



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 02:31 PM UTC

PDB ID : 4V8L / pdb_00004v8l
EMDB ID : EMD-2238
Title : Cryo-EM Structure of the Mycobacterial Fatty Acid Synthase
Authors : Boehringer, D.; Ban, N.; Leibundgut, M.
Deposited on : 2012-12-06
Resolution : 7.50 Å(reported)
Based on initial model : 2UV8

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:

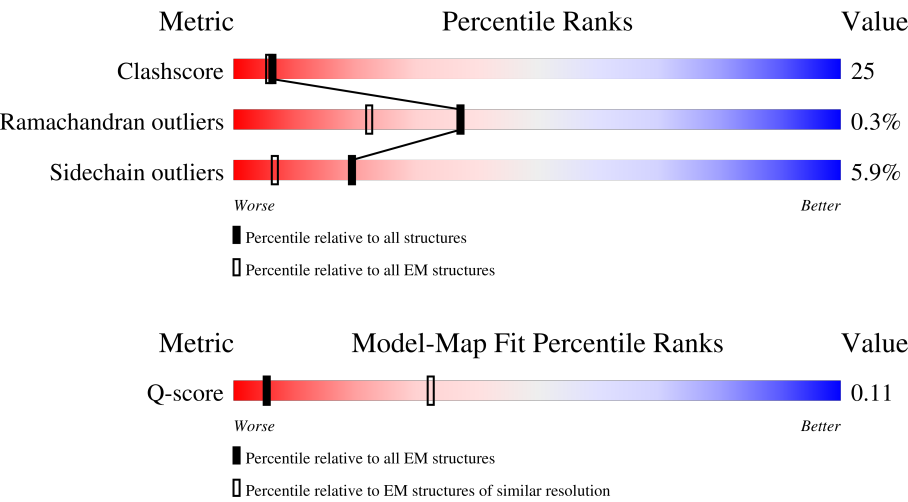
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

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

The reported resolution of this entry is 7.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	436 (7.00 - 8.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	3089	
1	B	3089	
1	C	3089	
1	D	3089	

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Mol	Chain	Length	Quality of chain
1	E	3089	17% 86% 5% 9%
1	F	3089	15% 86% 5% 9%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 126306 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 FATTY ACID SYNTHASE.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	D	2822	Total 21020	C 13294	N 3662	O 3998	S 66	0	0
1	E	2822	Total 21020	C 13294	N 3662	O 3998	S 66	0	0
1	F	2822	Total 21020	C 13294	N 3662	O 3998	S 66	0	0
1	A	2822	Total 21020	C 13294	N 3662	O 3998	S 66	0	0
1	B	2822	Total 21020	C 13294	N 3662	O 3998	S 66	0	0
1	C	2822	Total 21020	C 13294	N 3662	O 3998	S 66	0	0

There are 1086 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	929	UNK	GLU	conflict	UNP A0R1H7
D	930	UNK	PRO	conflict	UNP A0R1H7
D	931	UNK	VAL	conflict	UNP A0R1H7
D	932	UNK	GLU	conflict	UNP A0R1H7
D	933	UNK	VAL	conflict	UNP A0R1H7
D	934	UNK	LEU	conflict	UNP A0R1H7
D	935	UNK	SER	conflict	UNP A0R1H7
D	936	UNK	ARG	conflict	UNP A0R1H7
D	937	UNK	ARG	conflict	UNP A0R1H7
D	938	UNK	GLN	conflict	UNP A0R1H7
D	939	UNK	ALA	conflict	UNP A0R1H7
D	940	UNK	ARG	conflict	UNP A0R1H7
D	941	UNK	ARG	conflict	UNP A0R1H7
D	942	UNK	ASP	conflict	UNP A0R1H7
D	943	UNK	ALA	conflict	UNP A0R1H7
D	944	UNK	SER	conflict	UNP A0R1H7
D	974	UNK	THR	conflict	UNP A0R1H7
D	975	UNK	GLU	conflict	UNP A0R1H7

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Chain	Residue	Modelled	Actual	Comment	Reference
D	976	UNK	TRP	conflict	UNP A0R1H7
D	977	UNK	GLN	conflict	UNP A0R1H7
D	978	UNK	VAL	conflict	UNP A0R1H7
D	979	UNK	ARG	conflict	UNP A0R1H7
D	980	UNK	GLU	conflict	UNP A0R1H7
D	981	UNK	GLY	conflict	UNP A0R1H7
D	982	UNK	SER	conflict	UNP A0R1H7
D	983	UNK	ASP	conflict	UNP A0R1H7
D	984	UNK	ASN	conflict	UNP A0R1H7
D	985	UNK	ARG	conflict	UNP A0R1H7
D	986	UNK	SER	conflict	UNP A0R1H7
D	987	UNK	ALA	conflict	UNP A0R1H7
D	988	UNK	SER	conflict	UNP A0R1H7
D	989	UNK	HIS	conflict	UNP A0R1H7
D	990	UNK	PRO	conflict	UNP A0R1H7
D	991	UNK	SER	conflict	UNP A0R1H7
D	992	UNK	THR	conflict	UNP A0R1H7
D	993	UNK	GLY	conflict	UNP A0R1H7
D	994	UNK	ALA	conflict	UNP A0R1H7
D	995	UNK	ARG	conflict	UNP A0R1H7
D	996	UNK	LEU	conflict	UNP A0R1H7
D	997	UNK	GLU	conflict	UNP A0R1H7
D	998	UNK	VAL	conflict	UNP A0R1H7
D	999	UNK	ALA	conflict	UNP A0R1H7
D	1000	UNK	ASP	conflict	UNP A0R1H7
D	1001	UNK	ASP	conflict	UNP A0R1H7
D	1002	UNK	GLN	conflict	UNP A0R1H7
D	1003	UNK	HIS	conflict	UNP A0R1H7
D	1004	UNK	VAL	conflict	UNP A0R1H7
D	1005	UNK	VAL	conflict	UNP A0R1H7
D	1006	UNK	LEU	conflict	UNP A0R1H7
D	1007	UNK	SER	conflict	UNP A0R1H7
D	1008	UNK	VAL	conflict	UNP A0R1H7
D	1009	UNK	PRO	conflict	UNP A0R1H7
D	1010	UNK	LEU	conflict	UNP A0R1H7
D	1011	UNK	SER	conflict	UNP A0R1H7
D	1012	UNK	GLY	conflict	UNP A0R1H7
D	1013	UNK	THR	conflict	UNP A0R1H7
D	1014	UNK	TRP	conflict	UNP A0R1H7
D	1196	UNK	GLY	conflict	UNP A0R1H7
D	1197	UNK	ARG	conflict	UNP A0R1H7
D	1198	UNK	THR	conflict	UNP A0R1H7

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Chain	Residue	Modelled	Actual	Comment	Reference
D	1199	UNK	GLY	conflict	UNP A0R1H7
D	1200	UNK	ALA	conflict	UNP A0R1H7
D	1201	UNK	ALA	conflict	UNP A0R1H7
D	1202	UNK	GLU	conflict	UNP A0R1H7
D	1203	UNK	LEU	conflict	UNP A0R1H7
D	1204	UNK	THR	conflict	UNP A0R1H7
D	1205	UNK	ASP	conflict	UNP A0R1H7
D	1206	UNK	PRO	conflict	UNP A0R1H7
D	1207	UNK	VAL	conflict	UNP A0R1H7
D	1208	UNK	ARG	conflict	UNP A0R1H7
D	1209	UNK	ALA	conflict	UNP A0R1H7
D	1210	UNK	GLY	conflict	UNP A0R1H7
D	1211	UNK	GLY	conflict	UNP A0R1H7
D	1212	UNK	ALA	conflict	UNP A0R1H7
D	1213	UNK	ILE	conflict	UNP A0R1H7
D	1214	UNK	SER	conflict	UNP A0R1H7
D	1215	UNK	ASP	conflict	UNP A0R1H7
D	1216	UNK	ASN	conflict	UNP A0R1H7
D	1217	UNK	ALA	conflict	UNP A0R1H7
D	1218	UNK	THR	conflict	UNP A0R1H7
D	1219	UNK	ASP	conflict	UNP A0R1H7
D	1220	UNK	THR	conflict	UNP A0R1H7
D	1221	UNK	PRO	conflict	UNP A0R1H7
D	1222	UNK	ARG	conflict	UNP A0R1H7
D	1223	UNK	ARG	conflict	UNP A0R1H7
D	1224	UNK	ARG	conflict	UNP A0R1H7
D	1225	UNK	ARG	conflict	UNP A0R1H7
D	1226	UNK	ARG	conflict	UNP A0R1H7
D	1227	UNK	ASP	conflict	UNP A0R1H7
D	2076	UNK	GLY	conflict	UNP A0R1H7
D	2077	UNK	ASP	conflict	UNP A0R1H7
D	2078	UNK	ILE	conflict	UNP A0R1H7
D	2079	UNK	ASP	conflict	UNP A0R1H7
D	2080	UNK	ALA	conflict	UNP A0R1H7
D	2081	UNK	GLN	conflict	UNP A0R1H7
D	2082	UNK	TRP	conflict	UNP A0R1H7
D	2083	UNK	GLU	conflict	UNP A0R1H7
D	2084	UNK	GLN	conflict	UNP A0R1H7
D	2085	UNK	LEU	conflict	UNP A0R1H7
D	2086	UNK	SER	conflict	UNP A0R1H7
D	2087	UNK	GLN	conflict	UNP A0R1H7
D	2088	UNK	ARG	conflict	UNP A0R1H7

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Chain	Residue	Modelled	Actual	Comment	Reference
D	2089	UNK	PHE	conflict	UNP A0R1H7
D	2090	UNK	GLU	conflict	UNP A0R1H7
D	2091	UNK	GLY	conflict	UNP A0R1H7
D	2092	UNK	THR	conflict	UNP A0R1H7
D	2093	UNK	GLY	conflict	UNP A0R1H7
D	2094	UNK	HIS	conflict	UNP A0R1H7
D	2095	UNK	VAL	conflict	UNP A0R1H7
D	2096	UNK	VAL	conflict	UNP A0R1H7
D	2097	UNK	ALA	conflict	UNP A0R1H7
D	2098	UNK	THR	conflict	UNP A0R1H7
D	2099	UNK	GLN	conflict	UNP A0R1H7
D	2100	UNK	ALA	conflict	UNP A0R1H7
D	2101	UNK	ASN	conflict	UNP A0R1H7
D	2102	UNK	TRP	conflict	UNP A0R1H7
D	2103	UNK	TRP	conflict	UNP A0R1H7
D	2104	UNK	GLN	conflict	UNP A0R1H7
D	2105	UNK	GLY	conflict	UNP A0R1H7
D	2106	UNK	LYS	conflict	UNP A0R1H7
D	2107	UNK	ALA	conflict	UNP A0R1H7
D	2108	UNK	LEU	conflict	UNP A0R1H7
D	2109	UNK	ALA	conflict	UNP A0R1H7
D	2110	UNK	ALA	conflict	UNP A0R1H7
D	2111	UNK	GLY	conflict	UNP A0R1H7
D	2112	UNK	ARG	conflict	UNP A0R1H7
D	2113	UNK	ASN	conflict	UNP A0R1H7
D	2114	UNK	VAL	conflict	UNP A0R1H7
D	2115	UNK	HIS	conflict	UNP A0R1H7
D	2116	UNK	ALA	conflict	UNP A0R1H7
D	2117	UNK	SER	conflict	UNP A0R1H7
D	2118	UNK	LEU	conflict	UNP A0R1H7
D	2119	UNK	PHE	conflict	UNP A0R1H7
D	2120	UNK	GLY	conflict	UNP A0R1H7
D	2121	UNK	ARG	conflict	UNP A0R1H7
D	2122	UNK	ILE	conflict	UNP A0R1H7
D	2123	UNK	ALA	conflict	UNP A0R1H7
D	2124	UNK	ALA	conflict	UNP A0R1H7
D	2125	UNK	GLY	conflict	UNP A0R1H7
D	2126	UNK	ALA	conflict	UNP A0R1H7
D	2127	UNK	GLU	conflict	UNP A0R1H7
D	2128	UNK	ASN	conflict	UNP A0R1H7
D	2129	UNK	PRO	conflict	UNP A0R1H7
D	2130	UNK	GLY	conflict	UNP A0R1H7

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Chain	Residue	Modelled	Actual	Comment	Reference
D	2131	UNK	LYS	conflict	UNP A0R1H7
D	2132	UNK	GLY	conflict	UNP A0R1H7
D	2133	UNK	ARG	conflict	UNP A0R1H7
D	2134	UNK	TYR	conflict	UNP A0R1H7
D	2135	UNK	SER	conflict	UNP A0R1H7
D	2422	UNK	GLU	conflict	UNP A0R1H7
D	2423	UNK	SER	conflict	UNP A0R1H7
D	2424	UNK	ASP	conflict	UNP A0R1H7
D	2425	UNK	ASP	conflict	UNP A0R1H7
D	2426	UNK	GLU	conflict	UNP A0R1H7
D	2427	UNK	ALA	conflict	UNP A0R1H7
D	2428	UNK	PRO	conflict	UNP A0R1H7
D	2429	UNK	ALA	conflict	UNP A0R1H7
D	2430	UNK	GLY	conflict	UNP A0R1H7
D	2431	UNK	THR	conflict	UNP A0R1H7
D	2432	UNK	ILE	conflict	UNP A0R1H7
D	2433	UNK	ARG	conflict	UNP A0R1H7
D	2434	UNK	ALA	conflict	UNP A0R1H7
D	2435	UNK	LEU	conflict	UNP A0R1H7
D	2436	UNK	PRO	conflict	UNP A0R1H7
D	2437	UNK	SER	conflict	UNP A0R1H7
D	2438	UNK	PRO	conflict	UNP A0R1H7
D	2439	UNK	PRO	conflict	UNP A0R1H7
D	2440	UNK	ARG	conflict	UNP A0R1H7
D	2441	UNK	GLY	conflict	UNP A0R1H7
D	2442	UNK	TYR	conflict	UNP A0R1H7
D	2443	UNK	ASN	conflict	UNP A0R1H7
D	2444	UNK	PRO	conflict	UNP A0R1H7
D	2445	UNK	ALA	conflict	UNP A0R1H7
D	2446	UNK	PRO	conflict	UNP A0R1H7
D	2447	UNK	ALA	conflict	UNP A0R1H7
D	2448	UNK	PRO	conflict	UNP A0R1H7
D	2449	UNK	GLU	conflict	UNP A0R1H7
D	2450	UNK	TRP	conflict	UNP A0R1H7
D	2451	UNK	ASP	conflict	UNP A0R1H7
D	2452	UNK	ASP	conflict	UNP A0R1H7
D	2453	UNK	LEU	conflict	UNP A0R1H7
E	929	UNK	GLU	conflict	UNP A0R1H7
E	930	UNK	PRO	conflict	UNP A0R1H7
E	931	UNK	VAL	conflict	UNP A0R1H7
E	932	UNK	GLU	conflict	UNP A0R1H7
E	933	UNK	VAL	conflict	UNP A0R1H7

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Chain	Residue	Modelled	Actual	Comment	Reference
E	934	UNK	LEU	conflict	UNP A0R1H7
E	935	UNK	SER	conflict	UNP A0R1H7
E	936	UNK	ARG	conflict	UNP A0R1H7
E	937	UNK	ARG	conflict	UNP A0R1H7
E	938	UNK	GLN	conflict	UNP A0R1H7
E	939	UNK	ALA	conflict	UNP A0R1H7
E	940	UNK	ARG	conflict	UNP A0R1H7
E	941	UNK	ARG	conflict	UNP A0R1H7
E	942	UNK	ASP	conflict	UNP A0R1H7
E	943	UNK	ALA	conflict	UNP A0R1H7
E	944	UNK	SER	conflict	UNP A0R1H7
E	974	UNK	THR	conflict	UNP A0R1H7
E	975	UNK	GLU	conflict	UNP A0R1H7
E	976	UNK	TRP	conflict	UNP A0R1H7
E	977	UNK	GLN	conflict	UNP A0R1H7
E	978	UNK	VAL	conflict	UNP A0R1H7
E	979	UNK	ARG	conflict	UNP A0R1H7
E	980	UNK	GLU	conflict	UNP A0R1H7
E	981	UNK	GLY	conflict	UNP A0R1H7
E	982	UNK	SER	conflict	UNP A0R1H7
E	983	UNK	ASP	conflict	UNP A0R1H7
E	984	UNK	ASN	conflict	UNP A0R1H7
E	985	UNK	ARG	conflict	UNP A0R1H7
E	986	UNK	SER	conflict	UNP A0R1H7
E	987	UNK	ALA	conflict	UNP A0R1H7
E	988	UNK	SER	conflict	UNP A0R1H7
E	989	UNK	HIS	conflict	UNP A0R1H7
E	990	UNK	PRO	conflict	UNP A0R1H7
E	991	UNK	SER	conflict	UNP A0R1H7
E	992	UNK	THR	conflict	UNP A0R1H7
E	993	UNK	GLY	conflict	UNP A0R1H7
E	994	UNK	ALA	conflict	UNP A0R1H7
E	995	UNK	ARG	conflict	UNP A0R1H7
E	996	UNK	LEU	conflict	UNP A0R1H7
E	997	UNK	GLU	conflict	UNP A0R1H7
E	998	UNK	VAL	conflict	UNP A0R1H7
E	999	UNK	ALA	conflict	UNP A0R1H7
E	1000	UNK	ASP	conflict	UNP A0R1H7
E	1001	UNK	ASP	conflict	UNP A0R1H7
E	1002	UNK	GLN	conflict	UNP A0R1H7
E	1003	UNK	HIS	conflict	UNP A0R1H7
E	1004	UNK	VAL	conflict	UNP A0R1H7

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Chain	Residue	Modelled	Actual	Comment	Reference
E	1005	UNK	VAL	conflict	UNP A0R1H7
E	1006	UNK	LEU	conflict	UNP A0R1H7
E	1007	UNK	SER	conflict	UNP A0R1H7
E	1008	UNK	VAL	conflict	UNP A0R1H7
E	1009	UNK	PRO	conflict	UNP A0R1H7
E	1010	UNK	LEU	conflict	UNP A0R1H7
E	1011	UNK	SER	conflict	UNP A0R1H7
E	1012	UNK	GLY	conflict	UNP A0R1H7
E	1013	UNK	THR	conflict	UNP A0R1H7
E	1014	UNK	TRP	conflict	UNP A0R1H7
E	1196	UNK	GLY	conflict	UNP A0R1H7
E	1197	UNK	ARG	conflict	UNP A0R1H7
E	1198	UNK	THR	conflict	UNP A0R1H7
E	1199	UNK	GLY	conflict	UNP A0R1H7
E	1200	UNK	ALA	conflict	UNP A0R1H7
E	1201	UNK	ALA	conflict	UNP A0R1H7
E	1202	UNK	GLU	conflict	UNP A0R1H7
E	1203	UNK	LEU	conflict	UNP A0R1H7
E	1204	UNK	THR	conflict	UNP A0R1H7
E	1205	UNK	ASP	conflict	UNP A0R1H7
E	1206	UNK	PRO	conflict	UNP A0R1H7
E	1207	UNK	VAL	conflict	UNP A0R1H7
E	1208	UNK	ARG	conflict	UNP A0R1H7
E	1209	UNK	ALA	conflict	UNP A0R1H7
E	1210	UNK	GLY	conflict	UNP A0R1H7
E	1211	UNK	GLY	conflict	UNP A0R1H7
E	1212	UNK	ALA	conflict	UNP A0R1H7
E	1213	UNK	ILE	conflict	UNP A0R1H7
E	1214	UNK	SER	conflict	UNP A0R1H7
E	1215	UNK	ASP	conflict	UNP A0R1H7
E	1216	UNK	ASN	conflict	UNP A0R1H7
E	1217	UNK	ALA	conflict	UNP A0R1H7
E	1218	UNK	THR	conflict	UNP A0R1H7
E	1219	UNK	ASP	conflict	UNP A0R1H7
E	1220	UNK	THR	conflict	UNP A0R1H7
E	1221	UNK	PRO	conflict	UNP A0R1H7
E	1222	UNK	ARG	conflict	UNP A0R1H7
E	1223	UNK	ARG	conflict	UNP A0R1H7
E	1224	UNK	ARG	conflict	UNP A0R1H7
E	1225	UNK	ARG	conflict	UNP A0R1H7
E	1226	UNK	ARG	conflict	UNP A0R1H7
E	1227	UNK	ASP	conflict	UNP A0R1H7

