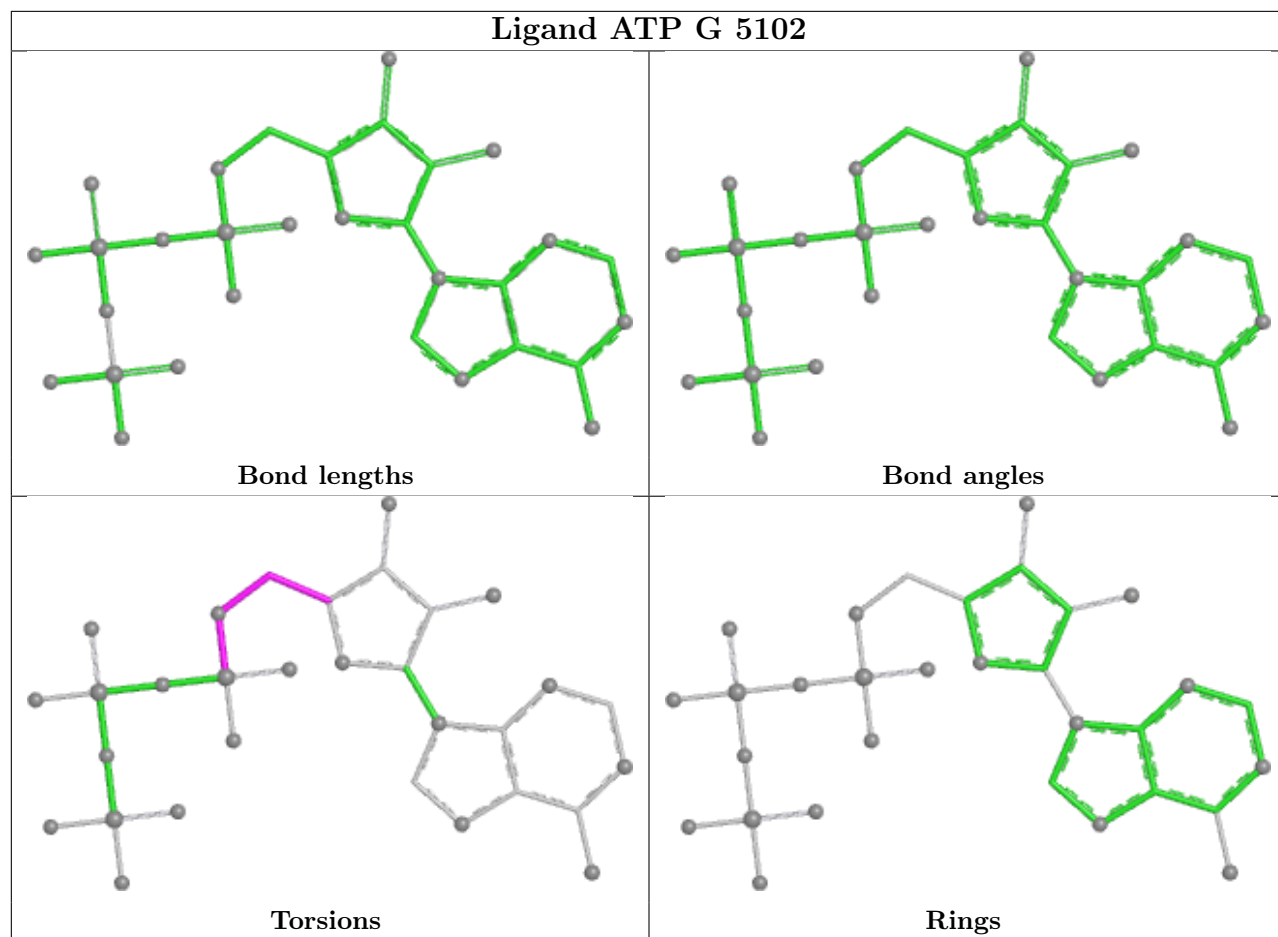


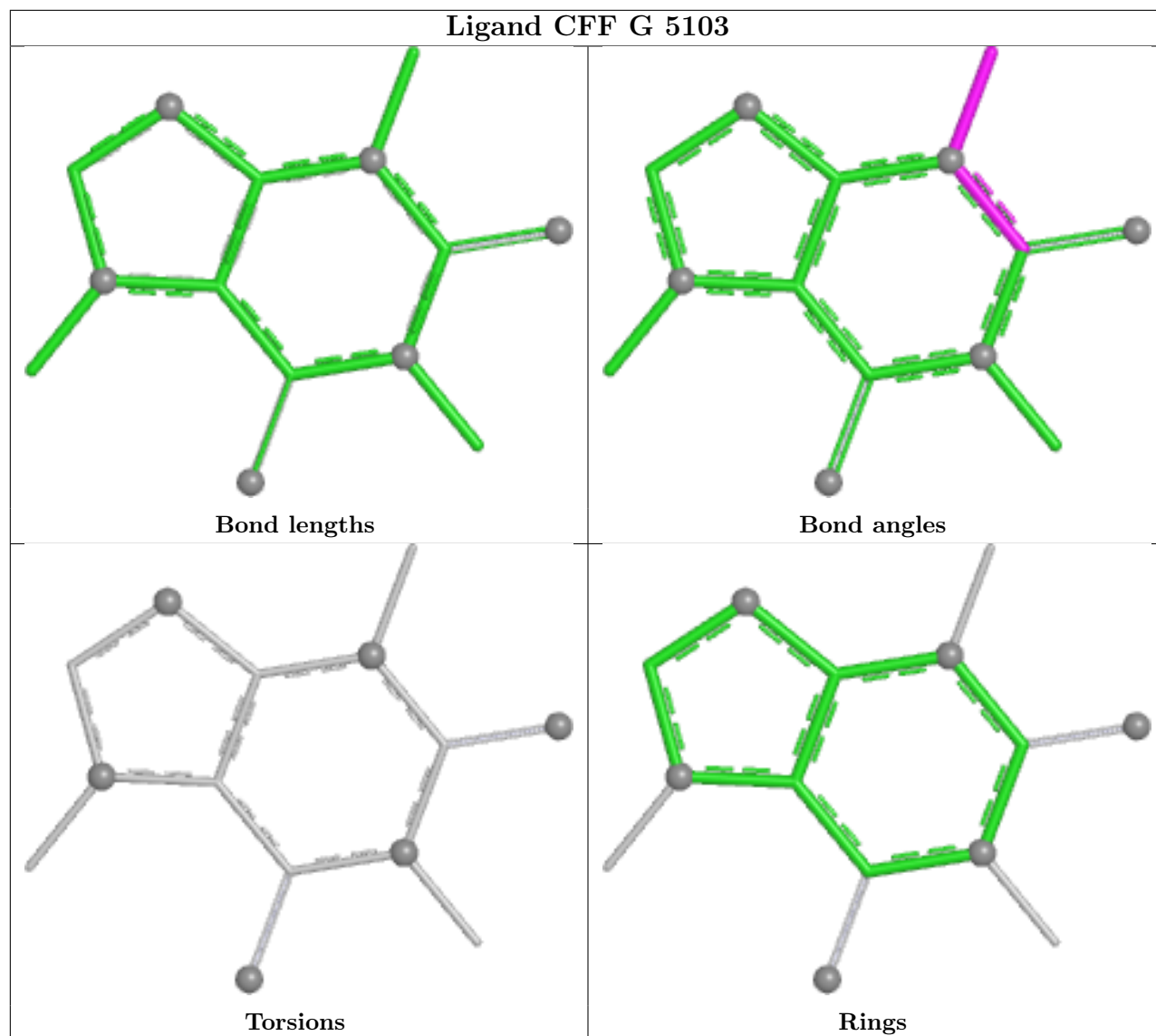












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

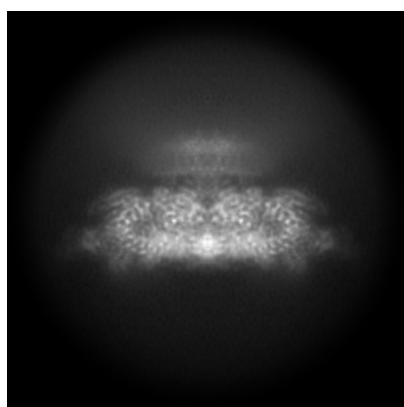
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-19464. These allow visual inspection of the internal detail of the map and identification of artifacts.

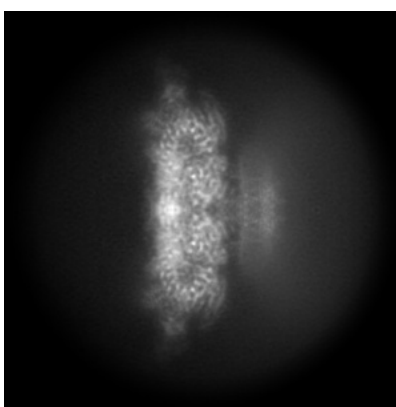
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