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Chain	Residue	Modelled	Actual	Comment	Reference
E	2076	UNK	GLY	conflict	UNP A0R1H7
E	2077	UNK	ASP	conflict	UNP A0R1H7
E	2078	UNK	ILE	conflict	UNP A0R1H7
E	2079	UNK	ASP	conflict	UNP A0R1H7
E	2080	UNK	ALA	conflict	UNP A0R1H7
E	2081	UNK	GLN	conflict	UNP A0R1H7
E	2082	UNK	TRP	conflict	UNP A0R1H7
E	2083	UNK	GLU	conflict	UNP A0R1H7
E	2084	UNK	GLN	conflict	UNP A0R1H7
E	2085	UNK	LEU	conflict	UNP A0R1H7
E	2086	UNK	SER	conflict	UNP A0R1H7
E	2087	UNK	GLN	conflict	UNP A0R1H7
E	2088	UNK	ARG	conflict	UNP A0R1H7
E	2089	UNK	PHE	conflict	UNP A0R1H7
E	2090	UNK	GLU	conflict	UNP A0R1H7
E	2091	UNK	GLY	conflict	UNP A0R1H7
E	2092	UNK	THR	conflict	UNP A0R1H7
E	2093	UNK	GLY	conflict	UNP A0R1H7
E	2094	UNK	HIS	conflict	UNP A0R1H7
E	2095	UNK	VAL	conflict	UNP A0R1H7
E	2096	UNK	VAL	conflict	UNP A0R1H7
E	2097	UNK	ALA	conflict	UNP A0R1H7
E	2098	UNK	THR	conflict	UNP A0R1H7
E	2099	UNK	GLN	conflict	UNP A0R1H7
E	2100	UNK	ALA	conflict	UNP A0R1H7
E	2101	UNK	ASN	conflict	UNP A0R1H7
E	2102	UNK	TRP	conflict	UNP A0R1H7
E	2103	UNK	TRP	conflict	UNP A0R1H7
E	2104	UNK	GLN	conflict	UNP A0R1H7
E	2105	UNK	GLY	conflict	UNP A0R1H7
E	2106	UNK	LYS	conflict	UNP A0R1H7
E	2107	UNK	ALA	conflict	UNP A0R1H7
E	2108	UNK	LEU	conflict	UNP A0R1H7
E	2109	UNK	ALA	conflict	UNP A0R1H7
E	2110	UNK	ALA	conflict	UNP A0R1H7
E	2111	UNK	GLY	conflict	UNP A0R1H7
E	2112	UNK	ARG	conflict	UNP A0R1H7
E	2113	UNK	ASN	conflict	UNP A0R1H7
E	2114	UNK	VAL	conflict	UNP A0R1H7
E	2115	UNK	HIS	conflict	UNP A0R1H7
E	2116	UNK	ALA	conflict	UNP A0R1H7
E	2117	UNK	SER	conflict	UNP A0R1H7

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Chain	Residue	Modelled	Actual	Comment	Reference
E	2118	UNK	LEU	conflict	UNP A0R1H7
E	2119	UNK	PHE	conflict	UNP A0R1H7
E	2120	UNK	GLY	conflict	UNP A0R1H7
E	2121	UNK	ARG	conflict	UNP A0R1H7
E	2122	UNK	ILE	conflict	UNP A0R1H7
E	2123	UNK	ALA	conflict	UNP A0R1H7
E	2124	UNK	ALA	conflict	UNP A0R1H7
E	2125	UNK	GLY	conflict	UNP A0R1H7
E	2126	UNK	ALA	conflict	UNP A0R1H7
E	2127	UNK	GLU	conflict	UNP A0R1H7
E	2128	UNK	ASN	conflict	UNP A0R1H7
E	2129	UNK	PRO	conflict	UNP A0R1H7
E	2130	UNK	GLY	conflict	UNP A0R1H7
E	2131	UNK	LYS	conflict	UNP A0R1H7
E	2132	UNK	GLY	conflict	UNP A0R1H7
E	2133	UNK	ARG	conflict	UNP A0R1H7
E	2134	UNK	TYR	conflict	UNP A0R1H7
E	2135	UNK	SER	conflict	UNP A0R1H7
E	2422	UNK	GLU	conflict	UNP A0R1H7
E	2423	UNK	SER	conflict	UNP A0R1H7
E	2424	UNK	ASP	conflict	UNP A0R1H7
E	2425	UNK	ASP	conflict	UNP A0R1H7
E	2426	UNK	GLU	conflict	UNP A0R1H7
E	2427	UNK	ALA	conflict	UNP A0R1H7
E	2428	UNK	PRO	conflict	UNP A0R1H7
E	2429	UNK	ALA	conflict	UNP A0R1H7
E	2430	UNK	GLY	conflict	UNP A0R1H7
E	2431	UNK	THR	conflict	UNP A0R1H7
E	2432	UNK	ILE	conflict	UNP A0R1H7
E	2433	UNK	ARG	conflict	UNP A0R1H7
E	2434	UNK	ALA	conflict	UNP A0R1H7
E	2435	UNK	LEU	conflict	UNP A0R1H7
E	2436	UNK	PRO	conflict	UNP A0R1H7
E	2437	UNK	SER	conflict	UNP A0R1H7
E	2438	UNK	PRO	conflict	UNP A0R1H7
E	2439	UNK	PRO	conflict	UNP A0R1H7
E	2440	UNK	ARG	conflict	UNP A0R1H7
E	2441	UNK	GLY	conflict	UNP A0R1H7
E	2442	UNK	TYR	conflict	UNP A0R1H7
E	2443	UNK	ASN	conflict	UNP A0R1H7
E	2444	UNK	PRO	conflict	UNP A0R1H7
E	2445	UNK	ALA	conflict	UNP A0R1H7

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Chain	Residue	Modelled	Actual	Comment	Reference
E	2446	UNK	PRO	conflict	UNP A0R1H7
E	2447	UNK	ALA	conflict	UNP A0R1H7
E	2448	UNK	PRO	conflict	UNP A0R1H7
E	2449	UNK	GLU	conflict	UNP A0R1H7
E	2450	UNK	TRP	conflict	UNP A0R1H7
E	2451	UNK	ASP	conflict	UNP A0R1H7
E	2452	UNK	ASP	conflict	UNP A0R1H7
E	2453	UNK	LEU	conflict	UNP A0R1H7
F	929	UNK	GLU	conflict	UNP A0R1H7
F	930	UNK	PRO	conflict	UNP A0R1H7
F	931	UNK	VAL	conflict	UNP A0R1H7
F	932	UNK	GLU	conflict	UNP A0R1H7
F	933	UNK	VAL	conflict	UNP A0R1H7
F	934	UNK	LEU	conflict	UNP A0R1H7
F	935	UNK	SER	conflict	UNP A0R1H7
F	936	UNK	ARG	conflict	UNP A0R1H7
F	937	UNK	ARG	conflict	UNP A0R1H7
F	938	UNK	GLN	conflict	UNP A0R1H7
F	939	UNK	ALA	conflict	UNP A0R1H7
F	940	UNK	ARG	conflict	UNP A0R1H7
F	941	UNK	ARG	conflict	UNP A0R1H7
F	942	UNK	ASP	conflict	UNP A0R1H7
F	943	UNK	ALA	conflict	UNP A0R1H7
F	944	UNK	SER	conflict	UNP A0R1H7
F	974	UNK	THR	conflict	UNP A0R1H7
F	975	UNK	GLU	conflict	UNP A0R1H7
F	976	UNK	TRP	conflict	UNP A0R1H7
F	977	UNK	GLN	conflict	UNP A0R1H7
F	978	UNK	VAL	conflict	UNP A0R1H7
F	979	UNK	ARG	conflict	UNP A0R1H7
F	980	UNK	GLU	conflict	UNP A0R1H7
F	981	UNK	GLY	conflict	UNP A0R1H7
F	982	UNK	SER	conflict	UNP A0R1H7
F	983	UNK	ASP	conflict	UNP A0R1H7
F	984	UNK	ASN	conflict	UNP A0R1H7
F	985	UNK	ARG	conflict	UNP A0R1H7
F	986	UNK	SER	conflict	UNP A0R1H7
F	987	UNK	ALA	conflict	UNP A0R1H7
F	988	UNK	SER	conflict	UNP A0R1H7
F	989	UNK	HIS	conflict	UNP A0R1H7
F	990	UNK	PRO	conflict	UNP A0R1H7
F	991	UNK	SER	conflict	UNP A0R1H7

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Chain	Residue	Modelled	Actual	Comment	Reference
F	992	UNK	THR	conflict	UNP A0R1H7
F	993	UNK	GLY	conflict	UNP A0R1H7
F	994	UNK	ALA	conflict	UNP A0R1H7
F	995	UNK	ARG	conflict	UNP A0R1H7
F	996	UNK	LEU	conflict	UNP A0R1H7
F	997	UNK	GLU	conflict	UNP A0R1H7
F	998	UNK	VAL	conflict	UNP A0R1H7
F	999	UNK	ALA	conflict	UNP A0R1H7
F	1000	UNK	ASP	conflict	UNP A0R1H7
F	1001	UNK	ASP	conflict	UNP A0R1H7
F	1002	UNK	GLN	conflict	UNP A0R1H7
F	1003	UNK	HIS	conflict	UNP A0R1H7
F	1004	UNK	VAL	conflict	UNP A0R1H7
F	1005	UNK	VAL	conflict	UNP A0R1H7
F	1006	UNK	LEU	conflict	UNP A0R1H7
F	1007	UNK	SER	conflict	UNP A0R1H7
F	1008	UNK	VAL	conflict	UNP A0R1H7
F	1009	UNK	PRO	conflict	UNP A0R1H7
F	1010	UNK	LEU	conflict	UNP A0R1H7
F	1011	UNK	SER	conflict	UNP A0R1H7
F	1012	UNK	GLY	conflict	UNP A0R1H7
F	1013	UNK	THR	conflict	UNP A0R1H7
F	1014	UNK	TRP	conflict	UNP A0R1H7
F	1196	UNK	GLY	conflict	UNP A0R1H7
F	1197	UNK	ARG	conflict	UNP A0R1H7
F	1198	UNK	THR	conflict	UNP A0R1H7
F	1199	UNK	GLY	conflict	UNP A0R1H7
F	1200	UNK	ALA	conflict	UNP A0R1H7
F	1201	UNK	ALA	conflict	UNP A0R1H7
F	1202	UNK	GLU	conflict	UNP A0R1H7
F	1203	UNK	LEU	conflict	UNP A0R1H7
F	1204	UNK	THR	conflict	UNP A0R1H7
F	1205	UNK	ASP	conflict	UNP A0R1H7
F	1206	UNK	PRO	conflict	UNP A0R1H7
F	1207	UNK	VAL	conflict	UNP A0R1H7
F	1208	UNK	ARG	conflict	UNP A0R1H7
F	1209	UNK	ALA	conflict	UNP A0R1H7
F	1210	UNK	GLY	conflict	UNP A0R1H7
F	1211	UNK	GLY	conflict	UNP A0R1H7
F	1212	UNK	ALA	conflict	UNP A0R1H7
F	1213	UNK	ILE	conflict	UNP A0R1H7
F	1214	UNK	SER	conflict	UNP A0R1H7

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Chain	Residue	Modelled	Actual	Comment	Reference
F	1215	UNK	ASP	conflict	UNP A0R1H7
F	1216	UNK	ASN	conflict	UNP A0R1H7
F	1217	UNK	ALA	conflict	UNP A0R1H7
F	1218	UNK	THR	conflict	UNP A0R1H7
F	1219	UNK	ASP	conflict	UNP A0R1H7
F	1220	UNK	THR	conflict	UNP A0R1H7
F	1221	UNK	PRO	conflict	UNP A0R1H7
F	1222	UNK	ARG	conflict	UNP A0R1H7
F	1223	UNK	ARG	conflict	UNP A0R1H7
F	1224	UNK	ARG	conflict	UNP A0R1H7
F	1225	UNK	ARG	conflict	UNP A0R1H7
F	1226	UNK	ARG	conflict	UNP A0R1H7
F	1227	UNK	ASP	conflict	UNP A0R1H7
F	2076	UNK	GLY	conflict	UNP A0R1H7
F	2077	UNK	ASP	conflict	UNP A0R1H7
F	2078	UNK	ILE	conflict	UNP A0R1H7
F	2079	UNK	ASP	conflict	UNP A0R1H7
F	2080	UNK	ALA	conflict	UNP A0R1H7
F	2081	UNK	GLN	conflict	UNP A0R1H7
F	2082	UNK	TRP	conflict	UNP A0R1H7
F	2083	UNK	GLU	conflict	UNP A0R1H7
F	2084	UNK	GLN	conflict	UNP A0R1H7
F	2085	UNK	LEU	conflict	UNP A0R1H7
F	2086	UNK	SER	conflict	UNP A0R1H7
F	2087	UNK	GLN	conflict	UNP A0R1H7
F	2088	UNK	ARG	conflict	UNP A0R1H7
F	2089	UNK	PHE	conflict	UNP A0R1H7
F	2090	UNK	GLU	conflict	UNP A0R1H7
F	2091	UNK	GLY	conflict	UNP A0R1H7
F	2092	UNK	THR	conflict	UNP A0R1H7
F	2093	UNK	GLY	conflict	UNP A0R1H7
F	2094	UNK	HIS	conflict	UNP A0R1H7
F	2095	UNK	VAL	conflict	UNP A0R1H7
F	2096	UNK	VAL	conflict	UNP A0R1H7
F	2097	UNK	ALA	conflict	UNP A0R1H7
F	2098	UNK	THR	conflict	UNP A0R1H7
F	2099	UNK	GLN	conflict	UNP A0R1H7
F	2100	UNK	ALA	conflict	UNP A0R1H7
F	2101	UNK	ASN	conflict	UNP A0R1H7
F	2102	UNK	TRP	conflict	UNP A0R1H7
F	2103	UNK	TRP	conflict	UNP A0R1H7
F	2104	UNK	GLN	conflict	UNP A0R1H7

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Chain	Residue	Modelled	Actual	Comment	Reference
F	2105	UNK	GLY	conflict	UNP A0R1H7
F	2106	UNK	LYS	conflict	UNP A0R1H7
F	2107	UNK	ALA	conflict	UNP A0R1H7
F	2108	UNK	LEU	conflict	UNP A0R1H7
F	2109	UNK	ALA	conflict	UNP A0R1H7
F	2110	UNK	ALA	conflict	UNP A0R1H7
F	2111	UNK	GLY	conflict	UNP A0R1H7
F	2112	UNK	ARG	conflict	UNP A0R1H7
F	2113	UNK	ASN	conflict	UNP A0R1H7
F	2114	UNK	VAL	conflict	UNP A0R1H7
F	2115	UNK	HIS	conflict	UNP A0R1H7
F	2116	UNK	ALA	conflict	UNP A0R1H7
F	2117	UNK	SER	conflict	UNP A0R1H7
F	2118	UNK	LEU	conflict	UNP A0R1H7
F	2119	UNK	PHE	conflict	UNP A0R1H7
F	2120	UNK	GLY	conflict	UNP A0R1H7
F	2121	UNK	ARG	conflict	UNP A0R1H7
F	2122	UNK	ILE	conflict	UNP A0R1H7
F	2123	UNK	ALA	conflict	UNP A0R1H7
F	2124	UNK	ALA	conflict	UNP A0R1H7
F	2125	UNK	GLY	conflict	UNP A0R1H7
F	2126	UNK	ALA	conflict	UNP A0R1H7
F	2127	UNK	GLU	conflict	UNP A0R1H7
F	2128	UNK	ASN	conflict	UNP A0R1H7
F	2129	UNK	PRO	conflict	UNP A0R1H7
F	2130	UNK	GLY	conflict	UNP A0R1H7
F	2131	UNK	LYS	conflict	UNP A0R1H7
F	2132	UNK	GLY	conflict	UNP A0R1H7
F	2133	UNK	ARG	conflict	UNP A0R1H7
F	2134	UNK	TYR	conflict	UNP A0R1H7
F	2135	UNK	SER	conflict	UNP A0R1H7
F	2422	UNK	GLU	conflict	UNP A0R1H7
F	2423	UNK	SER	conflict	UNP A0R1H7
F	2424	UNK	ASP	conflict	UNP A0R1H7
F	2425	UNK	ASP	conflict	UNP A0R1H7
F	2426	UNK	GLU	conflict	UNP A0R1H7
F	2427	UNK	ALA	conflict	UNP A0R1H7
F	2428	UNK	PRO	conflict	UNP A0R1H7
F	2429	UNK	ALA	conflict	UNP A0R1H7
F	2430	UNK	GLY	conflict	UNP A0R1H7
F	2431	UNK	THR	conflict	UNP A0R1H7
F	2432	UNK	ILE	conflict	UNP A0R1H7

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Chain	Residue	Modelled	Actual	Comment	Reference
F	2433	UNK	ARG	conflict	UNP A0R1H7
F	2434	UNK	ALA	conflict	UNP A0R1H7
F	2435	UNK	LEU	conflict	UNP A0R1H7
F	2436	UNK	PRO	conflict	UNP A0R1H7
F	2437	UNK	SER	conflict	UNP A0R1H7
F	2438	UNK	PRO	conflict	UNP A0R1H7
F	2439	UNK	PRO	conflict	UNP A0R1H7
F	2440	UNK	ARG	conflict	UNP A0R1H7
F	2441	UNK	GLY	conflict	UNP A0R1H7
F	2442	UNK	TYR	conflict	UNP A0R1H7
F	2443	UNK	ASN	conflict	UNP A0R1H7
F	2444	UNK	PRO	conflict	UNP A0R1H7
F	2445	UNK	ALA	conflict	UNP A0R1H7
F	2446	UNK	PRO	conflict	UNP A0R1H7
F	2447	UNK	ALA	conflict	UNP A0R1H7
F	2448	UNK	PRO	conflict	UNP A0R1H7
F	2449	UNK	GLU	conflict	UNP A0R1H7
F	2450	UNK	TRP	conflict	UNP A0R1H7
F	2451	UNK	ASP	conflict	UNP A0R1H7
F	2452	UNK	ASP	conflict	UNP A0R1H7
F	2453	UNK	LEU	conflict	UNP A0R1H7
A	929	UNK	GLU	conflict	UNP A0R1H7
A	930	UNK	PRO	conflict	UNP A0R1H7
A	931	UNK	VAL	conflict	UNP A0R1H7
A	932	UNK	GLU	conflict	UNP A0R1H7
A	933	UNK	VAL	conflict	UNP A0R1H7
A	934	UNK	LEU	conflict	UNP A0R1H7
A	935	UNK	SER	conflict	UNP A0R1H7
A	936	UNK	ARG	conflict	UNP A0R1H7
A	937	UNK	ARG	conflict	UNP A0R1H7
A	938	UNK	GLN	conflict	UNP A0R1H7
A	939	UNK	ALA	conflict	UNP A0R1H7
A	940	UNK	ARG	conflict	UNP A0R1H7
A	941	UNK	ARG	conflict	UNP A0R1H7
A	942	UNK	ASP	conflict	UNP A0R1H7
A	943	UNK	ALA	conflict	UNP A0R1H7
A	944	UNK	SER	conflict	UNP A0R1H7
A	974	UNK	THR	conflict	UNP A0R1H7
A	975	UNK	GLU	conflict	UNP A0R1H7
A	976	UNK	TRP	conflict	UNP A0R1H7
A	977	UNK	GLN	conflict	UNP A0R1H7
A	978	UNK	VAL	conflict	UNP A0R1H7

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Chain	Residue	Modelled	Actual	Comment	Reference
A	979	UNK	ARG	conflict	UNP A0R1H7
A	980	UNK	GLU	conflict	UNP A0R1H7
A	981	UNK	GLY	conflict	UNP A0R1H7
A	982	UNK	SER	conflict	UNP A0R1H7
A	983	UNK	ASP	conflict	UNP A0R1H7
A	984	UNK	ASN	conflict	UNP A0R1H7
A	985	UNK	ARG	conflict	UNP A0R1H7
A	986	UNK	SER	conflict	UNP A0R1H7
A	987	UNK	ALA	conflict	UNP A0R1H7
A	988	UNK	SER	conflict	UNP A0R1H7
A	989	UNK	HIS	conflict	UNP A0R1H7
A	990	UNK	PRO	conflict	UNP A0R1H7
A	991	UNK	SER	conflict	UNP A0R1H7
A	992	UNK	THR	conflict	UNP A0R1H7
A	993	UNK	GLY	conflict	UNP A0R1H7
A	994	UNK	ALA	conflict	UNP A0R1H7
A	995	UNK	ARG	conflict	UNP A0R1H7
A	996	UNK	LEU	conflict	UNP A0R1H7
A	997	UNK	GLU	conflict	UNP A0R1H7
A	998	UNK	VAL	conflict	UNP A0R1H7
A	999	UNK	ALA	conflict	UNP A0R1H7
A	1000	UNK	ASP	conflict	UNP A0R1H7
A	1001	UNK	ASP	conflict	UNP A0R1H7
A	1002	UNK	GLN	conflict	UNP A0R1H7
A	1003	UNK	HIS	conflict	UNP A0R1H7
A	1004	UNK	VAL	conflict	UNP A0R1H7
A	1005	UNK	VAL	conflict	UNP A0R1H7
A	1006	UNK	LEU	conflict	UNP A0R1H7
A	1007	UNK	SER	conflict	UNP A0R1H7
A	1008	UNK	VAL	conflict	UNP A0R1H7
A	1009	UNK	PRO	conflict	UNP A0R1H7
A	1010	UNK	LEU	conflict	UNP A0R1H7
A	1011	UNK	SER	conflict	UNP A0R1H7
A	1012	UNK	GLY	conflict	UNP A0R1H7
A	1013	UNK	THR	conflict	UNP A0R1H7
A	1014	UNK	TRP	conflict	UNP A0R1H7
A	1196	UNK	GLY	conflict	UNP A0R1H7
A	1197	UNK	ARG	conflict	UNP A0R1H7
A	1198	UNK	THR	conflict	UNP A0R1H7
A	1199	UNK	GLY	conflict	UNP A0R1H7
A	1200	UNK	ALA	conflict	UNP A0R1H7
A	1201	UNK	ALA	conflict	UNP A0R1H7

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1202	UNK	GLU	conflict	UNP A0R1H7
A	1203	UNK	LEU	conflict	UNP A0R1H7
A	1204	UNK	THR	conflict	UNP A0R1H7
A	1205	UNK	ASP	conflict	UNP A0R1H7
A	1206	UNK	PRO	conflict	UNP A0R1H7
A	1207	UNK	VAL	conflict	UNP A0R1H7
A	1208	UNK	ARG	conflict	UNP A0R1H7
A	1209	UNK	ALA	conflict	UNP A0R1H7
A	1210	UNK	GLY	conflict	UNP A0R1H7
A	1211	UNK	GLY	conflict	UNP A0R1H7
A	1212	UNK	ALA	conflict	UNP A0R1H7
A	1213	UNK	ILE	conflict	UNP A0R1H7
A	1214	UNK	SER	conflict	UNP A0R1H7
A	1215	UNK	ASP	conflict	UNP A0R1H7
A	1216	UNK	ASN	conflict	UNP A0R1H7
A	1217	UNK	ALA	conflict	UNP A0R1H7
A	1218	UNK	THR	conflict	UNP A0R1H7
A	1219	UNK	ASP	conflict	UNP A0R1H7
A	1220	UNK	THR	conflict	UNP A0R1H7
A	1221	UNK	PRO	conflict	UNP A0R1H7
A	1222	UNK	ARG	conflict	UNP A0R1H7
A	1223	UNK	ARG	conflict	UNP A0R1H7
A	1224	UNK	ARG	conflict	UNP A0R1H7
A	1225	UNK	ARG	conflict	UNP A0R1H7
A	1226	UNK	ARG	conflict	UNP A0R1H7
A	1227	UNK	ASP	conflict	UNP A0R1H7
A	2076	UNK	GLY	conflict	UNP A0R1H7
A	2077	UNK	ASP	conflict	UNP A0R1H7
A	2078	UNK	ILE	conflict	UNP A0R1H7
A	2079	UNK	ASP	conflict	UNP A0R1H7
A	2080	UNK	ALA	conflict	UNP A0R1H7
A	2081	UNK	GLN	conflict	UNP A0R1H7
A	2082	UNK	TRP	conflict	UNP A0R1H7
A	2083	UNK	GLU	conflict	UNP A0R1H7
A	2084	UNK	GLN	conflict	UNP A0R1H7
A	2085	UNK	LEU	conflict	UNP A0R1H7
A	2086	UNK	SER	conflict	UNP A0R1H7
A	2087	UNK	GLN	conflict	UNP A0R1H7
A	2088	UNK	ARG	conflict	UNP A0R1H7
A	2089	UNK	PHE	conflict	UNP A0R1H7
A	2090	UNK	GLU	conflict	UNP A0R1H7
A	2091	UNK	GLY	conflict	UNP A0R1H7

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Chain	Residue	Modelled	Actual	Comment	Reference
A	2092	UNK	THR	conflict	UNP A0R1H7
A	2093	UNK	GLY	conflict	UNP A0R1H7
A	2094	UNK	HIS	conflict	UNP A0R1H7
A	2095	UNK	VAL	conflict	UNP A0R1H7
A	2096	UNK	VAL	conflict	UNP A0R1H7
A	2097	UNK	ALA	conflict	UNP A0R1H7
A	2098	UNK	THR	conflict	UNP A0R1H7
A	2099	UNK	GLN	conflict	UNP A0R1H7
A	2100	UNK	ALA	conflict	UNP A0R1H7
A	2101	UNK	ASN	conflict	UNP A0R1H7
A	2102	UNK	TRP	conflict	UNP A0R1H7
A	2103	UNK	TRP	conflict	UNP A0R1H7
A	2104	UNK	GLN	conflict	UNP A0R1H7
A	2105	UNK	GLY	conflict	UNP A0R1H7
A	2106	UNK	LYS	conflict	UNP A0R1H7
A	2107	UNK	ALA	conflict	UNP A0R1H7
A	2108	UNK	LEU	conflict	UNP A0R1H7
A	2109	UNK	ALA	conflict	UNP A0R1H7
A	2110	UNK	ALA	conflict	UNP A0R1H7
A	2111	UNK	GLY	conflict	UNP A0R1H7
A	2112	UNK	ARG	conflict	UNP A0R1H7
A	2113	UNK	ASN	conflict	UNP A0R1H7
A	2114	UNK	VAL	conflict	UNP A0R1H7
A	2115	UNK	HIS	conflict	UNP A0R1H7
A	2116	UNK	ALA	conflict	UNP A0R1H7
A	2117	UNK	SER	conflict	UNP A0R1H7
A	2118	UNK	LEU	conflict	UNP A0R1H7
A	2119	UNK	PHE	conflict	UNP A0R1H7
A	2120	UNK	GLY	conflict	UNP A0R1H7
A	2121	UNK	ARG	conflict	UNP A0R1H7
A	2122	UNK	ILE	conflict	UNP A0R1H7
A	2123	UNK	ALA	conflict	UNP A0R1H7
A	2124	UNK	ALA	conflict	UNP A0R1H7
A	2125	UNK	GLY	conflict	UNP A0R1H7
A	2126	UNK	ALA	conflict	UNP A0R1H7
A	2127	UNK	GLU	conflict	UNP A0R1H7
A	2128	UNK	ASN	conflict	UNP A0R1H7
A	2129	UNK	PRO	conflict	UNP A0R1H7
A	2130	UNK	GLY	conflict	UNP A0R1H7
A	2131	UNK	LYS	conflict	UNP A0R1H7
A	2132	UNK	GLY	conflict	UNP A0R1H7
A	2133	UNK	ARG	conflict	UNP A0R1H7

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Chain	Residue	Modelled	Actual	Comment	Reference
A	2134	UNK	TYR	conflict	UNP A0R1H7
A	2135	UNK	SER	conflict	UNP A0R1H7
A	2422	UNK	GLU	conflict	UNP A0R1H7
A	2423	UNK	SER	conflict	UNP A0R1H7
A	2424	UNK	ASP	conflict	UNP A0R1H7
A	2425	UNK	ASP	conflict	UNP A0R1H7
A	2426	UNK	GLU	conflict	UNP A0R1H7
A	2427	UNK	ALA	conflict	UNP A0R1H7
A	2428	UNK	PRO	conflict	UNP A0R1H7
A	2429	UNK	ALA	conflict	UNP A0R1H7
A	2430	UNK	GLY	conflict	UNP A0R1H7
A	2431	UNK	THR	conflict	UNP A0R1H7
A	2432	UNK	ILE	conflict	UNP A0R1H7
A	2433	UNK	ARG	conflict	UNP A0R1H7
A	2434	UNK	ALA	conflict	UNP A0R1H7
A	2435	UNK	LEU	conflict	UNP A0R1H7
A	2436	UNK	PRO	conflict	UNP A0R1H7
A	2437	UNK	SER	conflict	UNP A0R1H7
A	2438	UNK	PRO	conflict	UNP A0R1H7
A	2439	UNK	PRO	conflict	UNP A0R1H7
A	2440	UNK	ARG	conflict	UNP A0R1H7
A	2441	UNK	GLY	conflict	UNP A0R1H7
A	2442	UNK	TYR	conflict	UNP A0R1H7
A	2443	UNK	ASN	conflict	UNP A0R1H7
A	2444	UNK	PRO	conflict	UNP A0R1H7
A	2445	UNK	ALA	conflict	UNP A0R1H7
A	2446	UNK	PRO	conflict	UNP A0R1H7
A	2447	UNK	ALA	conflict	UNP A0R1H7
A	2448	UNK	PRO	conflict	UNP A0R1H7
A	2449	UNK	GLU	conflict	UNP A0R1H7
A	2450	UNK	TRP	conflict	UNP A0R1H7
A	2451	UNK	ASP	conflict	UNP A0R1H7
A	2452	UNK	ASP	conflict	UNP A0R1H7
A	2453	UNK	LEU	conflict	UNP A0R1H7
B	929	UNK	GLU	conflict	UNP A0R1H7
B	930	UNK	PRO	conflict	UNP A0R1H7
B	931	UNK	VAL	conflict	UNP A0R1H7
B	932	UNK	GLU	conflict	UNP A0R1H7
B	933	UNK	VAL	conflict	UNP A0R1H7
B	934	UNK	LEU	conflict	UNP A0R1H7
B	935	UNK	SER	conflict	UNP A0R1H7
B	936	UNK	ARG	conflict	UNP A0R1H7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	937	UNK	ARG	conflict	UNP A0R1H7
B	938	UNK	GLN	conflict	UNP A0R1H7
B	939	UNK	ALA	conflict	UNP A0R1H7
B	940	UNK	ARG	conflict	UNP A0R1H7
B	941	UNK	ARG	conflict	UNP A0R1H7
B	942	UNK	ASP	conflict	UNP A0R1H7
B	943	UNK	ALA	conflict	UNP A0R1H7
B	944	UNK	SER	conflict	UNP A0R1H7
B	974	UNK	THR	conflict	UNP A0R1H7
B	975	UNK	GLU	conflict	UNP A0R1H7
B	976	UNK	TRP	conflict	UNP A0R1H7
B	977	UNK	GLN	conflict	UNP A0R1H7
B	978	UNK	VAL	conflict	UNP A0R1H7
B	979	UNK	ARG	conflict	UNP A0R1H7
B	980	UNK	GLU	conflict	UNP A0R1H7
B	981	UNK	GLY	conflict	UNP A0R1H7
B	982	UNK	SER	conflict	UNP A0R1H7
B	983	UNK	ASP	conflict	UNP A0R1H7
B	984	UNK	ASN	conflict	UNP A0R1H7
B	985	UNK	ARG	conflict	UNP A0R1H7
B	986	UNK	SER	conflict	UNP A0R1H7
B	987	UNK	ALA	conflict	UNP A0R1H7
B	988	UNK	SER	conflict	UNP A0R1H7
B	989	UNK	HIS	conflict	UNP A0R1H7
B	990	UNK	PRO	conflict	UNP A0R1H7
B	991	UNK	SER	conflict	UNP A0R1H7
B	992	UNK	THR	conflict	UNP A0R1H7
B	993	UNK	GLY	conflict	UNP A0R1H7
B	994	UNK	ALA	conflict	UNP A0R1H7
B	995	UNK	ARG	conflict	UNP A0R1H7
B	996	UNK	LEU	conflict	UNP A0R1H7
B	997	UNK	GLU	conflict	UNP A0R1H7
B	998	UNK	VAL	conflict	UNP A0R1H7
B	999	UNK	ALA	conflict	UNP A0R1H7
B	1000	UNK	ASP	conflict	UNP A0R1H7
B	1001	UNK	ASP	conflict	UNP A0R1H7
B	1002	UNK	GLN	conflict	UNP A0R1H7
B	1003	UNK	HIS	conflict	UNP A0R1H7
B	1004	UNK	VAL	conflict	UNP A0R1H7
B	1005	UNK	VAL	conflict	UNP A0R1H7
B	1006	UNK	LEU	conflict	UNP A0R1H7
B	1007	UNK	SER	conflict	UNP A0R1H7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1008	UNK	VAL	conflict	UNP A0R1H7
B	1009	UNK	PRO	conflict	UNP A0R1H7
B	1010	UNK	LEU	conflict	UNP A0R1H7
B	1011	UNK	SER	conflict	UNP A0R1H7
B	1012	UNK	GLY	conflict	UNP A0R1H7
B	1013	UNK	THR	conflict	UNP A0R1H7
B	1014	UNK	TRP	conflict	UNP A0R1H7
B	1196	UNK	GLY	conflict	UNP A0R1H7
B	1197	UNK	ARG	conflict	UNP A0R1H7
B	1198	UNK	THR	conflict	UNP A0R1H7
B	1199	UNK	GLY	conflict	UNP A0R1H7
B	1200	UNK	ALA	conflict	UNP A0R1H7
B	1201	UNK	ALA	conflict	UNP A0R1H7
B	1202	UNK	GLU	conflict	UNP A0R1H7
B	1203	UNK	LEU	conflict	UNP A0R1H7
B	1204	UNK	THR	conflict	UNP A0R1H7
B	1205	UNK	ASP	conflict	UNP A0R1H7
B	1206	UNK	PRO	conflict	UNP A0R1H7
B	1207	UNK	VAL	conflict	UNP A0R1H7
B	1208	UNK	ARG	conflict	UNP A0R1H7
B	1209	UNK	ALA	conflict	UNP A0R1H7
B	1210	UNK	GLY	conflict	UNP A0R1H7
B	1211	UNK	GLY	conflict	UNP A0R1H7
B	1212	UNK	ALA	conflict	UNP A0R1H7
B	1213	UNK	ILE	conflict	UNP A0R1H7
B	1214	UNK	SER	conflict	UNP A0R1H7
B	1215	UNK	ASP	conflict	UNP A0R1H7
B	1216	UNK	ASN	conflict	UNP A0R1H7
B	1217	UNK	ALA	conflict	UNP A0R1H7
B	1218	UNK	THR	conflict	UNP A0R1H7
B	1219	UNK	ASP	conflict	UNP A0R1H7
B	1220	UNK	THR	conflict	UNP A0R1H7
B	1221	UNK	PRO	conflict	UNP A0R1H7
B	1222	UNK	ARG	conflict	UNP A0R1H7
B	1223	UNK	ARG	conflict	UNP A0R1H7
B	1224	UNK	ARG	conflict	UNP A0R1H7
B	1225	UNK	ARG	conflict	UNP A0R1H7
B	1226	UNK	ARG	conflict	UNP A0R1H7
B	1227	UNK	ASP	conflict	UNP A0R1H7
B	2076	UNK	GLY	conflict	UNP A0R1H7
B	2077	UNK	ASP	conflict	UNP A0R1H7
B	2078	UNK	ILE	conflict	UNP A0R1H7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	2079	UNK	ASP	conflict	UNP A0R1H7
B	2080	UNK	ALA	conflict	UNP A0R1H7
B	2081	UNK	GLN	conflict	UNP A0R1H7
B	2082	UNK	TRP	conflict	UNP A0R1H7
B	2083	UNK	GLU	conflict	UNP A0R1H7
B	2084	UNK	GLN	conflict	UNP A0R1H7
B	2085	UNK	LEU	conflict	UNP A0R1H7
B	2086	UNK	SER	conflict	UNP A0R1H7
B	2087	UNK	GLN	conflict	UNP A0R1H7
B	2088	UNK	ARG	conflict	UNP A0R1H7
B	2089	UNK	PHE	conflict	UNP A0R1H7
B	2090	UNK	GLU	conflict	UNP A0R1H7
B	2091	UNK	GLY	conflict	UNP A0R1H7
B	2092	UNK	THR	conflict	UNP A0R1H7
B	2093	UNK	GLY	conflict	UNP A0R1H7
B	2094	UNK	HIS	conflict	UNP A0R1H7
B	2095	UNK	VAL	conflict	UNP A0R1H7
B	2096	UNK	VAL	conflict	UNP A0R1H7
B	2097	UNK	ALA	conflict	UNP A0R1H7
B	2098	UNK	THR	conflict	UNP A0R1H7
B	2099	UNK	GLN	conflict	UNP A0R1H7
B	2100	UNK	ALA	conflict	UNP A0R1H7
B	2101	UNK	ASN	conflict	UNP A0R1H7
B	2102	UNK	TRP	conflict	UNP A0R1H7
B	2103	UNK	TRP	conflict	UNP A0R1H7
B	2104	UNK	GLN	conflict	UNP A0R1H7
B	2105	UNK	GLY	conflict	UNP A0R1H7
B	2106	UNK	LYS	conflict	UNP A0R1H7
B	2107	UNK	ALA	conflict	UNP A0R1H7
B	2108	UNK	LEU	conflict	UNP A0R1H7
B	2109	UNK	ALA	conflict	UNP A0R1H7
B	2110	UNK	ALA	conflict	UNP A0R1H7
B	2111	UNK	GLY	conflict	UNP A0R1H7
B	2112	UNK	ARG	conflict	UNP A0R1H7
B	2113	UNK	ASN	conflict	UNP A0R1H7
B	2114	UNK	VAL	conflict	UNP A0R1H7
B	2115	UNK	HIS	conflict	UNP A0R1H7
B	2116	UNK	ALA	conflict	UNP A0R1H7
B	2117	UNK	SER	conflict	UNP A0R1H7
B	2118	UNK	LEU	conflict	UNP A0R1H7
B	2119	UNK	PHE	conflict	UNP A0R1H7
B	2120	UNK	GLY	conflict	UNP A0R1H7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	2121	UNK	ARG	conflict	UNP A0R1H7
B	2122	UNK	ILE	conflict	UNP A0R1H7
B	2123	UNK	ALA	conflict	UNP A0R1H7
B	2124	UNK	ALA	conflict	UNP A0R1H7
B	2125	UNK	GLY	conflict	UNP A0R1H7
B	2126	UNK	ALA	conflict	UNP A0R1H7
B	2127	UNK	GLU	conflict	UNP A0R1H7
B	2128	UNK	ASN	conflict	UNP A0R1H7
B	2129	UNK	PRO	conflict	UNP A0R1H7
B	2130	UNK	GLY	conflict	UNP A0R1H7
B	2131	UNK	LYS	conflict	UNP A0R1H7
B	2132	UNK	GLY	conflict	UNP A0R1H7
B	2133	UNK	ARG	conflict	UNP A0R1H7
B	2134	UNK	TYR	conflict	UNP A0R1H7
B	2135	UNK	SER	conflict	UNP A0R1H7
B	2422	UNK	GLU	conflict	UNP A0R1H7
B	2423	UNK	SER	conflict	UNP A0R1H7
B	2424	UNK	ASP	conflict	UNP A0R1H7
B	2425	UNK	ASP	conflict	UNP A0R1H7
B	2426	UNK	GLU	conflict	UNP A0R1H7
B	2427	UNK	ALA	conflict	UNP A0R1H7
B	2428	UNK	PRO	conflict	UNP A0R1H7
B	2429	UNK	ALA	conflict	UNP A0R1H7
B	2430	UNK	GLY	conflict	UNP A0R1H7
B	2431	UNK	THR	conflict	UNP A0R1H7
B	2432	UNK	ILE	conflict	UNP A0R1H7
B	2433	UNK	ARG	conflict	UNP A0R1H7
B	2434	UNK	ALA	conflict	UNP A0R1H7
B	2435	UNK	LEU	conflict	UNP A0R1H7
B	2436	UNK	PRO	conflict	UNP A0R1H7
B	2437	UNK	SER	conflict	UNP A0R1H7
B	2438	UNK	PRO	conflict	UNP A0R1H7
B	2439	UNK	PRO	conflict	UNP A0R1H7
B	2440	UNK	ARG	conflict	UNP A0R1H7
B	2441	UNK	GLY	conflict	UNP A0R1H7
B	2442	UNK	TYR	conflict	UNP A0R1H7
B	2443	UNK	ASN	conflict	UNP A0R1H7
B	2444	UNK	PRO	conflict	UNP A0R1H7
B	2445	UNK	ALA	conflict	UNP A0R1H7
B	2446	UNK	PRO	conflict	UNP A0R1H7
B	2447	UNK	ALA	conflict	UNP A0R1H7
B	2448	UNK	PRO	conflict	UNP A0R1H7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	2449	UNK	GLU	conflict	UNP A0R1H7
B	2450	UNK	TRP	conflict	UNP A0R1H7
B	2451	UNK	ASP	conflict	UNP A0R1H7
B	2452	UNK	ASP	conflict	UNP A0R1H7
B	2453	UNK	LEU	conflict	UNP A0R1H7
C	929	UNK	GLU	conflict	UNP A0R1H7
C	930	UNK	PRO	conflict	UNP A0R1H7
C	931	UNK	VAL	conflict	UNP A0R1H7
C	932	UNK	GLU	conflict	UNP A0R1H7
C	933	UNK	VAL	conflict	UNP A0R1H7
C	934	UNK	LEU	conflict	UNP A0R1H7
C	935	UNK	SER	conflict	UNP A0R1H7
C	936	UNK	ARG	conflict	UNP A0R1H7
C	937	UNK	ARG	conflict	UNP A0R1H7
C	938	UNK	GLN	conflict	UNP A0R1H7
C	939	UNK	ALA	conflict	UNP A0R1H7
C	940	UNK	ARG	conflict	UNP A0R1H7
C	941	UNK	ARG	conflict	UNP A0R1H7
C	942	UNK	ASP	conflict	UNP A0R1H7
C	943	UNK	ALA	conflict	UNP A0R1H7
C	944	UNK	SER	conflict	UNP A0R1H7
C	974	UNK	THR	conflict	UNP A0R1H7
C	975	UNK	GLU	conflict	UNP A0R1H7
C	976	UNK	TRP	conflict	UNP A0R1H7
C	977	UNK	GLN	conflict	UNP A0R1H7
C	978	UNK	VAL	conflict	UNP A0R1H7
C	979	UNK	ARG	conflict	UNP A0R1H7
C	980	UNK	GLU	conflict	UNP A0R1H7
C	981	UNK	GLY	conflict	UNP A0R1H7
C	982	UNK	SER	conflict	UNP A0R1H7
C	983	UNK	ASP	conflict	UNP A0R1H7
C	984	UNK	ASN	conflict	UNP A0R1H7
C	985	UNK	ARG	conflict	UNP A0R1H7
C	986	UNK	SER	conflict	UNP A0R1H7
C	987	UNK	ALA	conflict	UNP A0R1H7
C	988	UNK	SER	conflict	UNP A0R1H7
C	989	UNK	HIS	conflict	UNP A0R1H7
C	990	UNK	PRO	conflict	UNP A0R1H7
C	991	UNK	SER	conflict	UNP A0R1H7
C	992	UNK	THR	conflict	UNP A0R1H7
C	993	UNK	GLY	conflict	UNP A0R1H7
C	994	UNK	ALA	conflict	UNP A0R1H7