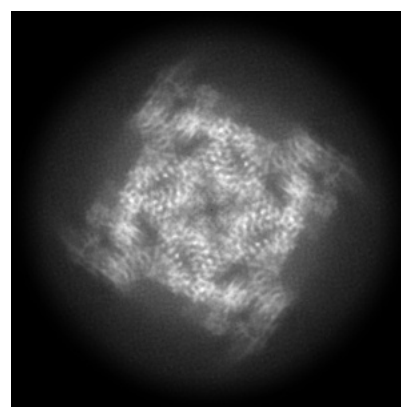
6.1.1 Primary map



X



Y

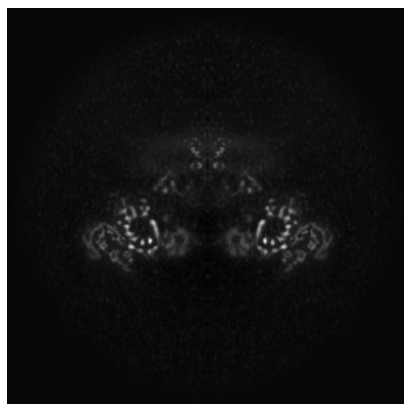


Z

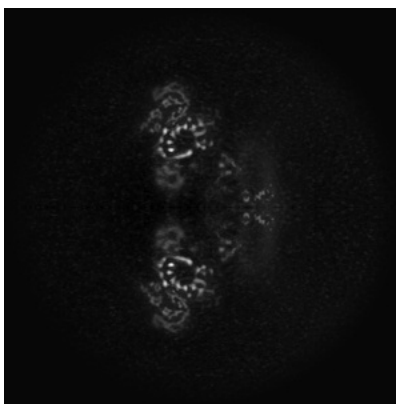
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

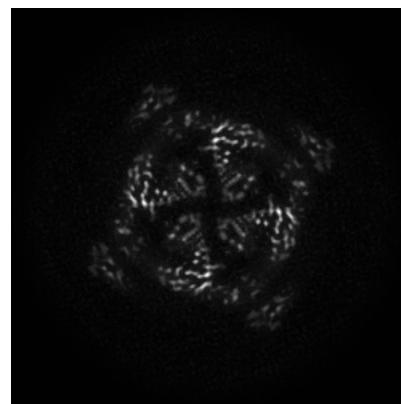
6.2.1 Primary map



X Index: 168



Y Index: 168

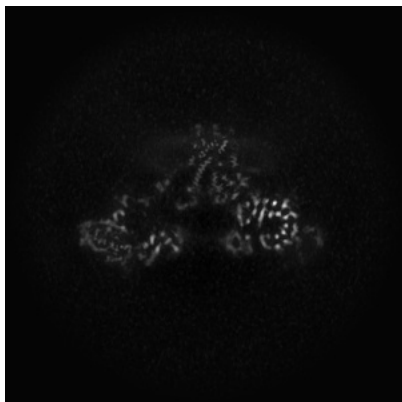


Z Index: 168

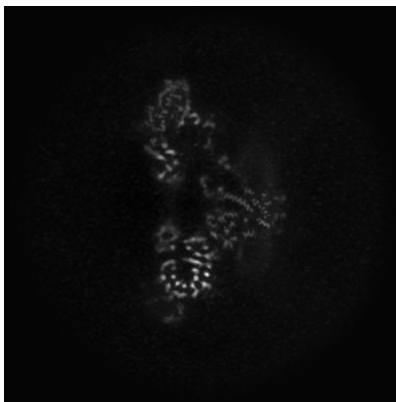
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

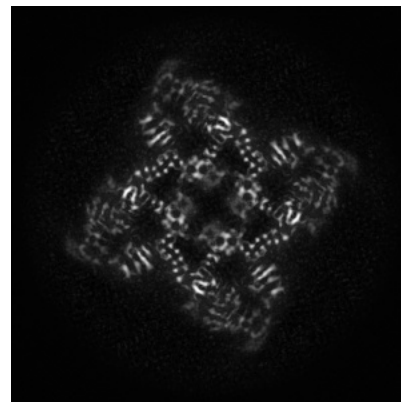
6.3.1 Primary map



X Index: 175



Y Index: 175

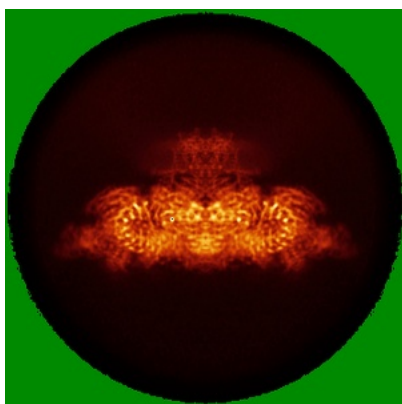


Z Index: 144

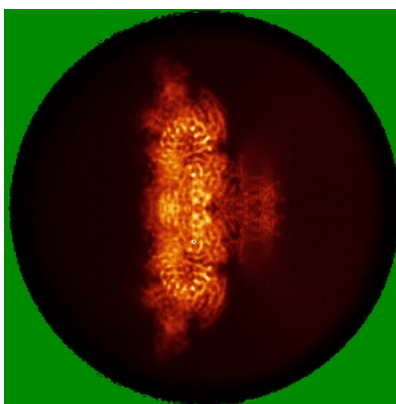
The images above show the largest variance slices of the map in three orthogonal directions.