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Chain	Residue	Modelled	Actual	Comment	Reference
C	995	UNK	ARG	conflict	UNP A0R1H7
C	996	UNK	LEU	conflict	UNP A0R1H7
C	997	UNK	GLU	conflict	UNP A0R1H7
C	998	UNK	VAL	conflict	UNP A0R1H7
C	999	UNK	ALA	conflict	UNP A0R1H7
C	1000	UNK	ASP	conflict	UNP A0R1H7
C	1001	UNK	ASP	conflict	UNP A0R1H7
C	1002	UNK	GLN	conflict	UNP A0R1H7
C	1003	UNK	HIS	conflict	UNP A0R1H7
C	1004	UNK	VAL	conflict	UNP A0R1H7
C	1005	UNK	VAL	conflict	UNP A0R1H7
C	1006	UNK	LEU	conflict	UNP A0R1H7
C	1007	UNK	SER	conflict	UNP A0R1H7
C	1008	UNK	VAL	conflict	UNP A0R1H7
C	1009	UNK	PRO	conflict	UNP A0R1H7
C	1010	UNK	LEU	conflict	UNP A0R1H7
C	1011	UNK	SER	conflict	UNP A0R1H7
C	1012	UNK	GLY	conflict	UNP A0R1H7
C	1013	UNK	THR	conflict	UNP A0R1H7
C	1014	UNK	TRP	conflict	UNP A0R1H7
C	1196	UNK	GLY	conflict	UNP A0R1H7
C	1197	UNK	ARG	conflict	UNP A0R1H7
C	1198	UNK	THR	conflict	UNP A0R1H7
C	1199	UNK	GLY	conflict	UNP A0R1H7
C	1200	UNK	ALA	conflict	UNP A0R1H7
C	1201	UNK	ALA	conflict	UNP A0R1H7
C	1202	UNK	GLU	conflict	UNP A0R1H7
C	1203	UNK	LEU	conflict	UNP A0R1H7
C	1204	UNK	THR	conflict	UNP A0R1H7
C	1205	UNK	ASP	conflict	UNP A0R1H7
C	1206	UNK	PRO	conflict	UNP A0R1H7
C	1207	UNK	VAL	conflict	UNP A0R1H7
C	1208	UNK	ARG	conflict	UNP A0R1H7
C	1209	UNK	ALA	conflict	UNP A0R1H7
C	1210	UNK	GLY	conflict	UNP A0R1H7
C	1211	UNK	GLY	conflict	UNP A0R1H7
C	1212	UNK	ALA	conflict	UNP A0R1H7
C	1213	UNK	ILE	conflict	UNP A0R1H7
C	1214	UNK	SER	conflict	UNP A0R1H7
C	1215	UNK	ASP	conflict	UNP A0R1H7
C	1216	UNK	ASN	conflict	UNP A0R1H7
C	1217	UNK	ALA	conflict	UNP A0R1H7

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1218	UNK	THR	conflict	UNP A0R1H7
C	1219	UNK	ASP	conflict	UNP A0R1H7
C	1220	UNK	THR	conflict	UNP A0R1H7
C	1221	UNK	PRO	conflict	UNP A0R1H7
C	1222	UNK	ARG	conflict	UNP A0R1H7
C	1223	UNK	ARG	conflict	UNP A0R1H7
C	1224	UNK	ARG	conflict	UNP A0R1H7
C	1225	UNK	ARG	conflict	UNP A0R1H7
C	1226	UNK	ARG	conflict	UNP A0R1H7
C	1227	UNK	ASP	conflict	UNP A0R1H7
C	2076	UNK	GLY	conflict	UNP A0R1H7
C	2077	UNK	ASP	conflict	UNP A0R1H7
C	2078	UNK	ILE	conflict	UNP A0R1H7
C	2079	UNK	ASP	conflict	UNP A0R1H7
C	2080	UNK	ALA	conflict	UNP A0R1H7
C	2081	UNK	GLN	conflict	UNP A0R1H7
C	2082	UNK	TRP	conflict	UNP A0R1H7
C	2083	UNK	GLU	conflict	UNP A0R1H7
C	2084	UNK	GLN	conflict	UNP A0R1H7
C	2085	UNK	LEU	conflict	UNP A0R1H7
C	2086	UNK	SER	conflict	UNP A0R1H7
C	2087	UNK	GLN	conflict	UNP A0R1H7
C	2088	UNK	ARG	conflict	UNP A0R1H7
C	2089	UNK	PHE	conflict	UNP A0R1H7
C	2090	UNK	GLU	conflict	UNP A0R1H7
C	2091	UNK	GLY	conflict	UNP A0R1H7
C	2092	UNK	THR	conflict	UNP A0R1H7
C	2093	UNK	GLY	conflict	UNP A0R1H7
C	2094	UNK	HIS	conflict	UNP A0R1H7
C	2095	UNK	VAL	conflict	UNP A0R1H7
C	2096	UNK	VAL	conflict	UNP A0R1H7
C	2097	UNK	ALA	conflict	UNP A0R1H7
C	2098	UNK	THR	conflict	UNP A0R1H7
C	2099	UNK	GLN	conflict	UNP A0R1H7
C	2100	UNK	ALA	conflict	UNP A0R1H7
C	2101	UNK	ASN	conflict	UNP A0R1H7
C	2102	UNK	TRP	conflict	UNP A0R1H7
C	2103	UNK	TRP	conflict	UNP A0R1H7
C	2104	UNK	GLN	conflict	UNP A0R1H7
C	2105	UNK	GLY	conflict	UNP A0R1H7
C	2106	UNK	LYS	conflict	UNP A0R1H7
C	2107	UNK	ALA	conflict	UNP A0R1H7

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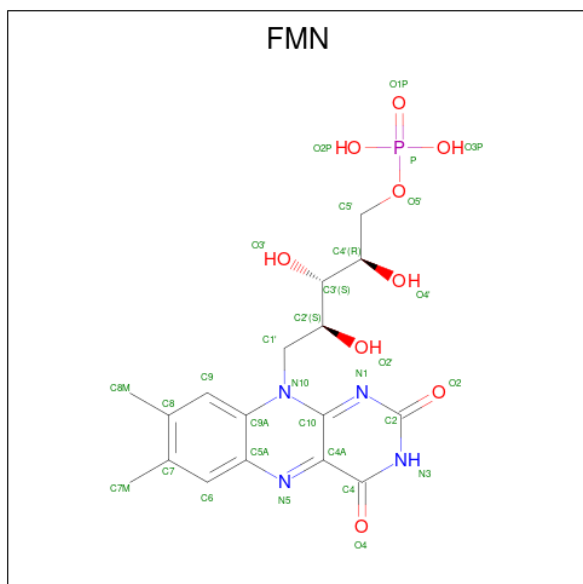
Chain	Residue	Modelled	Actual	Comment	Reference
C	2108	UNK	LEU	conflict	UNP A0R1H7
C	2109	UNK	ALA	conflict	UNP A0R1H7
C	2110	UNK	ALA	conflict	UNP A0R1H7
C	2111	UNK	GLY	conflict	UNP A0R1H7
C	2112	UNK	ARG	conflict	UNP A0R1H7
C	2113	UNK	ASN	conflict	UNP A0R1H7
C	2114	UNK	VAL	conflict	UNP A0R1H7
C	2115	UNK	HIS	conflict	UNP A0R1H7
C	2116	UNK	ALA	conflict	UNP A0R1H7
C	2117	UNK	SER	conflict	UNP A0R1H7
C	2118	UNK	LEU	conflict	UNP A0R1H7
C	2119	UNK	PHE	conflict	UNP A0R1H7
C	2120	UNK	GLY	conflict	UNP A0R1H7
C	2121	UNK	ARG	conflict	UNP A0R1H7
C	2122	UNK	ILE	conflict	UNP A0R1H7
C	2123	UNK	ALA	conflict	UNP A0R1H7
C	2124	UNK	ALA	conflict	UNP A0R1H7
C	2125	UNK	GLY	conflict	UNP A0R1H7
C	2126	UNK	ALA	conflict	UNP A0R1H7
C	2127	UNK	GLU	conflict	UNP A0R1H7
C	2128	UNK	ASN	conflict	UNP A0R1H7
C	2129	UNK	PRO	conflict	UNP A0R1H7
C	2130	UNK	GLY	conflict	UNP A0R1H7
C	2131	UNK	LYS	conflict	UNP A0R1H7
C	2132	UNK	GLY	conflict	UNP A0R1H7
C	2133	UNK	ARG	conflict	UNP A0R1H7
C	2134	UNK	TYR	conflict	UNP A0R1H7
C	2135	UNK	SER	conflict	UNP A0R1H7
C	2422	UNK	GLU	conflict	UNP A0R1H7
C	2423	UNK	SER	conflict	UNP A0R1H7
C	2424	UNK	ASP	conflict	UNP A0R1H7
C	2425	UNK	ASP	conflict	UNP A0R1H7
C	2426	UNK	GLU	conflict	UNP A0R1H7
C	2427	UNK	ALA	conflict	UNP A0R1H7
C	2428	UNK	PRO	conflict	UNP A0R1H7
C	2429	UNK	ALA	conflict	UNP A0R1H7
C	2430	UNK	GLY	conflict	UNP A0R1H7
C	2431	UNK	THR	conflict	UNP A0R1H7
C	2432	UNK	ILE	conflict	UNP A0R1H7
C	2433	UNK	ARG	conflict	UNP A0R1H7
C	2434	UNK	ALA	conflict	UNP A0R1H7
C	2435	UNK	LEU	conflict	UNP A0R1H7

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Chain	Residue	Modelled	Actual	Comment	Reference
C	2436	UNK	PRO	conflict	UNP A0R1H7
C	2437	UNK	SER	conflict	UNP A0R1H7
C	2438	UNK	PRO	conflict	UNP A0R1H7
C	2439	UNK	PRO	conflict	UNP A0R1H7
C	2440	UNK	ARG	conflict	UNP A0R1H7
C	2441	UNK	GLY	conflict	UNP A0R1H7
C	2442	UNK	TYR	conflict	UNP A0R1H7
C	2443	UNK	ASN	conflict	UNP A0R1H7
C	2444	UNK	PRO	conflict	UNP A0R1H7
C	2445	UNK	ALA	conflict	UNP A0R1H7
C	2446	UNK	PRO	conflict	UNP A0R1H7
C	2447	UNK	ALA	conflict	UNP A0R1H7
C	2448	UNK	PRO	conflict	UNP A0R1H7
C	2449	UNK	GLU	conflict	UNP A0R1H7
C	2450	UNK	TRP	conflict	UNP A0R1H7
C	2451	UNK	ASP	conflict	UNP A0R1H7
C	2452	UNK	ASP	conflict	UNP A0R1H7
C	2453	UNK	LEU	conflict	UNP A0R1H7

- Molecule 2 is FLAVIN MONONUCLEOTIDE (CCD ID: FMN) (formula: $C_{17}H_{21}N_4O_9P$).



Mol	Chain	Residues	Atoms					AltConf
2	D	1	Total	C	N	O	P	0
			31	17	4	9	1	
2	E	1	Total	C	N	O	P	0
			31	17	4	9	1	

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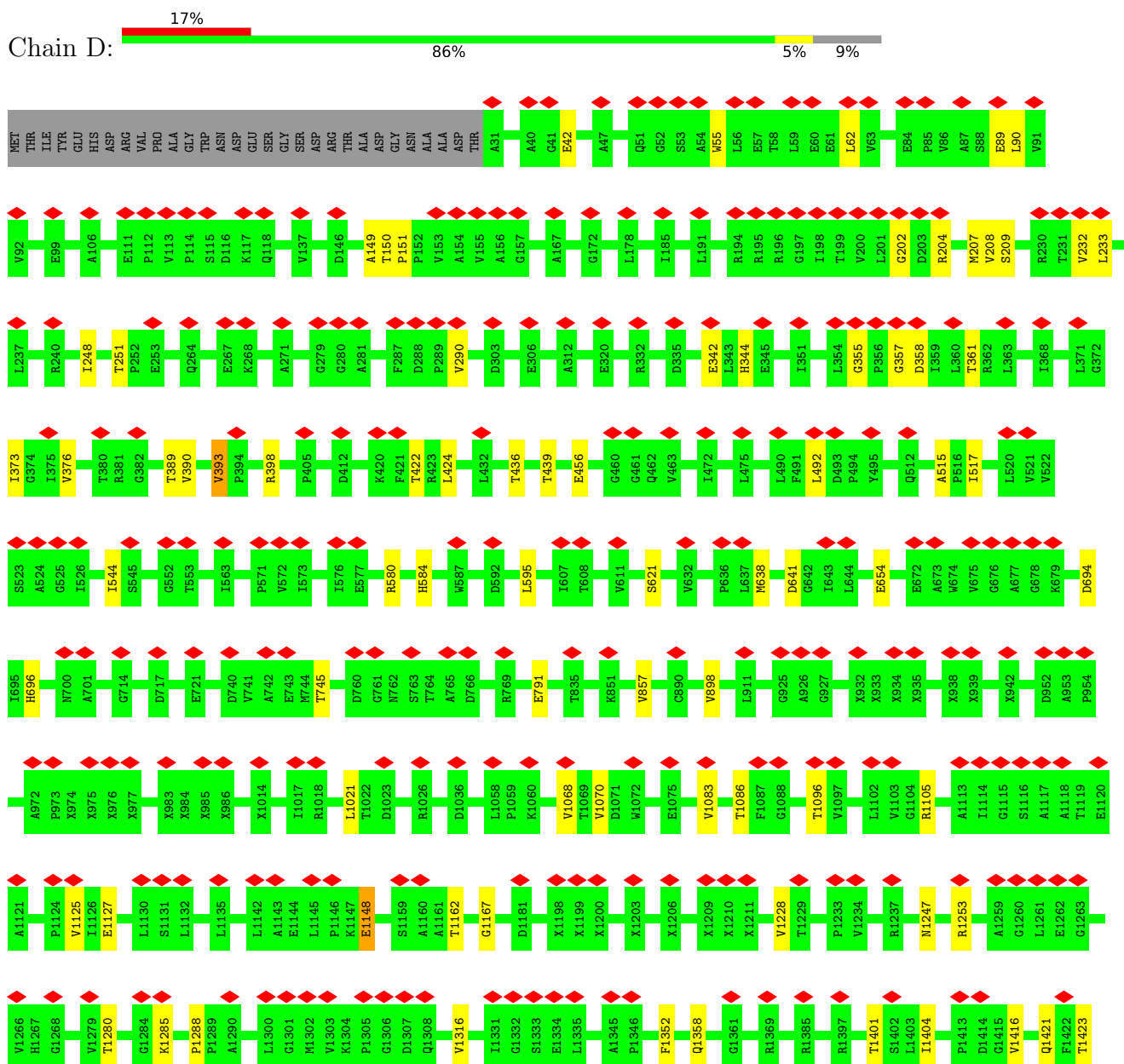
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Mol	Chain	Residues	Atoms					AltConf
2	F	1	Total 31	C 17	N 4	O 9	P 1	0
2	A	1	Total 31	C 17	N 4	O 9	P 1	0
2	B	1	Total 31	C 17	N 4	O 9	P 1	0
2	C	1	Total 31	C 17	N 4	O 9	P 1	0

3 Residue-property plots

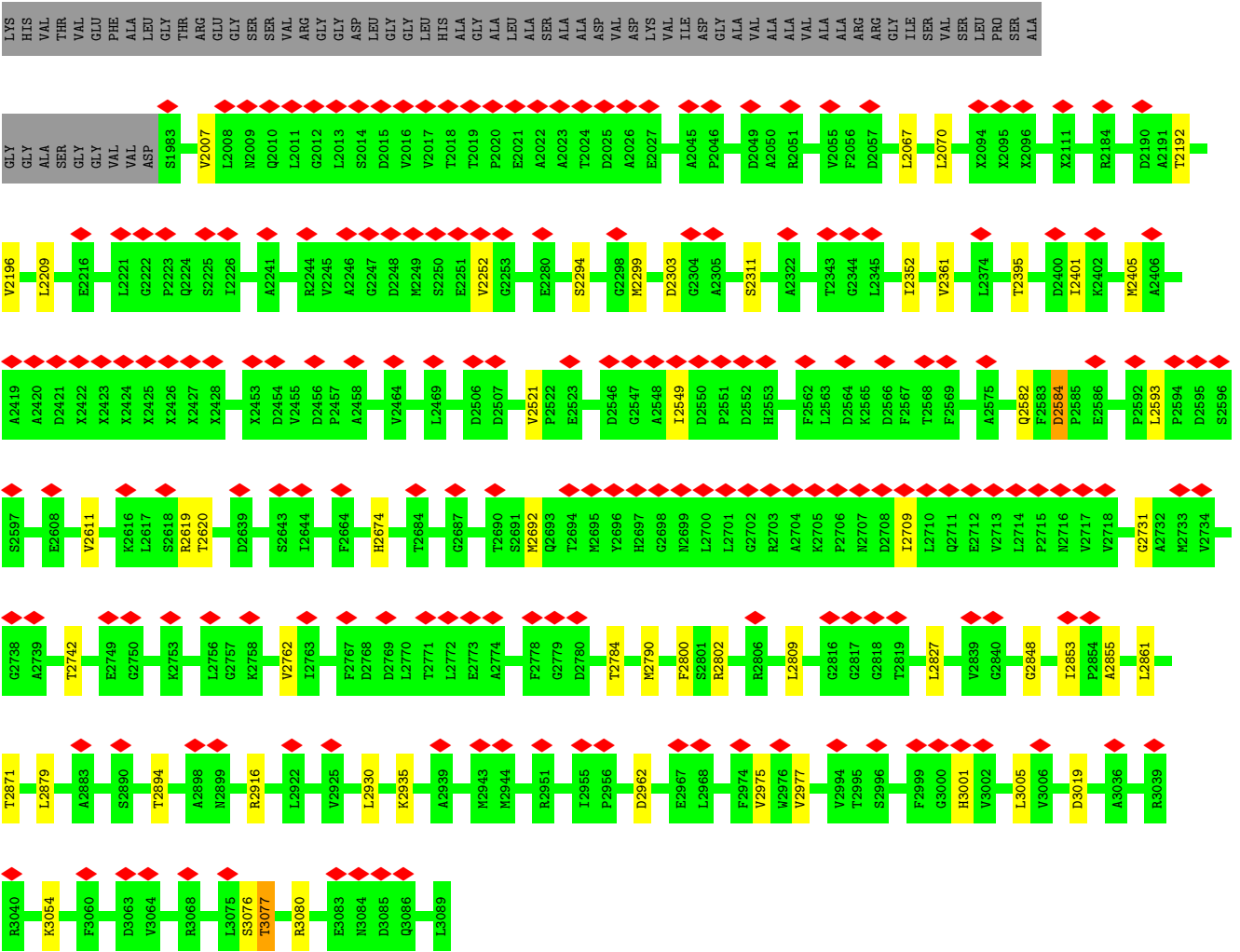
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

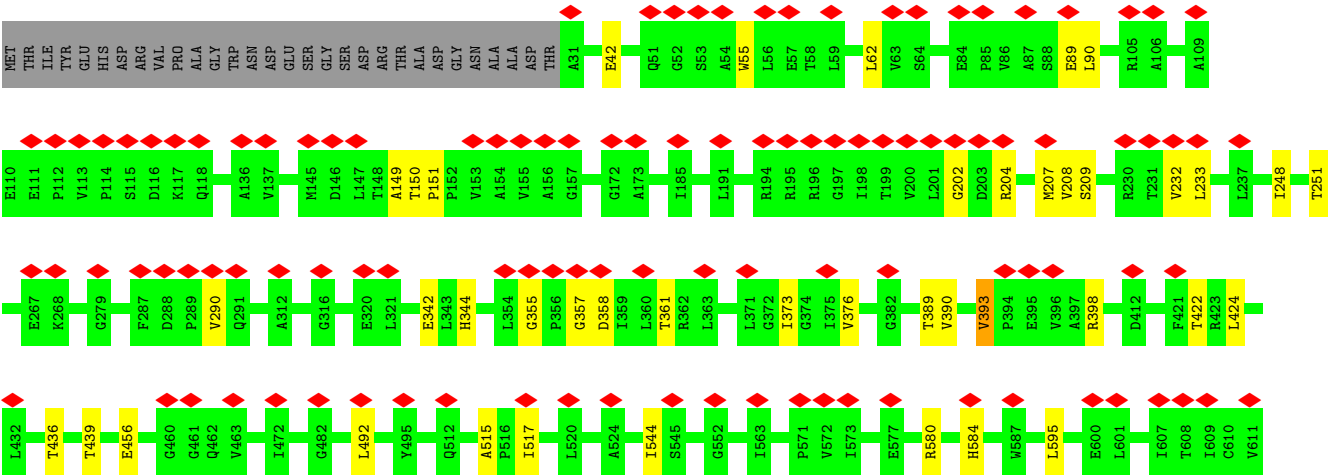
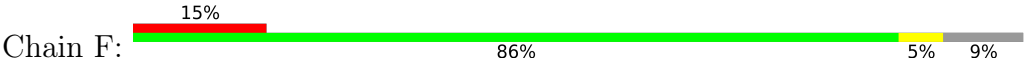




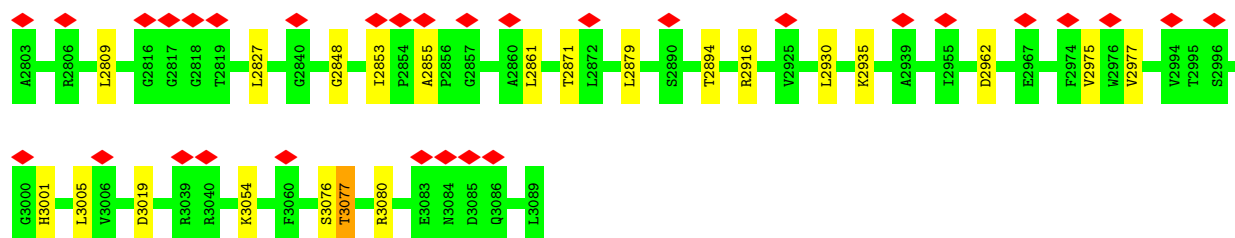




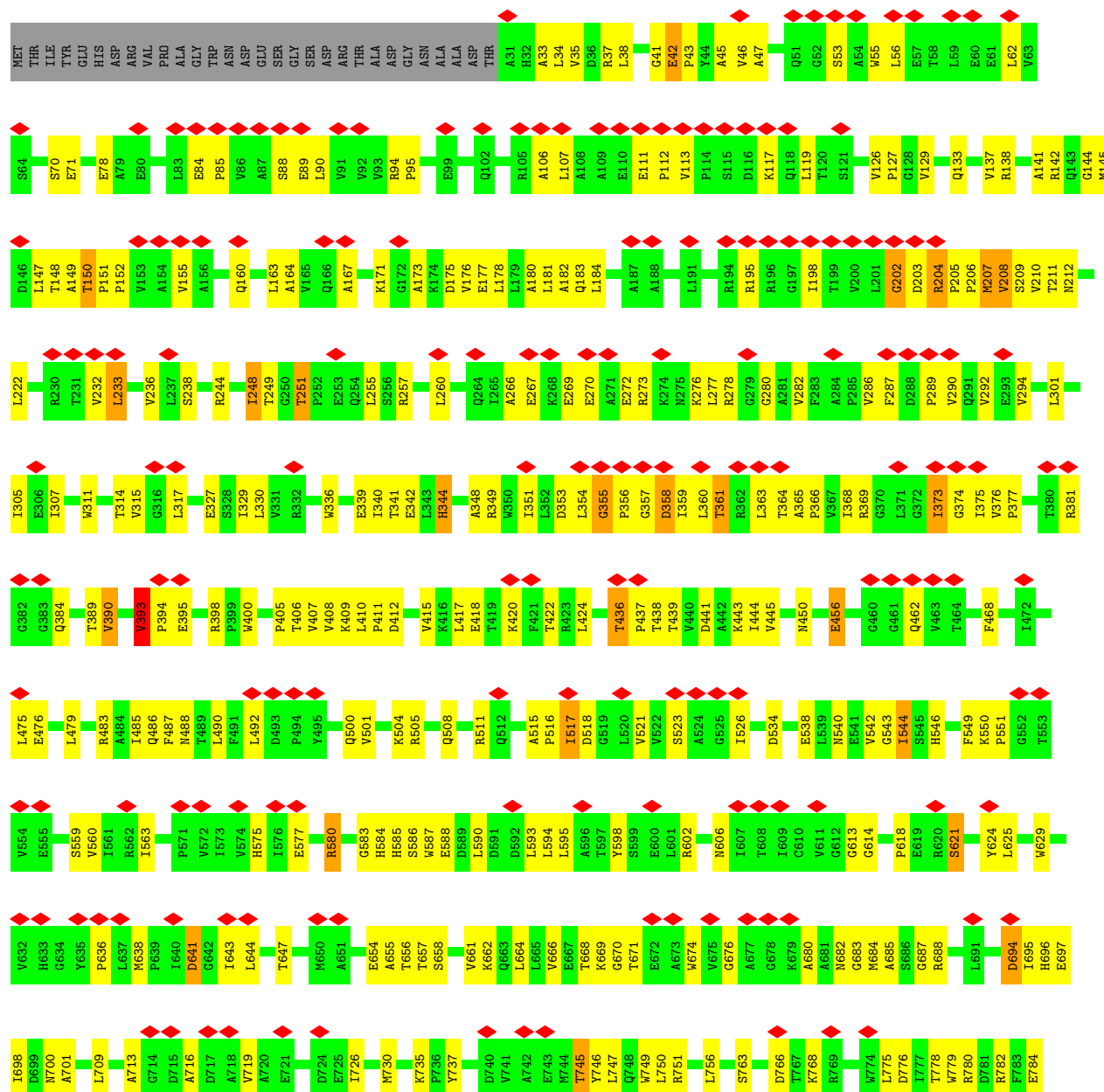
● Molecule 1: FATTY ACID SYNTHASE





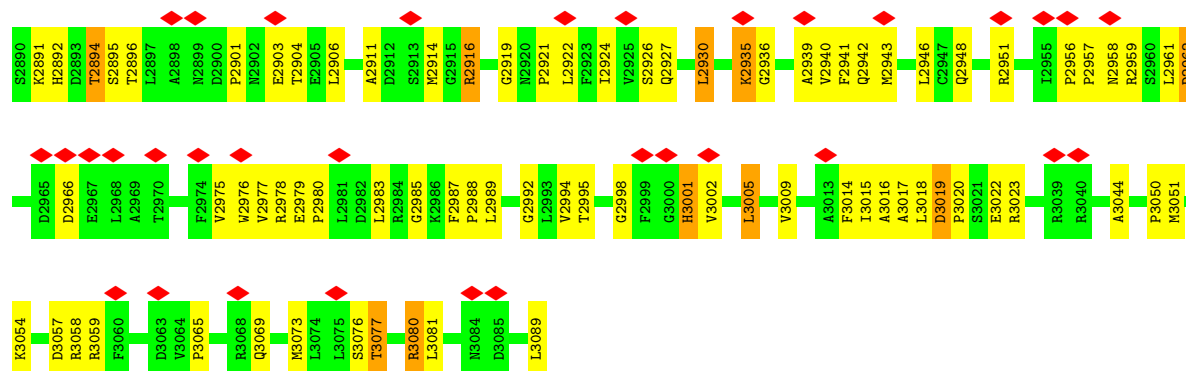


• Molecule 1: FATTY ACID SYNTHASE

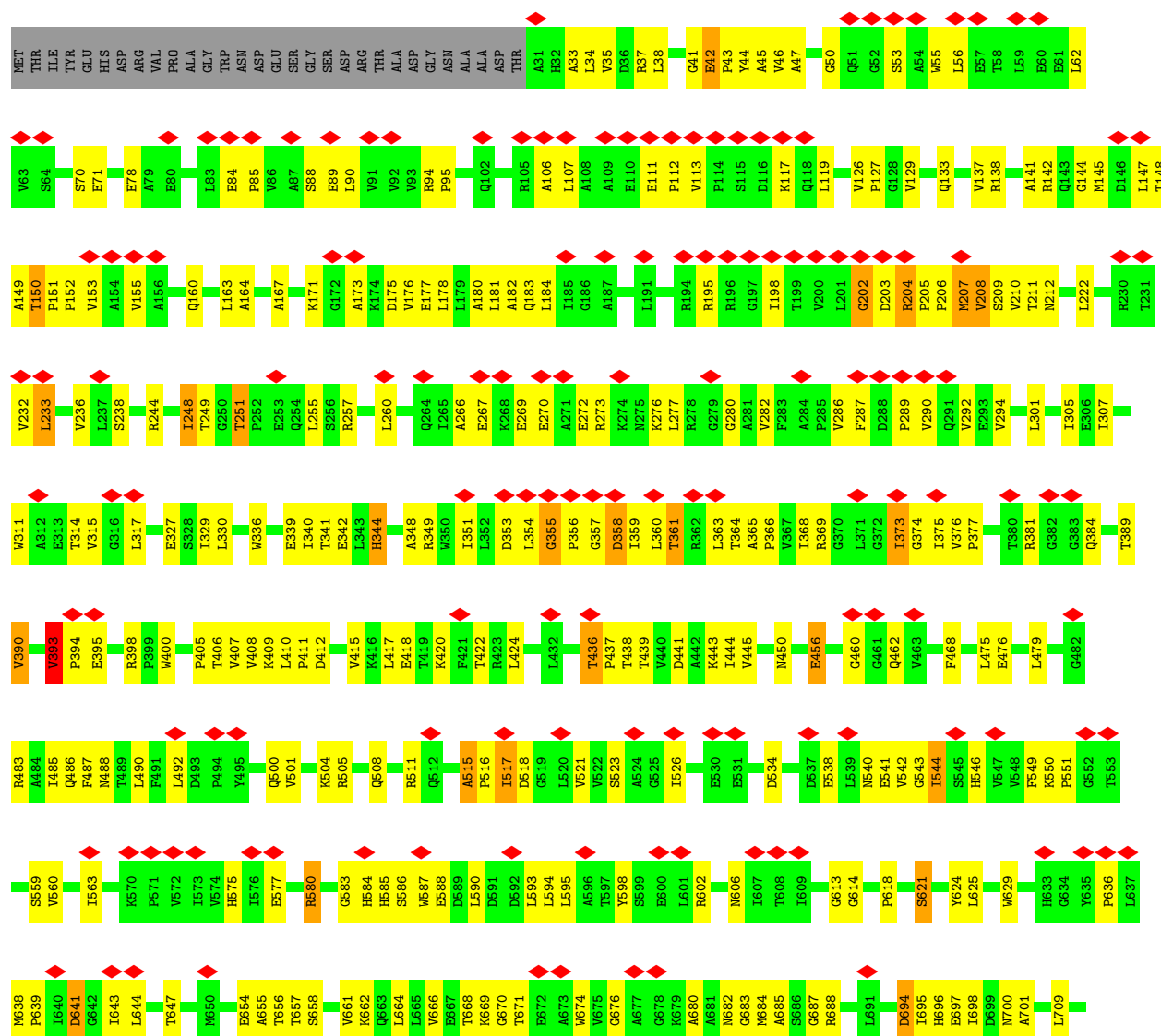




F2811	G2740	V2673	R2603	E2523	X2433	Q2348	E2251	R2175	X2095	G2012	ALA
L2812	A2741	H2674	R2604	C2524	X2434	N2349	V2252	L2176	X2096	L2013	GLY
Q2815	T2742	S2675	A2605	E2525	X2435	I2352	R2255	F2179	X2097	S2014	ALA
G2816	A2743	S2676	G2606	I2526	X2436	V2353	R2256	K2180	X2098	D2015	LEU
G2817	A2744	A2679	T2607	V2527	X2437	S2354	K2261		X2099	D2016	ALA
L2820	T2745	S2680	E2608	E2528	X2441	E2358	V2265	R2184	X2100	V2017	ALA
L2821	T2746	S2681	T2609	R2529	X2442	A2359	Q2268	R2188	X2101	V2018	VAL
L2822	T2747	T2684	R2610	Y2530	X2443	G2360	Q2269	F2189	X2102	T2019	ASP
L2823	T2748	G2685	P2612	A2533	X2444	V2361	L2270	D2190	X2103	T2018	VAL
L2824	T2749	G2686	R2613	R2541	X2445	V2362	L2271	D2191	X2104	T2019	ASP
L2827	K2753	G2687	K2614	E2542	X2448	M2369	L2274	T2192	X2105	P2020	LEU
L2828	T2754	G2688	T2615	F2543	X2449	M2372	L2277	T2193	X2106	A2022	ALA
L2829	T2755	T2690	K2616	D2546	X2450	L2373	T2277	K2194	X2107	A2023	GLY
K2830	L2756	S2691	L2617	G2547	X2451	L2374	T2278	W2195	X2108	T2024	PRO
M2831	G2757	M2692	X2452	A2548	X2453	L2375	E2280	F2196		D2025	ALA
G2832	K2758	Q2693	R2618	A2549	X2454	L2376	R2286	A2198		A2026	ALA
L2833	A2759	T2694	T2620	I2549	D2454		L2287	A2199		E2027	VAL
P2834			D2550	D2550	D2455	V2379	L2288	M2200			ALA
V2835	V2762	M2695	P2551	D2551	D2456	K2391	H2288			A2045	ALA
L2836	A2763	M2696	D2552	D2552	F2457	V2392	L2291	D2205		T2046	VAL
V2839	G2764	H2697	H2553	H2553	A2458	L2393				T2047	THR
G2840	G2765	G2698	D2554	D2554	D2459	L2394	S2284	L2209		F2048	THR
Q2843	T2766	M2699	S2555	S2555	V2461	L2395	F2295	V2210		D2049	TRP
S2844	T2767	L2700	P2556	P2556	V2462		M2296	W2211		A2050	GLY
F2845	D2768	G2701	L2557	L2558		L2398	G2298	W2212		K2051	LEU
A2846	T2769	Q2702	V2559	V2559	G2470	G2399	M2299	W2213		K2052	PRO
D2847	R2703	R2703	T2632	T2632	T2471	D2400	F2300	G2214		A2054	GLY
G2848	A2704	A2704	V2633	V2633	V2472	L2401		T2215		D2054	TRP
	L2705	K2705	D2639	D2639	R2478	K2402	D2303	E2216		V2055	ALA
	P2706	P2706	M2640	M2640		L2403	G2304	Q2217		D2056	ALA
	A2774	N2707	S2643	S2643	M2481	D2404	K2310	T2218		V2055	LYS
	L2775	D2708	T2644	T2644	E2482	M2405	E2219	E2219		D2057	VAL
	L2776	L2709	L2645	L2645	F2567	A2406	S2311	S2220		K2058	THR
	P2854	Q2711	R2646	R2646	L2487	E2407		L2221		W2060	VAL
	A2855	Q2712	V2647	V2647	V2492	A2408	R2319	G2222		R2064	PHE
	G2856	V2713	A2648	A2648		A2409		Q2223			VAL
	G2857	L2714	L2649	L2649	L2495	A2412	A2322	Q2224		L2067	LEU
	L2858	L2715	N2651	N2650	M2501	M2416	E2323	Q2225		S1983	GLY
	A2860	P2716	L2652	L2652	V2502	S2417	K2324	L2226		L2070	THR
	L2861	V2717	V2653	V2653	K2503	G2418	S2325			L1986	ARG
	T2871	V2718	T2655	T2655	E2504	A2419	S2331	K2229		F1989	GLY
	L2876	V2719	T2656	T2656	E2505	A2420	L2332			K1992	SER
	L2879	A2720	A2658	A2658	D2506	D2421	A2333	P2234		X2077	VAL
	G2880	H2721	F2659	F2659	D2507	X2422	H2334	T2235		X2078	ARG
	V2881	V2722	S2662	S2662	W2512	X2423	T2337	L2237		X2080	GLY
	G2882	V2727			V2513	X2424	G2338	F2238		X2081	GLY
	A2883	Y2730	P2666	P2666	E2516	X2425	W2339	A2241		X2082	ASP
	D2885	G2731	T2667	T2667		X2426		R2244		X2084	LEU
	P2806	A2732	E2668	E2668	L2520	X2427	T2343	R2245		X2085	GLY
	L2886	M2733	L2669	L2669	V2521	X2428	G2344	X2246		X2086	GLY
	L2889	V2734	M2670	M2670	P2594	X2429	L2345	A2246		X2087	LEU
		L2809	R2671	R2671	D2595	X2430	M2346	G2247		X2088	
		V2735	V2672	V2672	S2596	X2431	G2347	D2248		X2089	
		P2736			S2597	X2432		M2249		X2090	
		G2737			D2598			S2250		X2093	
		A2739			W2599					X2094	