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

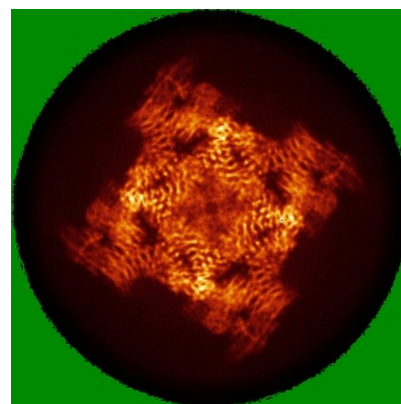
6.4.1 Primary map



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



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.2. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

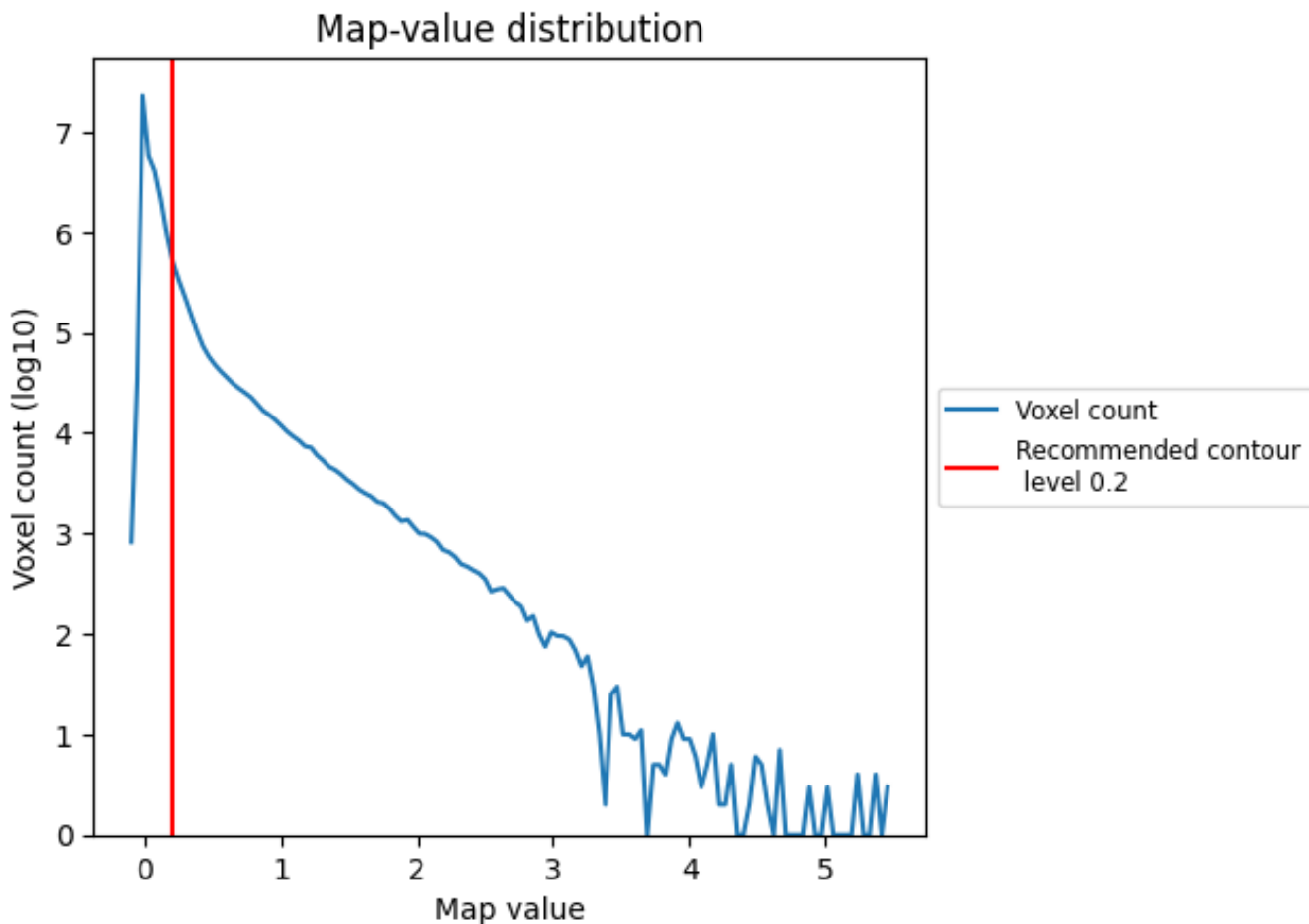
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