• Molecule 1: FATTY ACID SYNTHASE



G1713	A713	X986	D1073	E1143	L1219	P1305	D1381	V1464	Y1542	F1623	G1713	THR
L1714	A716	X987	P1074	E1149	X1220	G1306	R1385	V1467	A1543	T1624	L1714	ASP
R1717	A719	X988	E1075	E1150	X1221	D1307	R1386	Y1468	I1544	L1625	L1717	PRO
L1721	A720	X989	L1076	E1151	X1224	Q1308	S1391	E1469	A1549	R1634	R1717	GLU
E1726	A721	X990	V1083	S1159	X1225	D1310	R1397	L1470	G1550	D1635	L1721	PRO
L1730	A726	X991	A1085	A1161	X1226	F1311	R1397	E1471	L1551	L1636	P1722	GLU
K735	A730	X992	T1086	A1162	V1228	V1313	P1400	L1474	A1552	P1637	E1723	ALA
P736	K736	X993	F1087	T1164	T1229	D1314	T1401	V1477	L1553	P1638	Y1724	ALA
Y737	P736	X994	G1088	G1167	V1230	V1316	S1402	R1480	E1555	E1640	S1725	ALA
D740	D740	X995	A1089	R1168	V1234	V1317	I1404	K1483	E1556	T1650	H1726	ALA
V741	V741	X996	P1090	R1168	D1235	G1317	S1406	M1484	I1557	T1651	T1727	ALA
A742	A742	X997	A1092	P1171	D1236	V1320	G1407	H1485	R1560	W1652	T1728	ALA
E743	E743	X998	P1093	P1172	R1237	V1321	V1408	D1486	R1561	K1656	E1730	ALA
M744	M744	X999	T1094	V1173	N1247	L1325	H1412	I1487	R1562	P1657	L1731	ALA
L746	L746	X1000	T1095	V1174	R1253	E1326	Y1410	V1488	Q1563	K1658	N1733	ALA
Y747	Y747	X1001	L1096	R1177	A1259	F1327	H1411	P1499	I1564	E1659	S1734	ALA
L748	L748	X1002	V1097	N1178	G1260	S1328	H1412	R1490	T1565	G1661	E1735	ALA
Q748	Q748	X1003	P1098	A1180	L1261	A1329	P1413	D1491	G1566	R1662	R1736	ALA
W749	W749	X1004	D1100	D1181	L1262	R1330	G1415	E1492	G1567	K1663	D1737	ALA
L750	L750	X1005	L1102	G1182	E1262	L1331	V1416	L1493	I1572	I1666	A1738	ALA
R751	R751	X1006	V1103	A1183	V1266	G1332	L1417	G1494	I1573	E1667	V1740	ALA
L756	L756	X1007	G1104	L1185	H1267	E1334	T1420	R1495	L1574	Q1672	L1741	ALA
S763	S763	X1008	R1105	L1188	G1268	L1335	F1422	S1496	P1575	F1673	D1745	ALA
D766	D766	X1009	C1106	L1188	H1267	M1336	G1424	N1497	G1576	A1674	THR	
T767	T767	X1010	V1110	R1191	I1270	A1337	A1425	I1503	I1577	W1679	PRO	
K768	K768	X1011	F1111	F1192	L1271	A1339	V1426	R1504	D1578	D1684	GLU	
R769	R769	X1012	T1114	A1193	A1274	R1342	A1426	Q1507	I1579	I1685	GLU	
L775	L775	X1013	G1115	I1194	A1275	L1343	V1430	I1508	P1580	L1686	PRO	
D776	D776	X1014	S1116	X1195	Q1276	L1344	A1431	D1509	F1581	F1687	GLU	
I777	I777	X1015	A1117	X1196	H1277	A1344	A1431	L1510	H1582	L1687	ALA	
T778	T778	X1016	A1118	X1197	V1278	A1345	V1435	D1511	S1583	F1687	ALA	
W779	W779	X1017	T1119	X1198	V1279	P1346	V1435	D1514	S1584	E1690	ASP	
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F782	F782	X1019	F1123	X1200	T1282	A1350	Q1441	V1519	L1586	L1695	PRO	
E784	E784	X1020	V1125	X1201	D1283	A1351	V1445	R1525	E1590	G1696	ALA	
L787	L787	X1021	G1126	X1202	G1284	F1352	E1446	T1526	E1598	R1699	ALA	
A790	A790	X1022	E1127	X1203	K1285	P1353	G1447	G1527	D1604	F1700	ALA	
E791	E791	X1023	G1128	X1204	P1286	Q1355	A1448	E1528	K1605	E1701	ALA	
A792	A792	X1024	L1129	X1205	V1287	G1356	A1449	F1529	I1611	I1703	ALA	
R793	R793	X1025	L1130	X1206	P1288	I1357	H1453	L1530	G1612	G1704	ALA	
L794	L794	X1026	S1131	X1207	P1289	H1358	S1454	E1531	R1613	W1705	ALA	
H795	H795	X1027	V1133	X1208	K1291	H1359	V1455	I1532	Y1614	K1706	ALA	
G900	G900	X1028	L1132	X1209	L1292	G1360	G1456	V1533	P1616	S1707	ALA	
Q901	Q901	X1029	L1142	X1210	W1295	M1362	E1457	F1535	N1617	T1710	PRO	
D979	D979	X1030	A1144	X1211	L1300	E1365	T1458	L1536	L1618	V1711	ALA	
D798	D798	X1031	P1146	X1212	G1301	V1376	A1460	L1537	P1619	A1712	PRO	
		X1032	L1145	X1213	M1302	A1380	A1462	R1538	P1621		ALA	
		X1033	P1147	X1214	V1303		C1463	G1539	P1622		ALA	
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		X1134		X1315								ALA
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E2788	V2717	D2645	F2562	V2462	D2393	S2294	X2115	T2047	ALA
M2789	V2718	V2646	L2563	L2469	G2394	P2295	X2116	D2048	ALA
R2790	V2719	V2647	L2564	G2470	N2296	G2214	X2117	D2049	ALA
K2791	A2719	A2648	D2564	P2471	G2297	T2215	X2118	A2050	ALA
L2792	V2722	L2649	K2565	Y2472	G2298	T2216	X2119	R2051	ALA
F2800	V2727	V2650	D2566	Y2478	D2400	G2217	X2120	K2052	ALA
S2801	V2730	V2651	F2567	R2478	I2401	T2218	X2121	V2053	ALA
R2802	G2731	L2652	F2568	M2481	K2402	T2219	X2122	A2054	ALA
D2805	A2732	V2653	F2569	V2482	L2403	E2219	X2123	V2055	ALA
R2806	G2733	G2662	F2580	V2483	M2404	S2220	X2124	F2056	ALA
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L2809	H2735	T2665	F2583	V2492	E2407	P2223	X2127	G2059	ALA
G2810	V2736	T2666	P2584	V2495	L2408	Q2224	X2128	V2060	ALA
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L2822	S2746	S2680	D2598	L2516	X2424	R2244	X2138	X2080	ALA
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G2832	T2758	S2692	L2609	E2527	X2432	S2252	X2146	X2088	ALA
L2833	A2759	Q2693	R2610	E2528	X2433	R2255	X2147	X2089	ALA
V2834	V2762	T2694	V2611	E2529	X2434	M2260	X2148	X2090	ALA
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S2852	G2777	K2705	A2622	L2549	X2449	G2278	X2159	X2101	ALA
L2853	F2778	P2706	G2623	D2550	X2450	E2280	X2160	X2102	ALA
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T1668	H1744	T1668	T1745	V1747	K1673	P1673	R1578	L1491	H1411	D1328	X1242	T1176	X1003	D814	E817	L747
T1669	H1745	T1669	T1746	V1748	K1674	P1674	R1579	L1492	H1412	D1329	X1243	T1177	X1004	D815	E818	Q748
T1670	H1746	T1670	T1747	V1749	K1675	P1675	R1580	L1493	H1413	D1330	X1244	T1178	X1005	D816	E819	W749
T1671	H1747	T1671	T1748	V1750	K1676	P1676	R1581	L1494	H1414	D1331	X1245	T1179	X1006	D817	E820	L750
T1672	H1748	T1672	T1749	V1751	K1677	P1677	R1582	L1495	H1415	D1332	X1246	T1180	X1007	D818	E821	R751
T1673	H1749	T1673	T1750	V1752	K1678	P1678	R1583	L1496	H1416	D1333	X1247	T1181	X1008	D819	E822	L756
T1674	H1750	T1674	T1751	V1753	K1679	P1679	R1584	L1497	H1417	D1334	X1248	T1182	X1009	D820	E823	D760
T1675	H1751	T1675	T1752	V1754	K1680	P1680	R1585	L1498	H1418	D1335	X1249	T1183	X1010	D821	E824	G761
T1676	H1752	T1676	T1753	V1755	K1681	P1681	R1586	L1499	H1419	D1336	X1250	T1184	X1011	D822	E825	N762
T1677	H1753	T1677	T1754	V1756	K1682	P1682	R1587	L1500	H1420	D1337	X1251	T1185	X1012	D823	E826	S763
T1678	H1754	T1678	T1755	V1757	K1683	P1683	R1588	L1501	H1421	D1338	X1252	T1186	X1013	D824	E827	T764
T1679	H1755	T1679	T1756	V1758	K1684	P1684	R1589	L1502	H1422	D1339	X1253	T1187	X1014	D825	E828	A765
T1680	H1756	T1680	T1757	V1759	K1685	P1685	R1590	L1503	H1423	D1340	X1254	T1188	X1015	D826	E829	D766
T1681	H1757	T1681	T1758	V1760	K1686	P1686	R1591	L1504	H1424	D1341	X1255	T1189	X1016	D827	E830	T767
T1682	H1758	T1682	T1759	V1761	K1687	P1687	R1592	L1505	H1425	D1342	X1256	T1190	X1017	D828	E831	K768
T1683	H1759	T1683	T1760	V1762	K1688	P1688	R1593	L1506	H1426	D1343	X1257	T1191	X1018	D829	E832	R769
T1684	H1760	T1684	T1761	V1763	K1689	P1689	R1594	L1507	H1427	D1344	X1258	T1192	X1019	D830	E833	L775
T1685	H1761	T1685	T1762	V1764	K1690	P1690	R1595	L1508	H1428	D1345	X1259	T1193	X1020	D831	E834	D776
T1686	H1762	T1686	T1763	V1765	K1691	P1691	R1596	L1509	H1429	D1346	X1260	T1194	X1021	D832	E835	I777
T1687	H1763	T1687	T1764	V1766	K1692	P1692	R1597	L1510	H1430	D1347	X1261	T1195	X1022	D833	E836	W779
T1688	H1764	T1688	T1765	V1767	K1693	P1693	R1598	L1511	H1431	D1348	X1262	T1196	X1023	D834	E837	R780
T1689	H1765	T1689	T1766	V1768	K1694	P1694	R1599	L1512	H1432	D1349	X1263	T1197	X1024	D835	E838	D781
T1690	H1766	T1690	T1767	V1769	K1695	P1695	R1600	L1513	H1433	D1350	X1264	T1198	X1025	D836	E839	F782
T1691	H1767	T1691	T1768	V1770	K1696	P1696	R1601	L1514	H1434	D1351	X1265	T1199	X1026	D837	E840	E784
T1692	H1768	T1692	T1769	V1771	K1697	P1697	R1602	L1515	H1435	D1352	X1266	T1200	X1027	D838	E841	L787
T1693	H1769	T1693	T1770	V1772	K1698	P1698	R1603	L1516	H1436	D1353	X1267	T1201	X1028	D839	E842	A790
T1694	H1770	T1694	T1771	V1773	K1699	P1699	R1604	L1517	H1437	D1354	X1268	T1202	X1029	D840	E843	E791
T1695	H1771	T1695	T1772	V1774	K1700	P1700	R1605	L1518	H1438	D1355	X1269	T1203	X1030	D841	E844	A792
T1696	H1772	T1696	T1773	V1775	K1701	P1701	R1606	L1519	H1439	D1356	X1270	T1204	X1031	D842	E845	E793
T1697	H1773	T1697	T1774	V1776	K1702	P1702	R1607	L1520	H1440	D1357	X1271	T1205	X1032	D843	E846	R794
T1698	H1774	T1698	T1775	V1777	K1703	P1703	R1608	L1521	H1441	D1358	X1272	T1206	X1033	D844	E847	L795
T1699	H1775	T1699	T1776	V1778	K1704	P1704	R1609	L1522	H1442	D1359	X1273	T1207	X1034	D845	E848	P796
T1700	H1776	T1700	T1777	V1779	K1705	P1705	R1610	L1523	H1443	D1360	X1274	T1208	X1035	D846	E849	
T1701	H1777	T1701	T1778	V1780	K1706	P1706	R1611	L1524	H1444	D1361	X1275	T1209	X1036	D847	E850	
T1702	H1778	T1702	T1779	V1781	K1707	P1707	R1612	L1525	H1445	D1362	X1276	T1210	X1037	D848	E851	
T1703	H1779	T1703	T1780	V1782	K1708	P1708	R1613	L1526	H1446	D1363	X1277	T1211	X1038	D849	E852	
T1704	H1780	T1704	T1781	V1783	K1709	P1709	R1614	L1527	H1447	D1364	X1278	T1212	X1039	D850	E853	
T1705	H1781	T1705	T1782	V1784	K1710	P1710	R1615	L1528	H1448	D1365	X1279	T1213	X1040	D851	E854	
T1706	H1782	T1706	T1783	V1785	K1711	P1711	R1616	L1529	H1449	D1366	X1280	T1214	X1041	D852	E855	
T1707	H1783	T1707	T1784	V1786	K1712	P1712	R1617	L1530	H1450	D1367	X1281	T1215	X1042	D853	E856	
T1708	H1784	T1708	T1785	V1787	K1713	P1713	R1618	L1531	H1451	D1368	X1282	T1216	X1043	D854	E857	
T1709	H1785	T1709	T1786	V1788	K1714	P1714	R1619	L1532	H1452	D1369	X1283	T1217	X1044	D855	E858	
T1710	H1786	T1710	T1787	V1789	K1715	P1715	R1620	L1533	H1453	D1370	X1284	T1218	X1045	D856	E859	
T1711	H1787	T1711	T1788	V1790	K1716	P1716	R1621	L1534	H1454	D1371	X1285	T1219	X1046	D857	E860	
T1712	H1788	T1712	T1789	V1791	K1717	P1717	R1622	L1535	H1455	D1372	X1286	T1220	X1047	D858	E861	
T1713	H1789	T1713	T1790	V1792	K1718	P1718	R1623	L1536	H1456	D1373	X1287	T1221	X1048	D859	E862	
T1714	H1790	T1714	T1791	V1793	K1719	P1719	R1624	L1537	H1457	D1374	X1288	T1222	X1049	D860	E863	
T1715	H1791	T1715	T1792	V1794	K1720	P1720	R1625	L1538	H1458	D1375	X1289	T1223	X1050	D861	E864	
T1716	H1792	T1716	T1793	V1795	K1721	P1721	R1626	L1539	H1459	D1376	X1290	T1224	X1051	D862	E865	
T1717	H1793	T1717	T1794	V1796	K1722	P1722	R1627	L1540	H1460	D1377	X1291	T1225	X1052	D863	E866	
T1718	H1794	T1718	T1795	V1797	K1723	P1723	R1628	L1541	H1461	D1378	X1292	T1226	X1053	D864	E867	
T1719	H1795	T1719	T1796	V1798	K1724	P1724	R1629	L1542	H1462	D1379	X1293	T1227	X1054	D865	E868	
T1720	H1796	T1720	T1797	V1799	K1725	P1725	R1630	L1543	H1463	D1380	X1294	T1228	X1055	D866	E869	
T1721	H1797	T1721	T1798	V1800	K1726	P1726	R1631	L1544	H1464	D1381	X1295	T1229	X1056	D867	E870	
T1722	H1798	T1722	T1799	V1801	K1727	P1727	R1632	L1545	H1465	D1382	X1296	T1230	X1057	D868	E871	
T1723	H1799	T1723	T1800	V1802	K1728	P1728	R1633	L1546	H1466	D1383	X1297	T1231	X1058	D869	E872	
T1724	H1800	T1724	T1801	V1803	K1729	P1729	R1634	L1547	H1467	D1384	X1298	T1232	X1059	D870	E873	
T1725	H1801	T1725	T1802	V1804	K1730	P1730	R1635	L1548	H1468	D1385	X1299	T1233	X1060	D871	E874	
T1726	H1802	T1726	T1803	V1805	K1731	P1731	R1636	L1549	H1469	D1386	X1300	T1234	X1061	D872	E875	
T1727	H1803	T1727	T1804	V1806	K1732	P1732	R1637	L1550	H1470	D1387	X1301	T1235	X1062	D873	E876	
T1728	H1804	T1728	T1805	V1807	K1733	P1733	R1638	L1551	H1471	D1388	X1302	T1236	X1063	D874	E877	
T1729	H1805	T1729	T1806	V1808	K1734	P1734	R1639	L1552	H1472	D1389	X1303	T1237	X1064	D875	E878	
T1730	H1806	T1730	T1807													





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D3	Depositor
Number of particles used	106884	Depositor
Resolution determination method	Not provided	
CTF correction method	EACH IMAGE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	100000	Depositor
Image detector	FEI FALCON I (4k x 4k)	Depositor
Maximum map value	14.936	Depositor
Minimum map value	-7.793	Depositor
Average map value	-0.133	Depositor
Map value standard deviation	1.076	Depositor
Recommended contour level	2.7	Depositor
Map size ($\text{\AA}$)	392.0, 392.0, 392.0	wwPDB
Map dimensions	160, 160, 160	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	2.45, 2.45, 2.45	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.35	0/20319	0.87	42/27667 (0.2%)
1	B	0.35	0/20319	0.87	45/27667 (0.2%)
1	C	0.35	0/20319	0.87	42/27667 (0.2%)
1	D	0.35	0/20319	0.87	44/27667 (0.2%)
1	E	0.35	0/20319	0.87	45/27667 (0.2%)
1	F	0.35	0/20319	0.87	41/27667 (0.1%)
All	All	0.35	0/121914	0.87	259/166002 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	5
1	B	0	5
1	C	0	5
1	D	0	5
1	E	0	5
1	F	0	5
All	All	0	30

There are no bond length outliers.

The worst 5 of 259 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	151	PRO	N-CA-C	10.68	123.73	110.70
1	D	151	PRO	N-CA-C	10.67	123.71	110.70
1	C	151	PRO	N-CA-C	10.65	123.69	110.70
1	E	151	PRO	N-CA-C	10.63	123.67	110.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	151	PRO	N-CA-C	10.63	123.67	110.70

There are no chirality outliers.

5 of 30 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	1148	GLU	Peptide
1	D	150	THR	Peptide
1	D	202	GLY	Peptide
1	D	2584	ASP	Peptide
1	D	357	GLY	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	21020	0	20990	1082	0
1	B	21020	0	20990	1100	0
1	C	21020	0	20990	1083	0
1	D	21020	0	20990	0	0
1	E	21020	0	20990	0	0
1	F	21020	0	20990	0	0
2	A	31	0	19	4	0
2	B	31	0	19	5	0
2	C	31	0	19	4	0
2	D	31	0	19	0	0
2	E	31	0	19	0	0
2	F	31	0	19	0	0
All	All	126306	0	126054	3210	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 25.

The worst 5 of 3210 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:793:ARG:O	1:A:2435:UNK:HG2	1.31	1.30
1:B:793:ARG:O	1:B:2435:UNK:HG2	1.31	1.28
1:B:2100:UNK:O	1:B:2103:UNK:HG3	1.36	1.26
1:A:2105:UNK:O	1:A:2108:UNK:HG3	1.34	1.25
1:B:2105:UNK:O	1:B:2108:UNK:HG3	1.34	1.25

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	2637/3089 (85%)	2489 (94%)	140 (5%)	8 (0%)	36	72
1	B	2637/3089 (85%)	2489 (94%)	140 (5%)	8 (0%)	36	72
1	C	2637/3089 (85%)	2489 (94%)	139 (5%)	9 (0%)	36	72
1	D	2637/3089 (85%)	2488 (94%)	140 (5%)	9 (0%)	36	72
1	E	2637/3089 (85%)	2488 (94%)	141 (5%)	8 (0%)	36	72
1	F	2637/3089 (85%)	2488 (94%)	140 (5%)	9 (0%)	36	72
All	All	15822/18534 (85%)	14931 (94%)	840 (5%)	51 (0%)	37	72

5 of 51 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	1148	GLU
1	E	1148	GLU
1	F	1148	GLU
1	A	1148	GLU
1	B	1148	GLU

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	2076/2264 (92%)	1953 (94%)	123 (6%)	18	39
1	B	2076/2264 (92%)	1953 (94%)	123 (6%)	18	39
1	C	2076/2264 (92%)	1953 (94%)	123 (6%)	18	39
1	D	2076/2264 (92%)	1953 (94%)	123 (6%)	18	39
1	E	2076/2264 (92%)	1953 (94%)	123 (6%)	18	39
1	F	2076/2264 (92%)	1953 (94%)	123 (6%)	18	39
All	All	12456/13584 (92%)	11718 (94%)	738 (6%)	19	39

5 of 738 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2582	GLN
1	B	2209	LEU
1	A	2861	LEU
1	A	2549	ILE
1	B	595	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 78 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	633	HIS
1	C	2651	ASN
1	C	1134	HIS
1	C	1617	ASN
1	C	2927	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

6 ligands are modelled in this entry.

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
2	FMN	D	4000	-	33,33,33	1.04	2 (6%)	48,50,50	1.28	8 (16%)
2	FMN	E	4000	-	33,33,33	1.04	2 (6%)	48,50,50	1.29	7 (14%)
2	FMN	A	4000	-	33,33,33	1.03	2 (6%)	48,50,50	1.28	8 (16%)
2	FMN	C	4000	-	33,33,33	1.04	2 (6%)	48,50,50	1.28	8 (16%)
2	FMN	F	4000	-	33,33,33	1.03	2 (6%)	48,50,50	1.28	8 (16%)
2	FMN	B	4000	-	33,33,33	1.04	2 (6%)	48,50,50	1.29	9 (18%)

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
2	FMN	D	4000	-	-	5/18/18/18	0/3/3/3
2	FMN	E	4000	-	-	5/18/18/18	0/3/3/3
2	FMN	A	4000	-	-	5/18/18/18	0/3/3/3
2	FMN	C	4000	-	-	5/18/18/18	0/3/3/3
2	FMN	F	4000	-	-	5/18/18/18	0/3/3/3
2	FMN	B	4000	-	-	5/18/18/18	0/3/3/3

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	4000	FMN	C4A-N5	3.72	1.38	1.30
2	E	4000	FMN	C4A-N5	3.70	1.38	1.30
2	F	4000	FMN	C4A-N5	3.67	1.38	1.30
2	C	4000	FMN	C4A-N5	3.67	1.38	1.30
2	D	4000	FMN	C4A-N5	3.67	1.38	1.30

The worst 5 of 48 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	4000	FMN	C4-N3-C2	-3.13	120.08	125.64
2	F	4000	FMN	C4-N3-C2	-3.12	120.09	125.64
2	E	4000	FMN	C4-N3-C2	-3.11	120.11	125.64
2	B	4000	FMN	C4-N3-C2	-3.10	120.13	125.64
2	D	4000	FMN	C4-N3-C2	-3.09	120.15	125.64

There are no chirality outliers.

5 of 30 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	4000	FMN	O3'-C3'-C4'-C5'
2	E	4000	FMN	O3'-C3'-C4'-C5'
2	F	4000	FMN	O3'-C3'-C4'-C5'
2	A	4000	FMN	O3'-C3'-C4'-C5'
2	B	4000	FMN	O3'-C3'-C4'-C5'

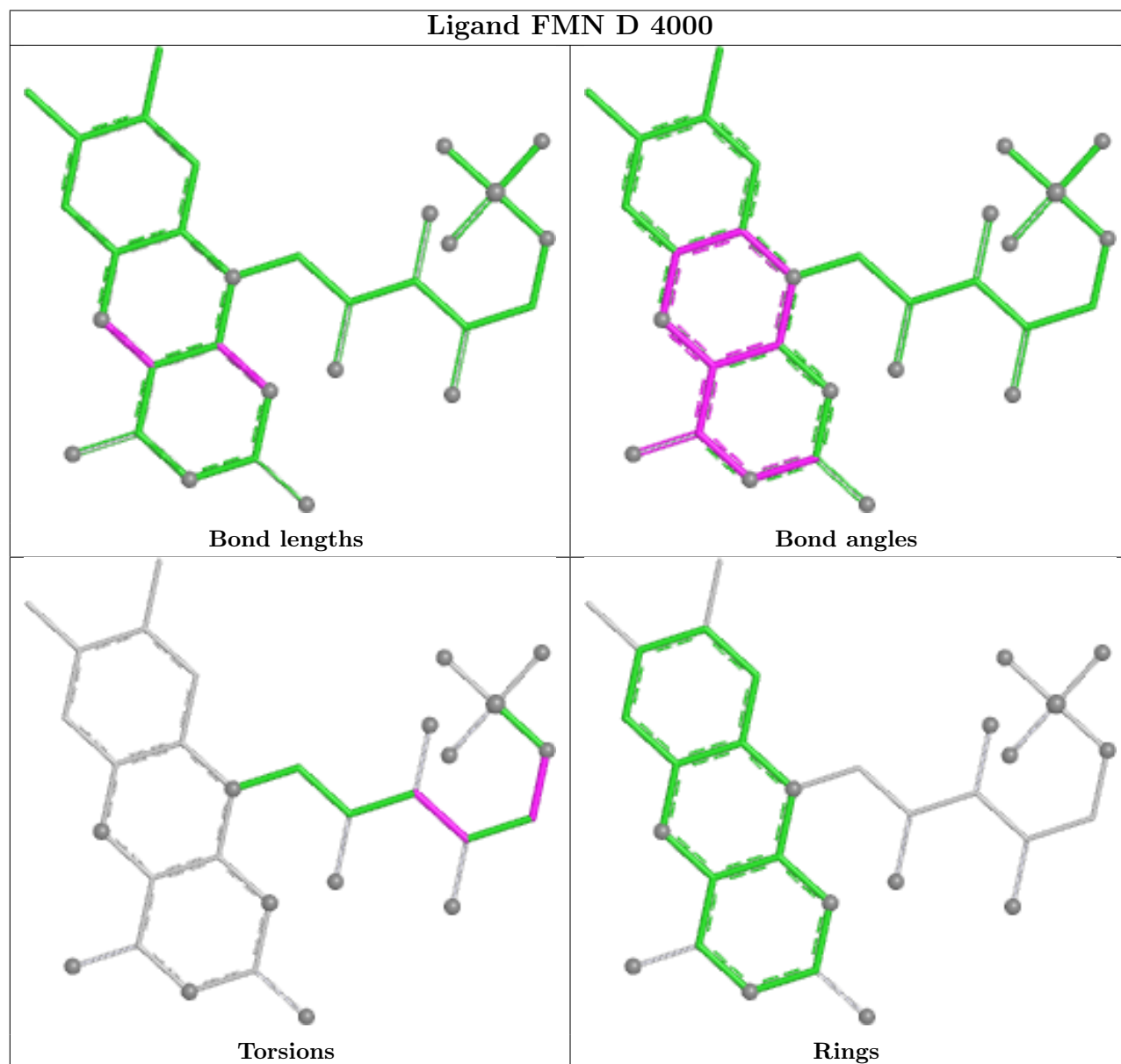
There are no ring outliers.

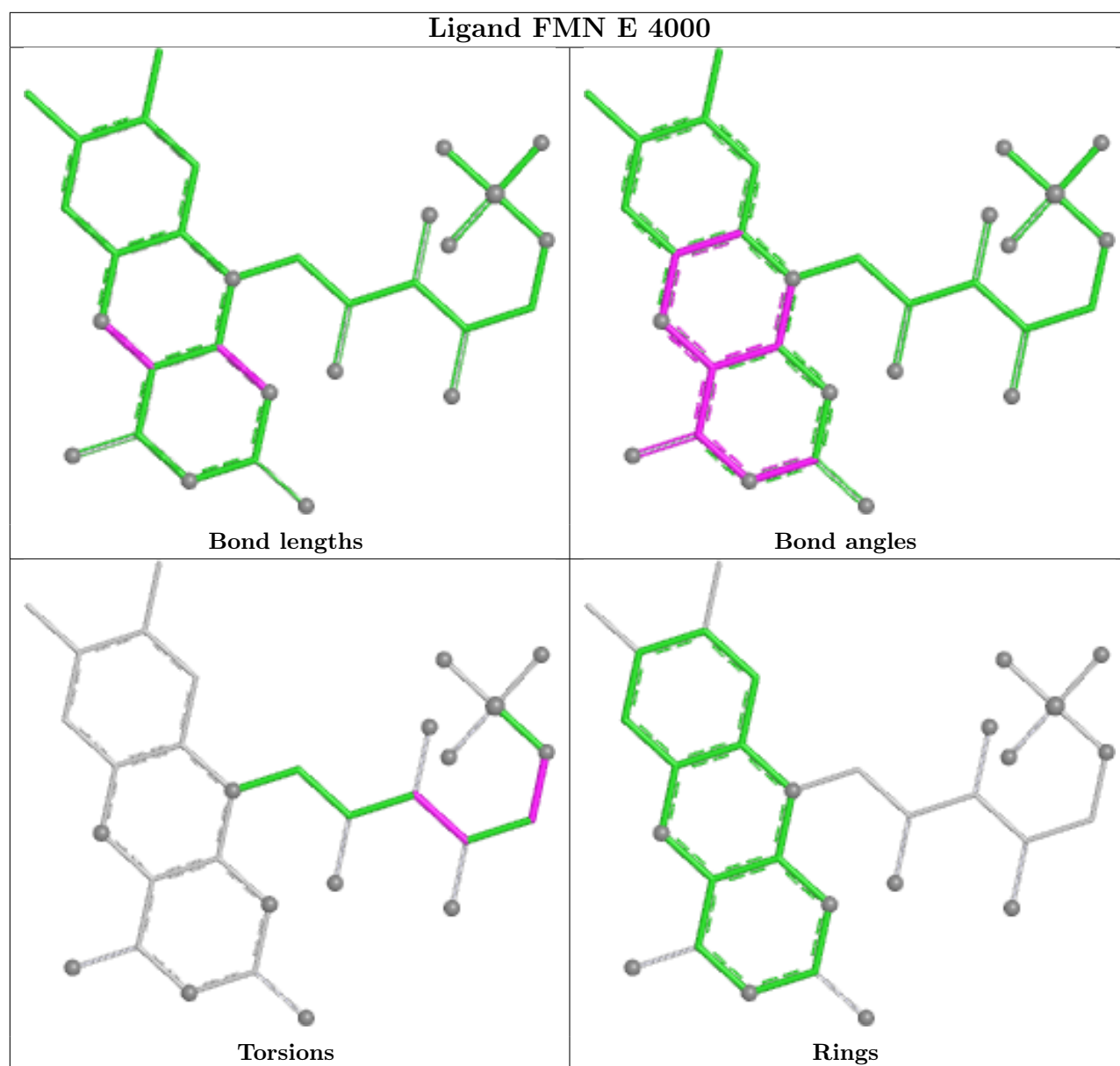
3 monomers are involved in 13 short contacts:

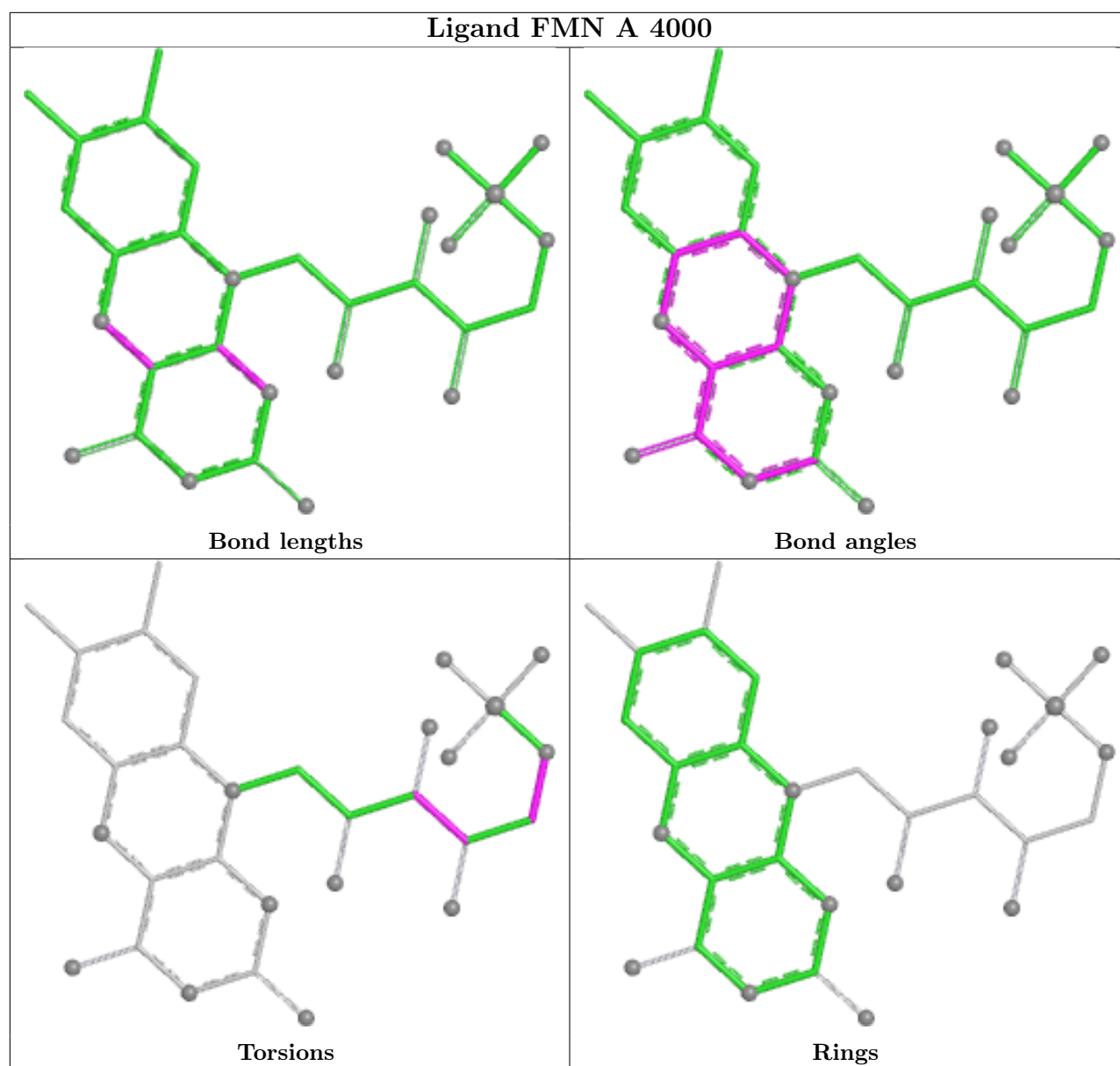
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	4000	FMN	4	0
2	C	4000	FMN	4	0
2	B	4000	FMN	5	0

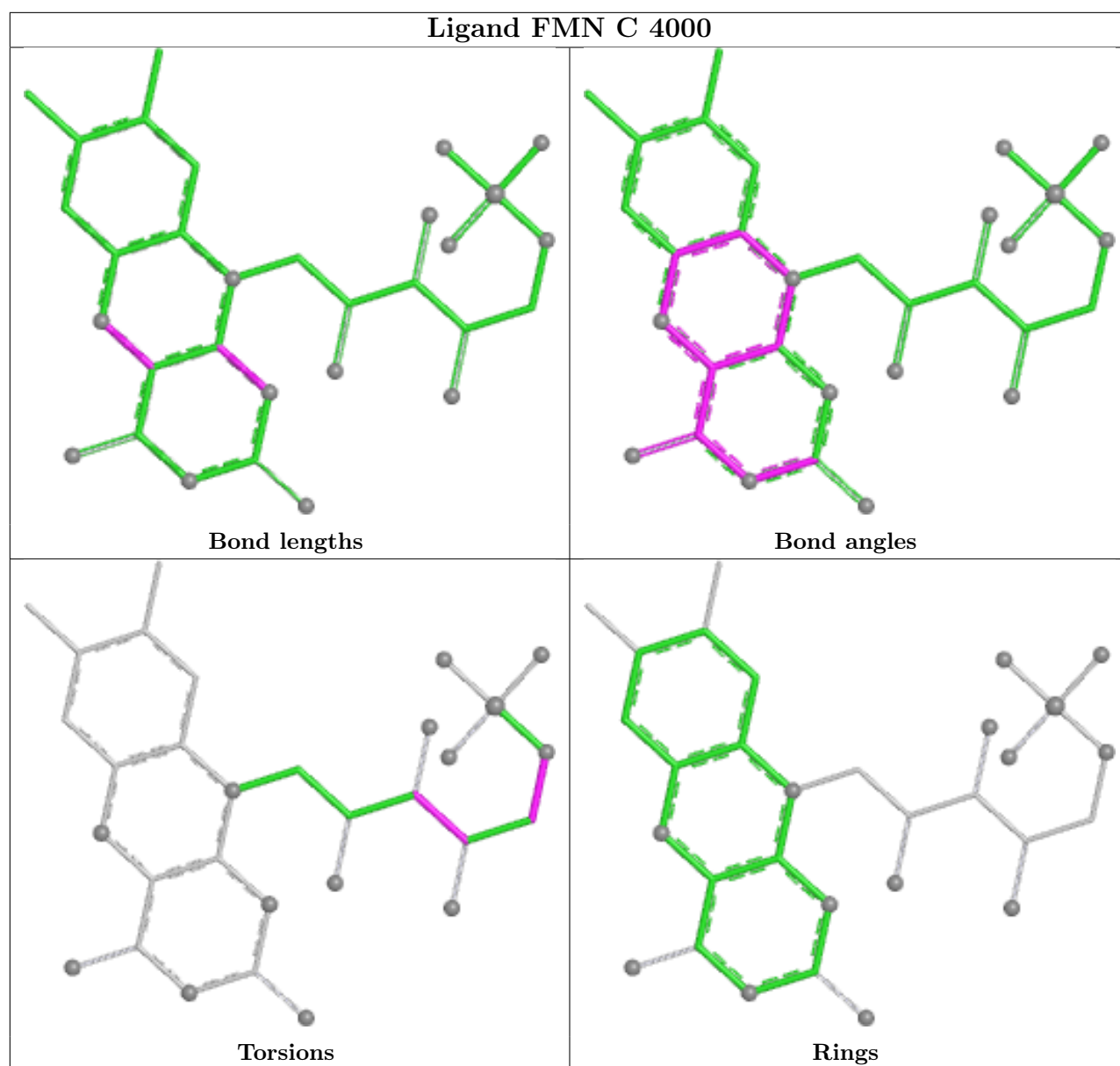
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

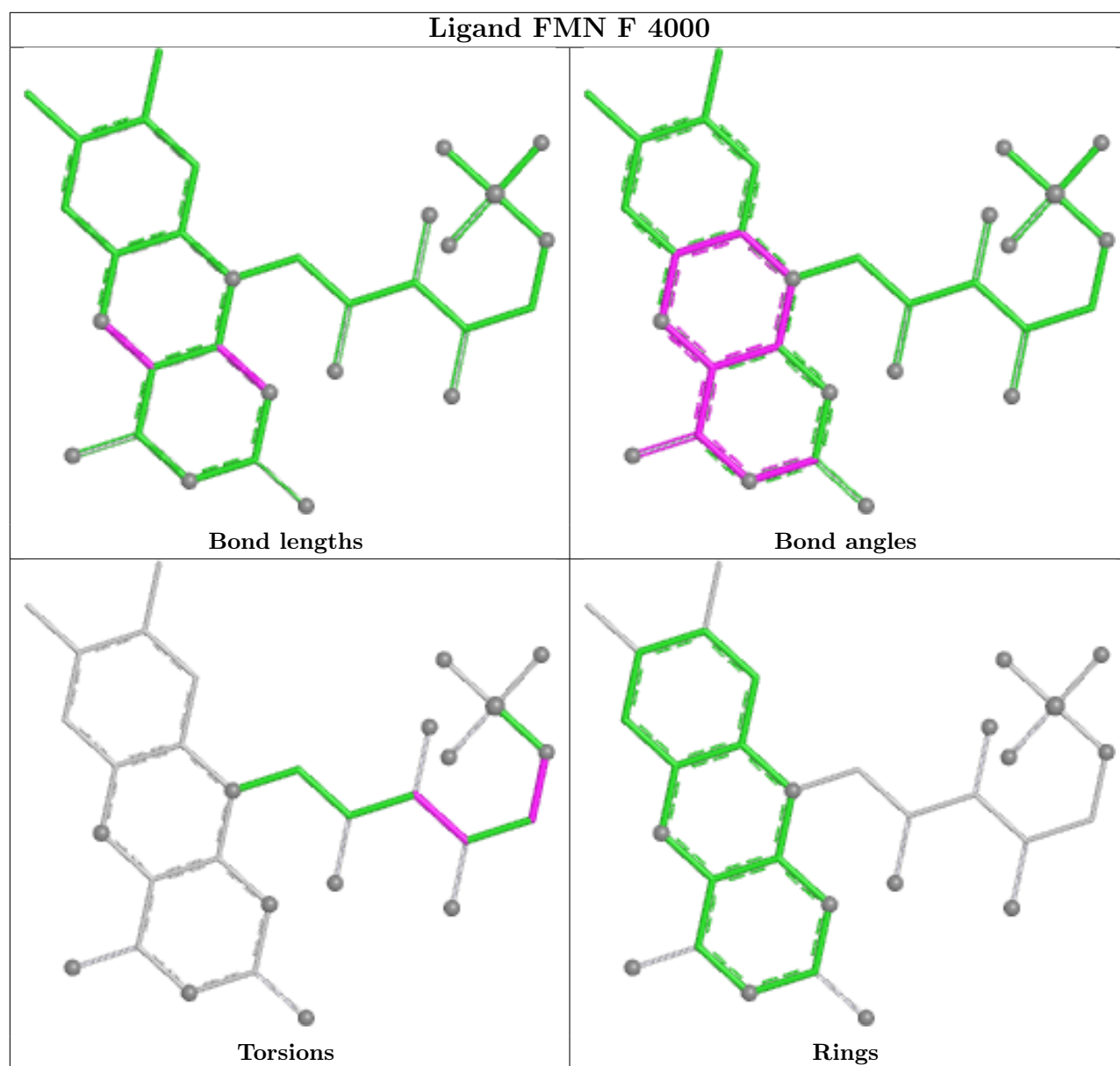
average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

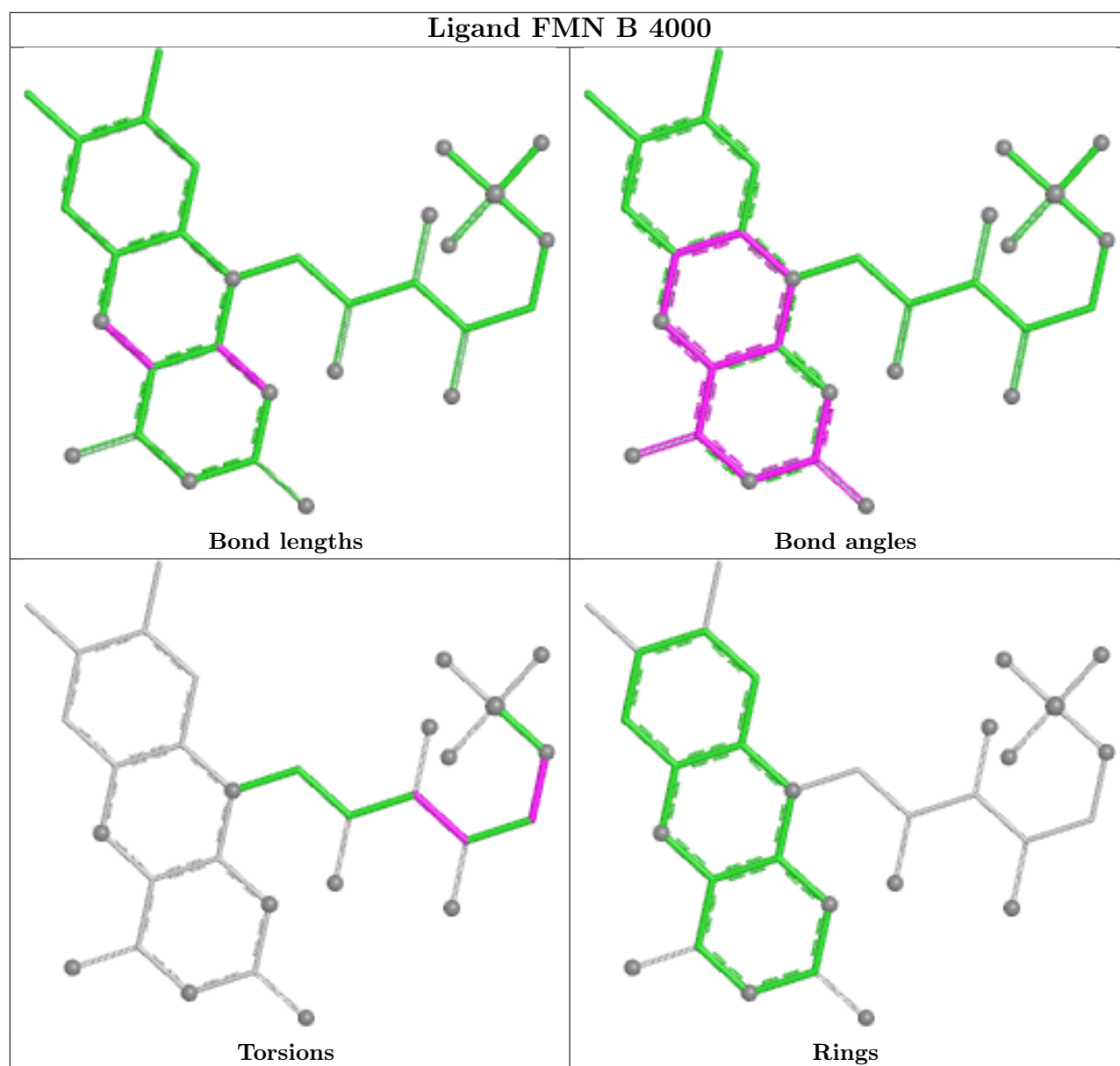












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

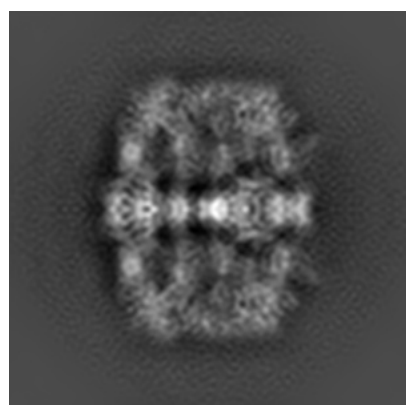
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2238. These allow visual inspection of the internal detail of the map and identification of artifacts.

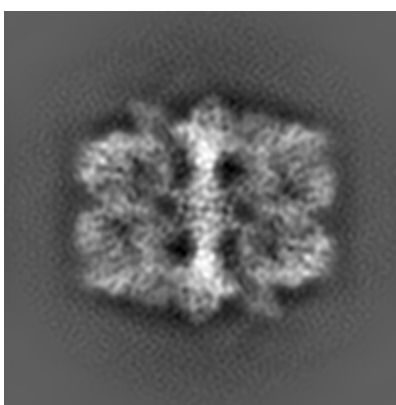
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

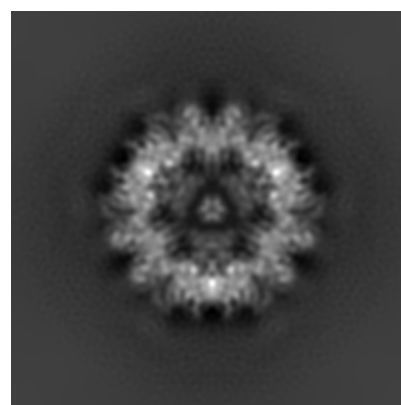
6.1.1 Primary map



X



Y

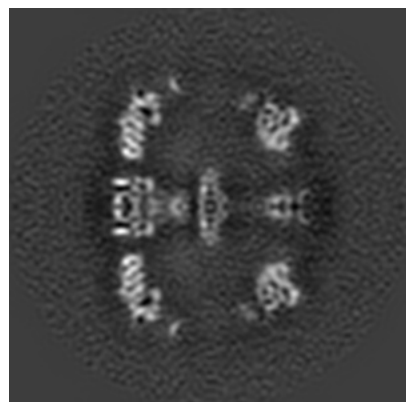


Z

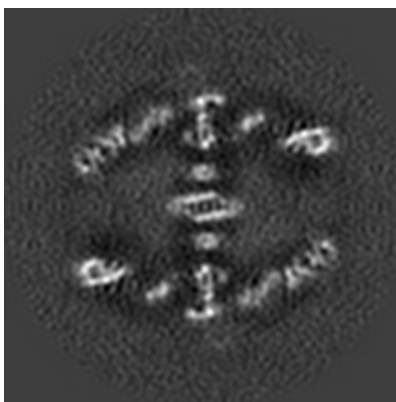
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

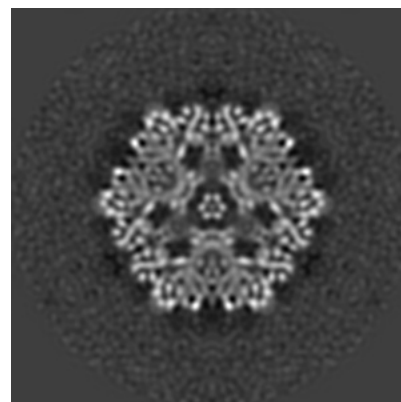
6.2.1 Primary map



X Index: 80



Y Index: 80

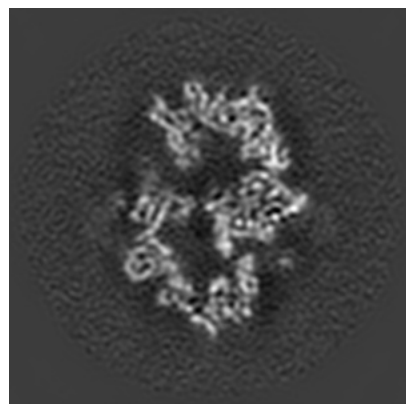


Z Index: 80

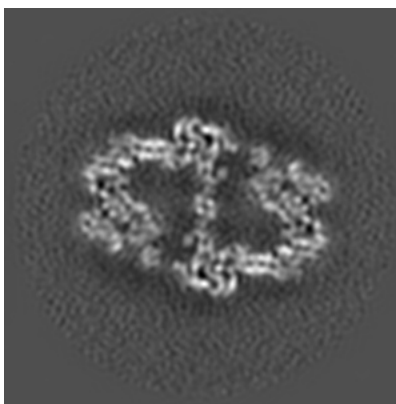
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

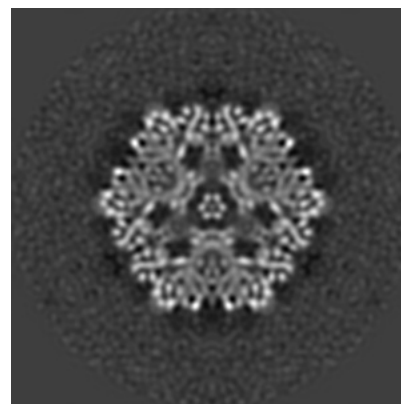
6.3.1 Primary map



X Index: 55



Y Index: 105

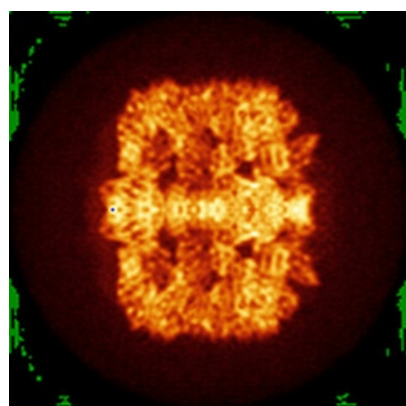


Z Index: 80

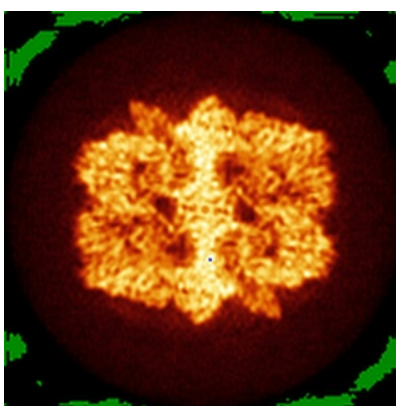
The images above show the largest variance slices of the map in three orthogonal directions.