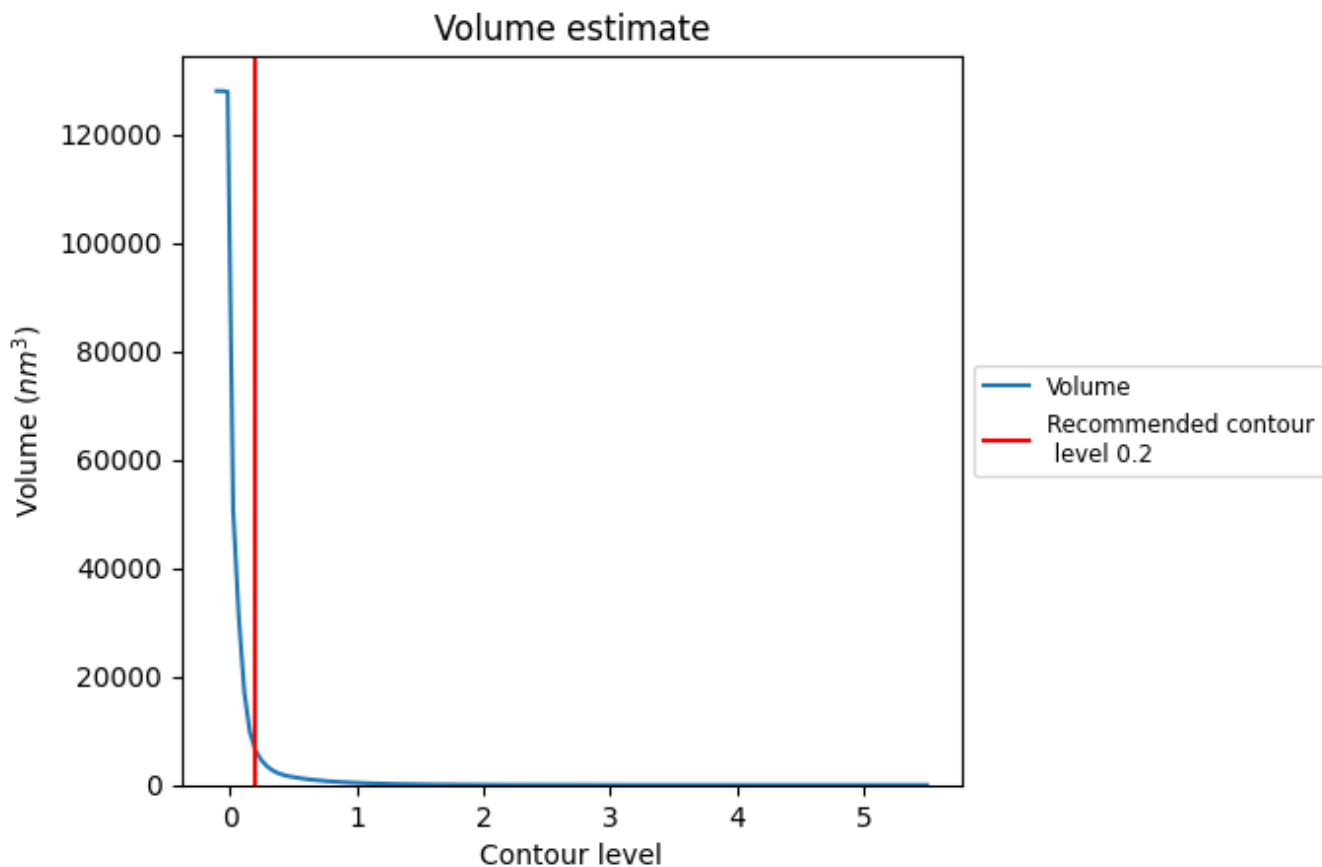
This section contains the results of statistical analysis of the map.

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.