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

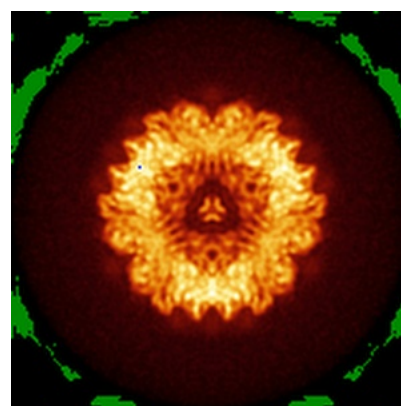
6.4.1 Primary map



X



Y

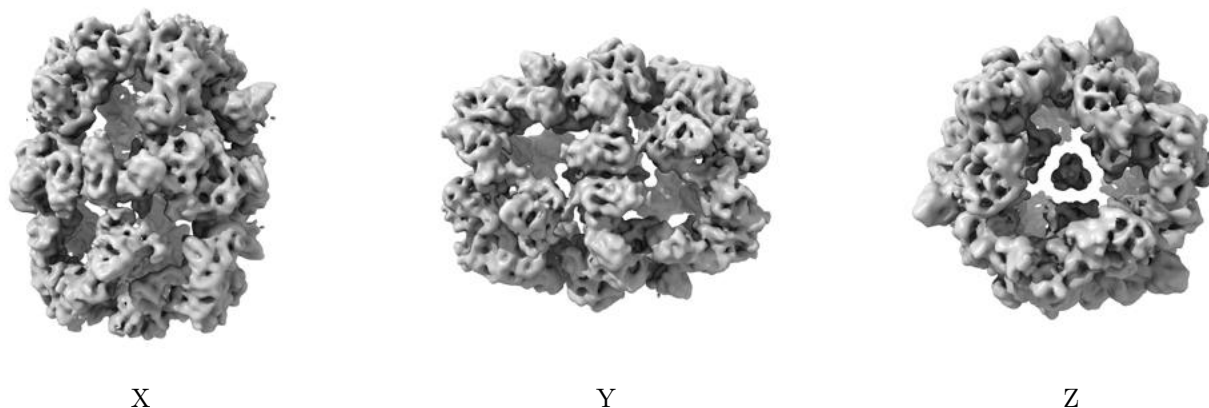


Z

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 2.7. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

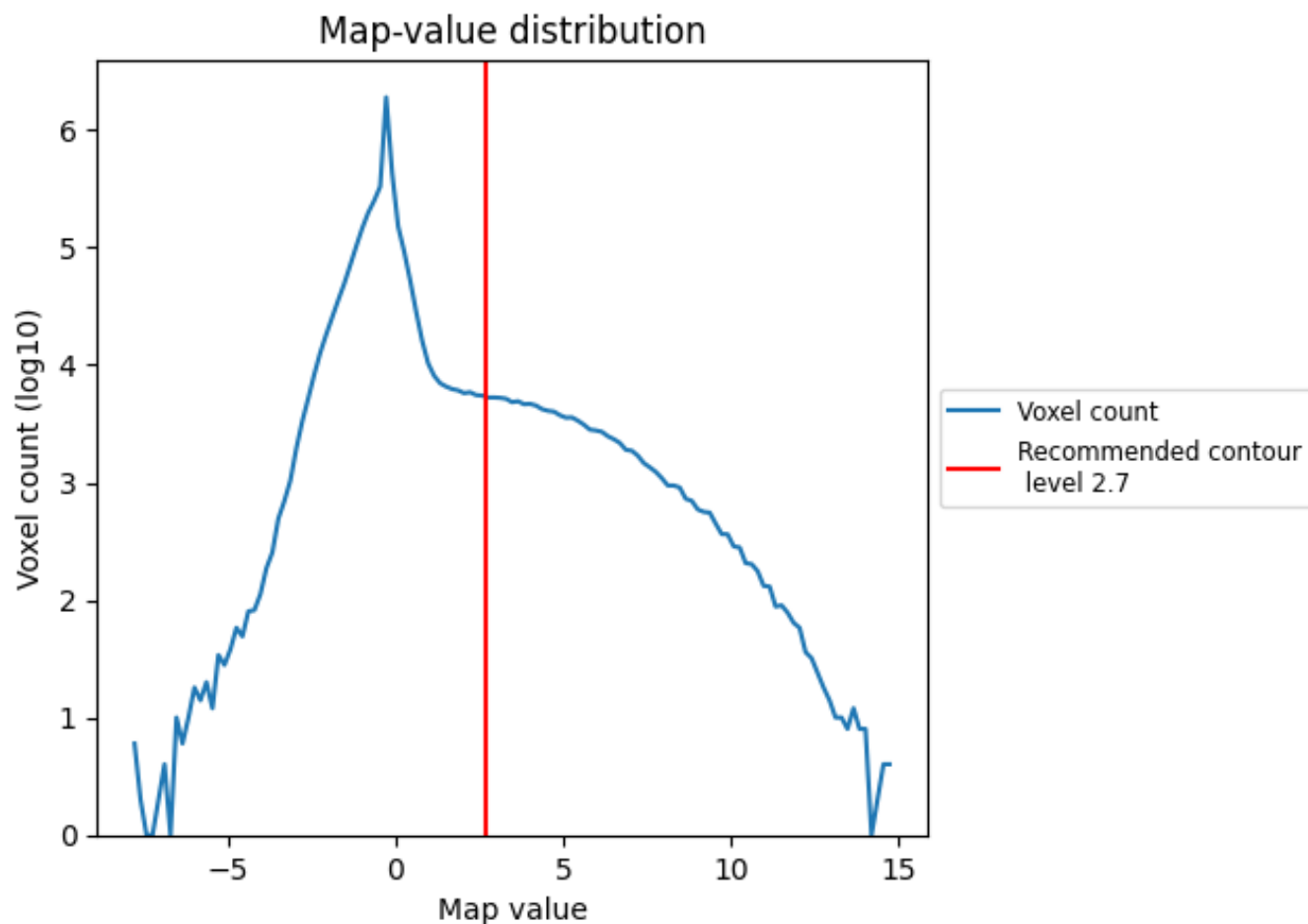
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

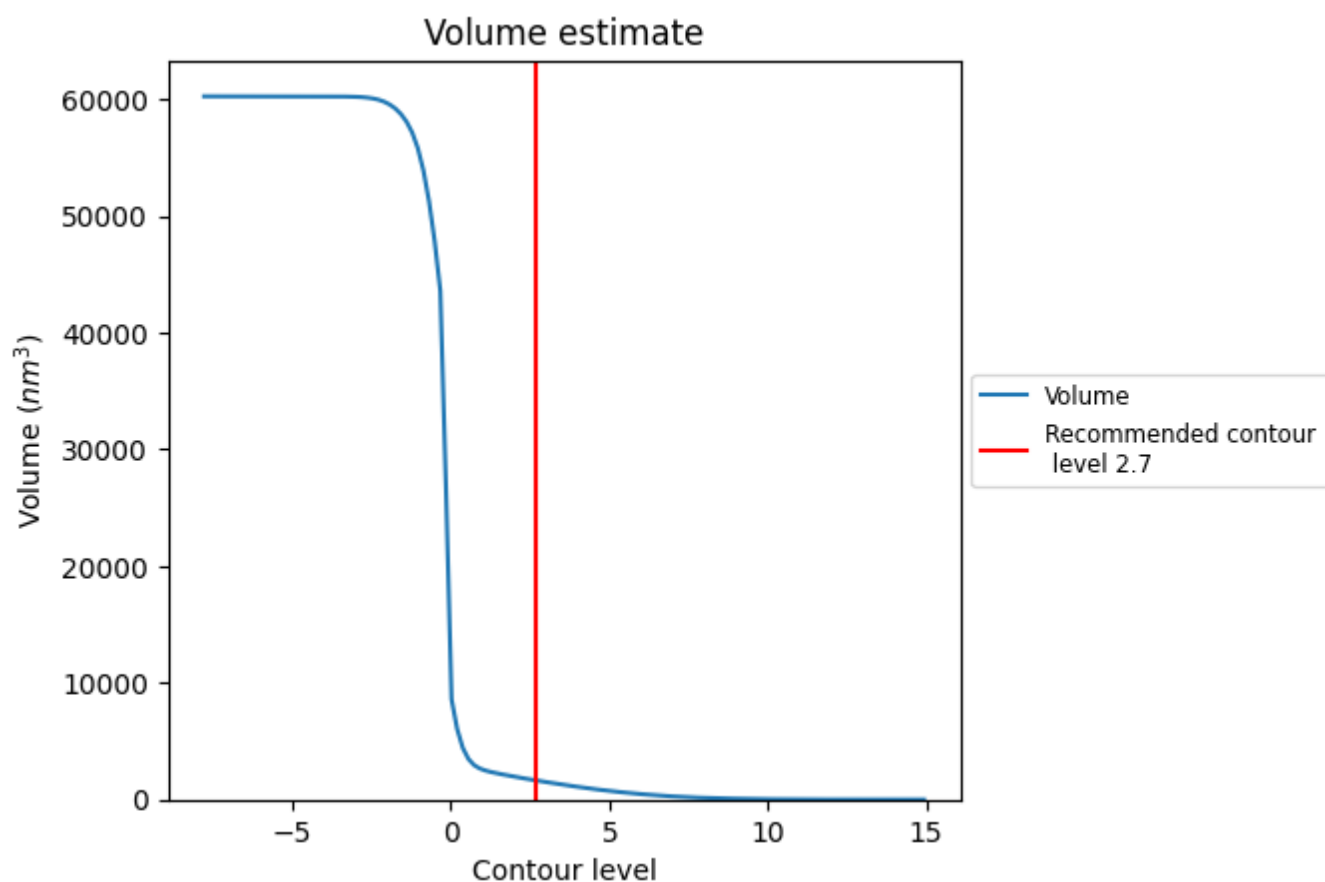
This section contains the results of statistical analysis of the map.

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.

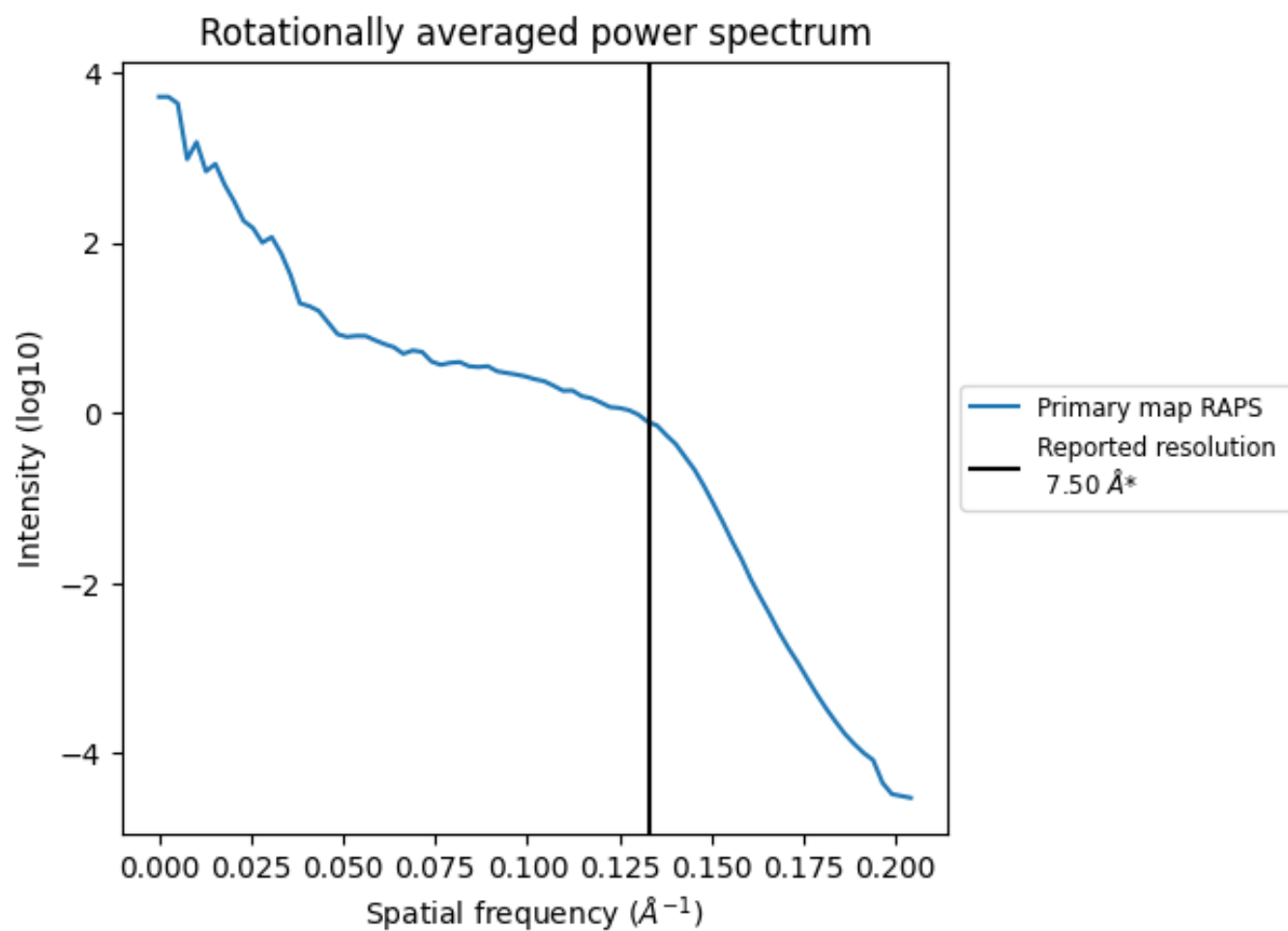
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1634 nm³; this corresponds to an approximate mass of 1476 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 0.133 Å⁻¹

8 Fourier-Shell correlation ⓘ

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

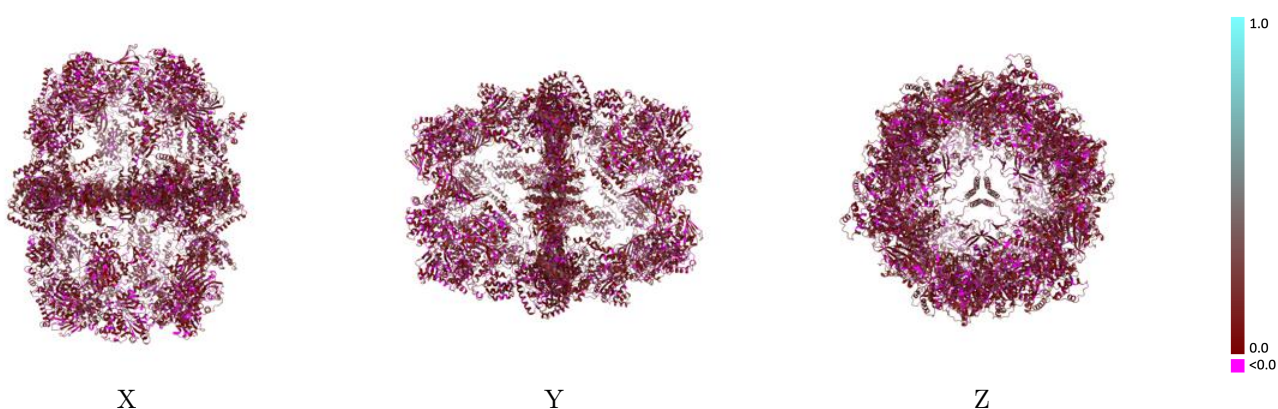
9 Map-model fit ⓘ

This section contains information regarding the fit between EMDB map EMD-2238 and PDB model 4V8L. Per-residue inclusion information can be found in section 3 on page 32.

9.1 Map-model overlay ⓘ

This section was not generated.

9.2 Q-score mapped to coordinate model ⓘ

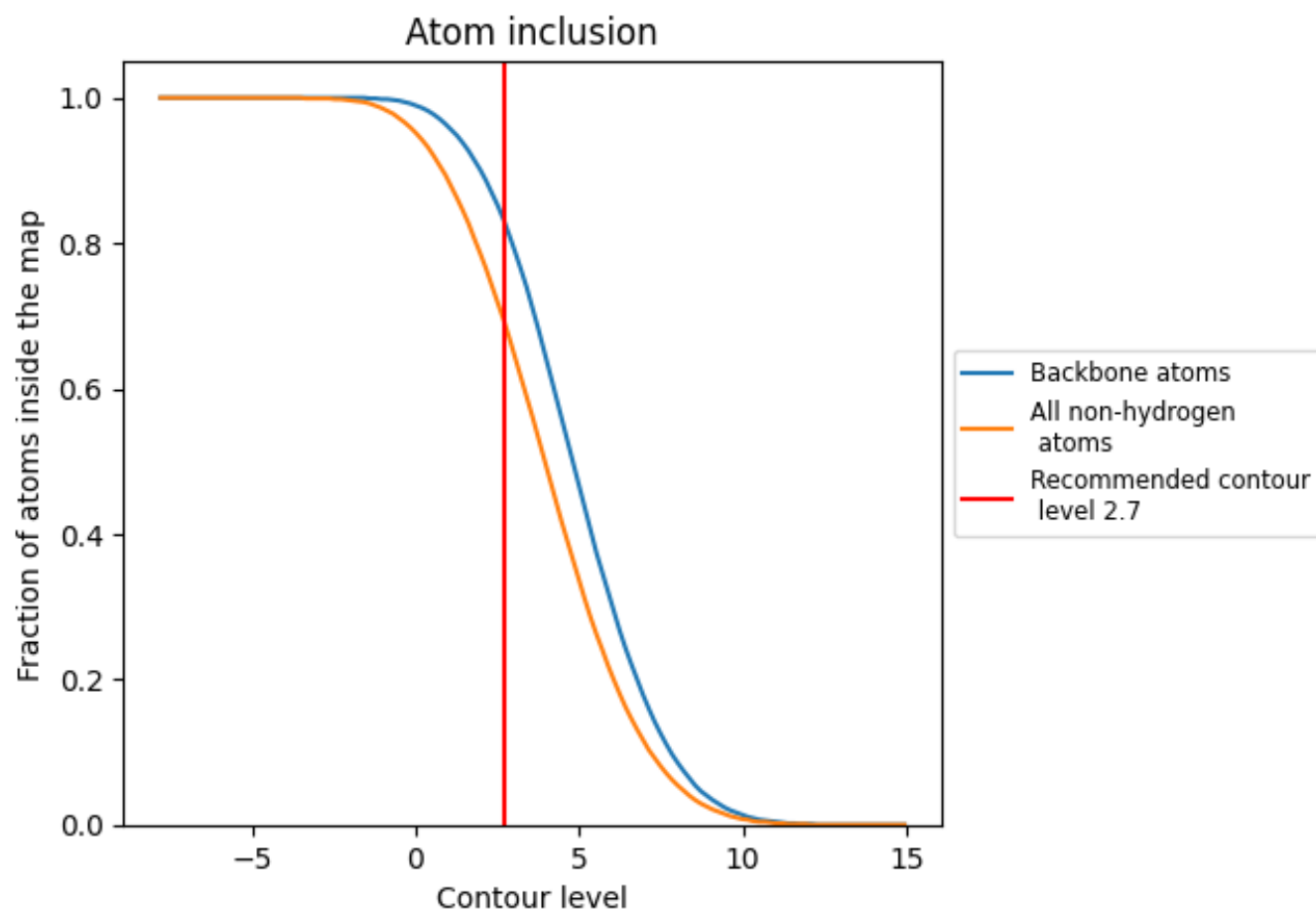


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 69% 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 (2.7) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6930	0.1100
A	0.6750	0.1000
B	0.6950	0.1130
C	0.6890	0.1090
D	0.6980	0.1120
E	0.6910	0.1080
F	0.7120	0.1200

1.0

0.0

<0.0