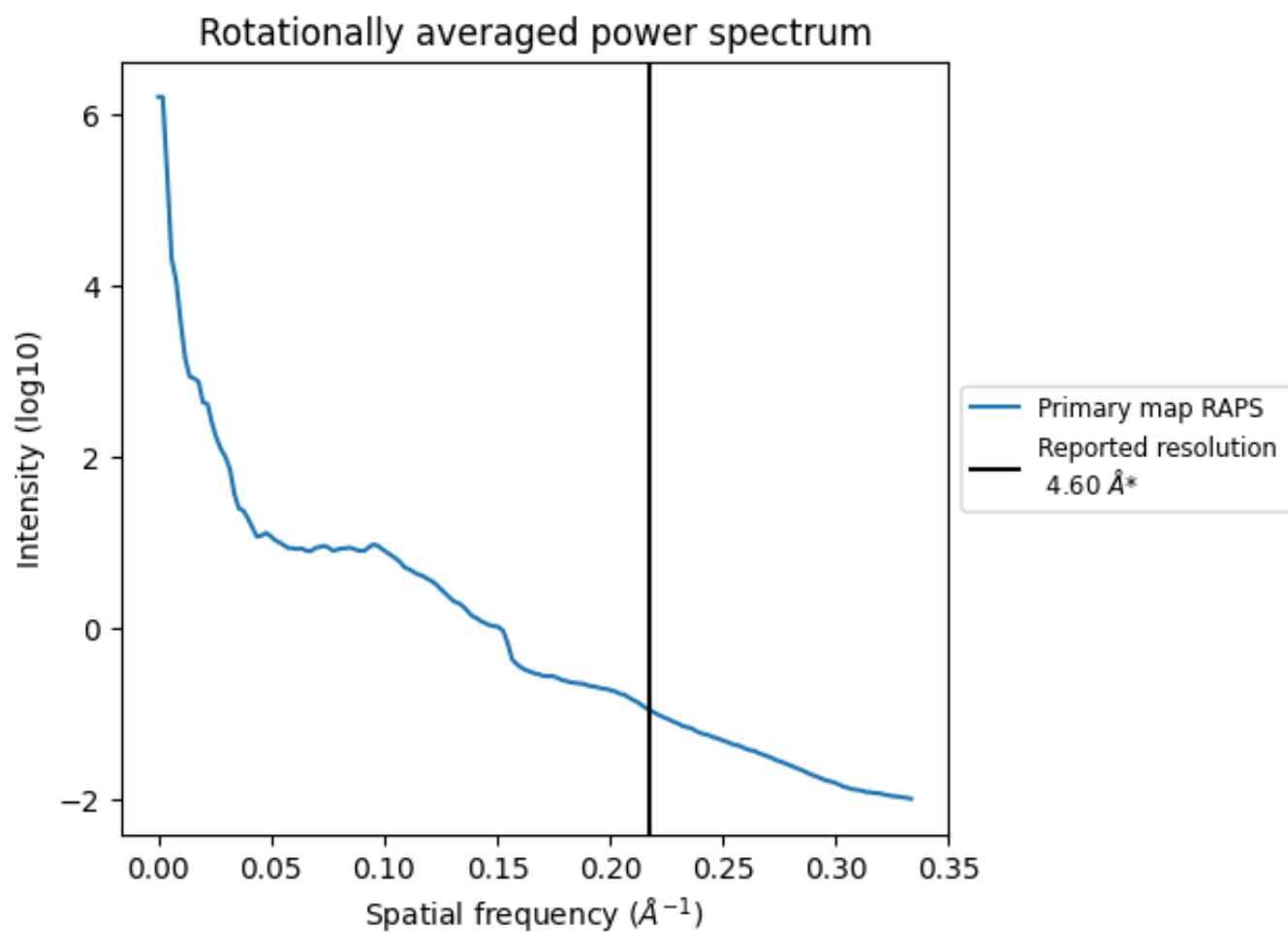
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 6569 nm^3 ; this corresponds to an approximate mass of 5934 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 i

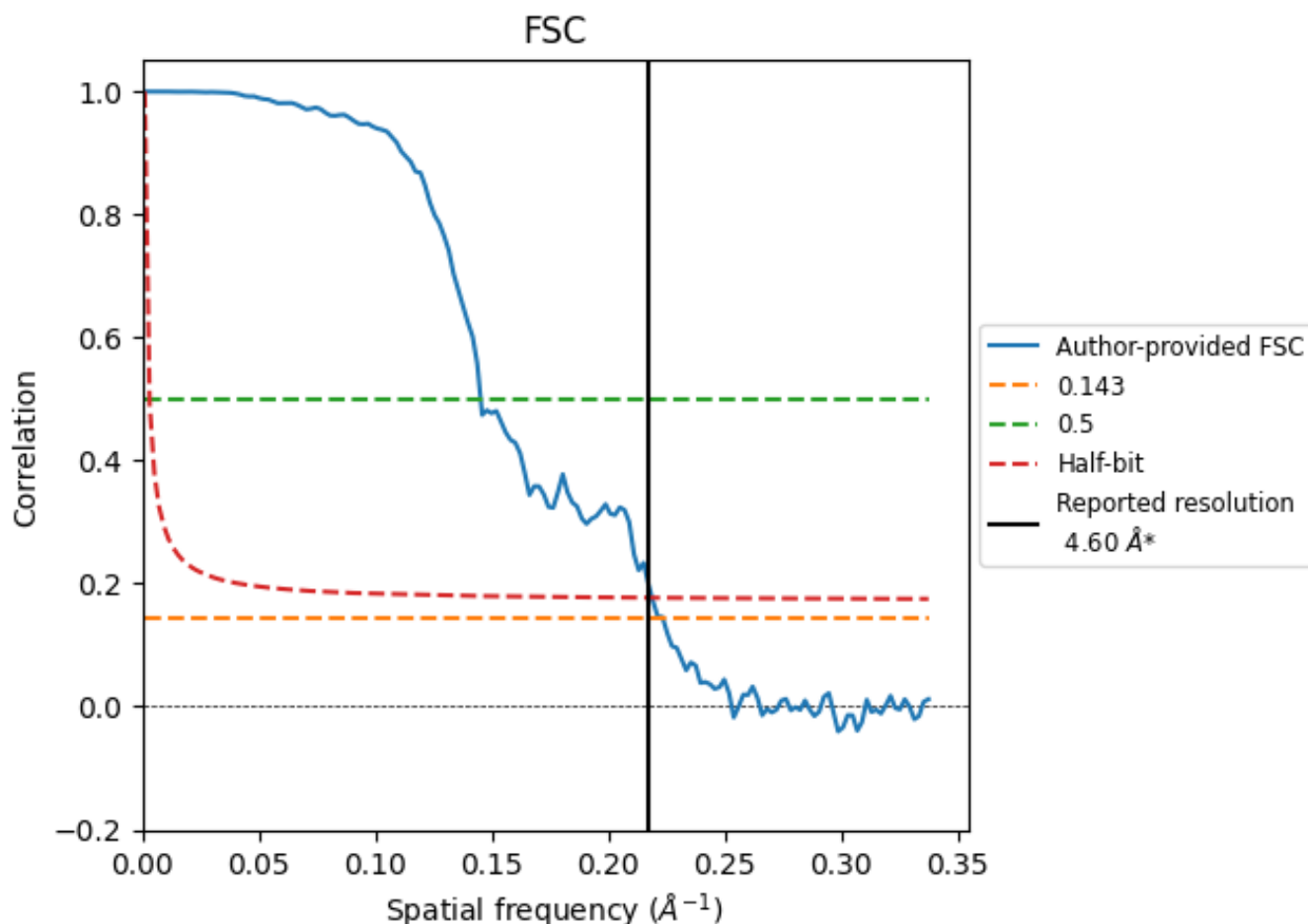


*Reported resolution corresponds to spatial frequency of 0.217 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.217 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.60	-	-
Author-provided FSC curve	4.48	6.89	4.57
Unmasked-calculated*	-	-	-

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

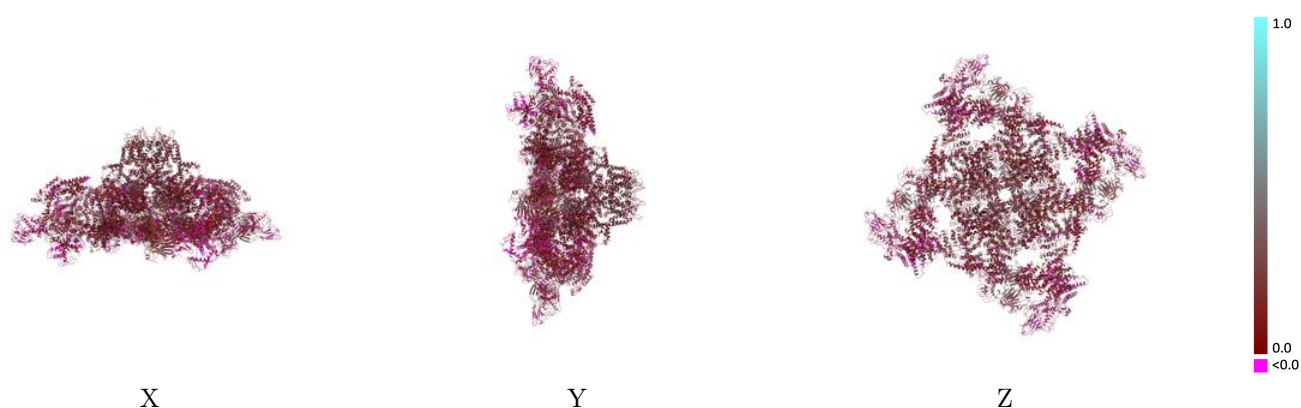
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-19464 and PDB model 8RRT. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlay [i](#)

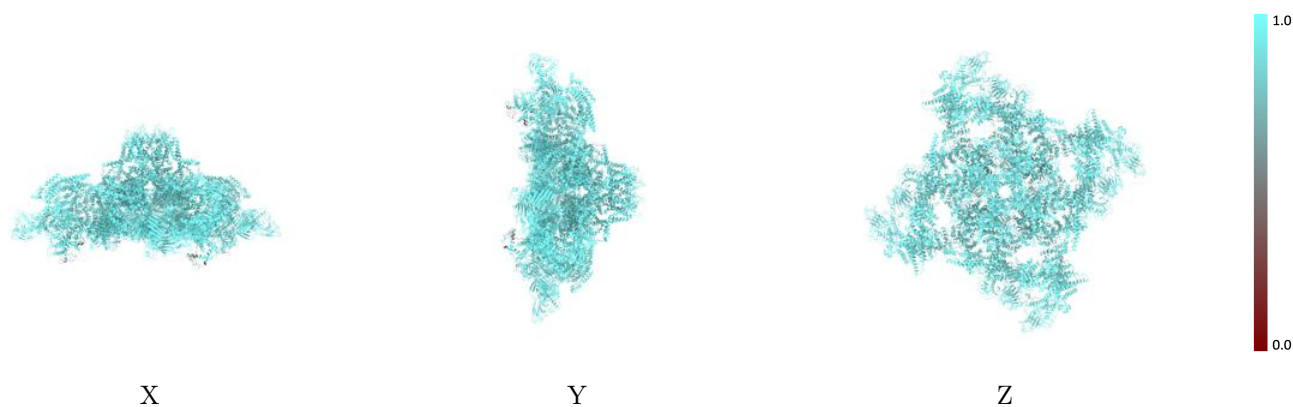
This section was not generated.

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



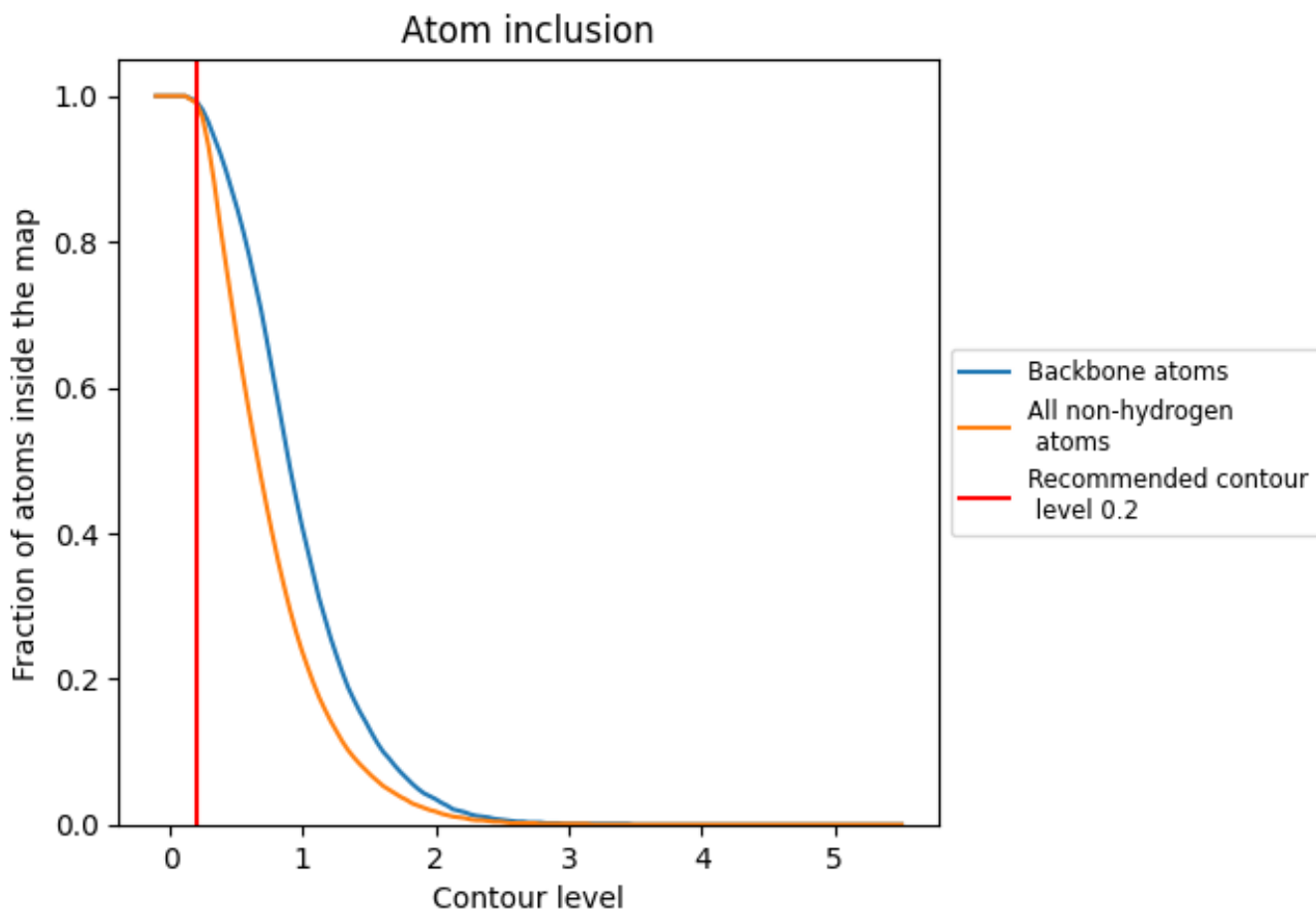
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



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 (0.2).



























9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 99% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary [i](#)

The table lists the average atom inclusion at the recommended contour level (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9900	 0.1540
A	 0.9980	 0.1450
B	 0.9910	 0.1570
C	 0.9680	 0.0830
D	 0.9980	 0.1380
E	 0.9910	 0.1560
F	 0.9680	 0.0820
G	 0.9910	 0.1570
H	 0.9980	 0.1350
I	 0.9980	 0.1380
J	 0.9910	 0.1560
K	 0.9680	 0.0800
M	 0.9670	 0.0810

