WORLDWIDE wwPDB PROTEIN DATA BANK

wwPDB EM Validation Summary Report (i)

Nov 20, 2022 – 01:48 am GMT

|		
PDB ID	:	4V8L
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

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1   Overall quality at a glance ⓘ

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

The reported resolution of this entry is 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	Percentile Ranks	Value
Clashscore		25
Ramachandran outliers		0.3%
Sidechain outliers		4.3%

Worse　　　　　　　*Better*

▮ Percentile relative to all structures
▯ Percentile relative to all EM structures
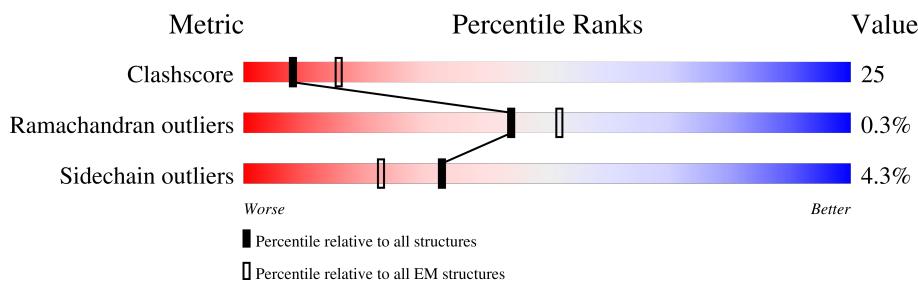
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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 <=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	20% / 56% / 33% / • / 9%
1	B	3089	17% / 56% / 33% / • / 9%
1	C	3089	18% / 56% / 33% / • / 9%
1	D	3089	17% / 88% / • / 9%
1	E	3089	17% / 88% / • / 9%
1	F	3089	15% / 88% / • / 9%
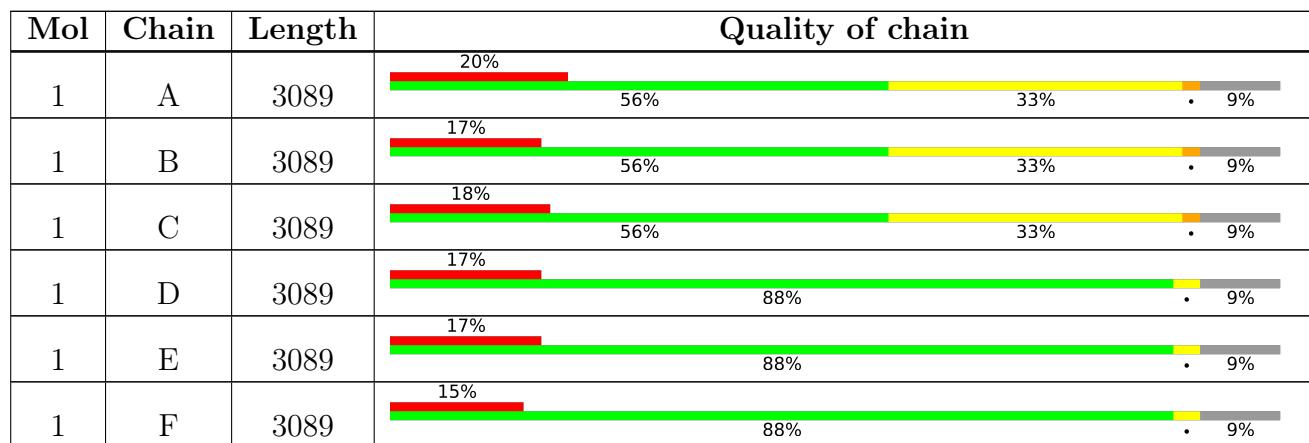
2 Entry composition ⓘ

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	C	N	O	S	0	0
			21020	13294	3662	3998	66		
1	E	2822	Total	C	N	O	S	0	0
			21020	13294	3662	3998	66		
1	F	2822	Total	C	N	O	S	0	0
			21020	13294	3662	3998	66		
1	A	2822	Total	C	N	O	S	0	0
			21020	13294	3662	3998	66		
1	B	2822	Total	C	N	O	S	0	0
			21020	13294	3662	3998	66		
1	C	2822	Total	C	N	O	S	0	0
			21020	13294	3662	3998	66		

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 (three-letter code: FMN) (formula: $C_{17}H_{21}N_4O_9P$).
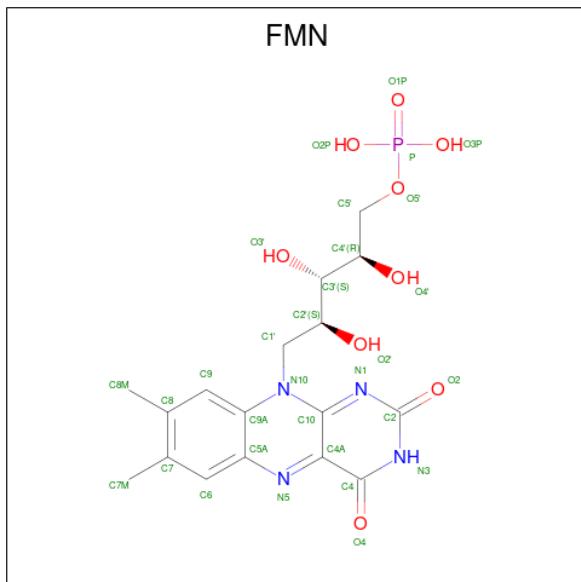
Mol	Chain	Residues	Atoms					AltConf
2	D	1	Total	C	N	O	P	0
			31	17	4	9	1	
2	E	1	Total	C	N	O	P	0
			31	17	4	9	1	

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

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
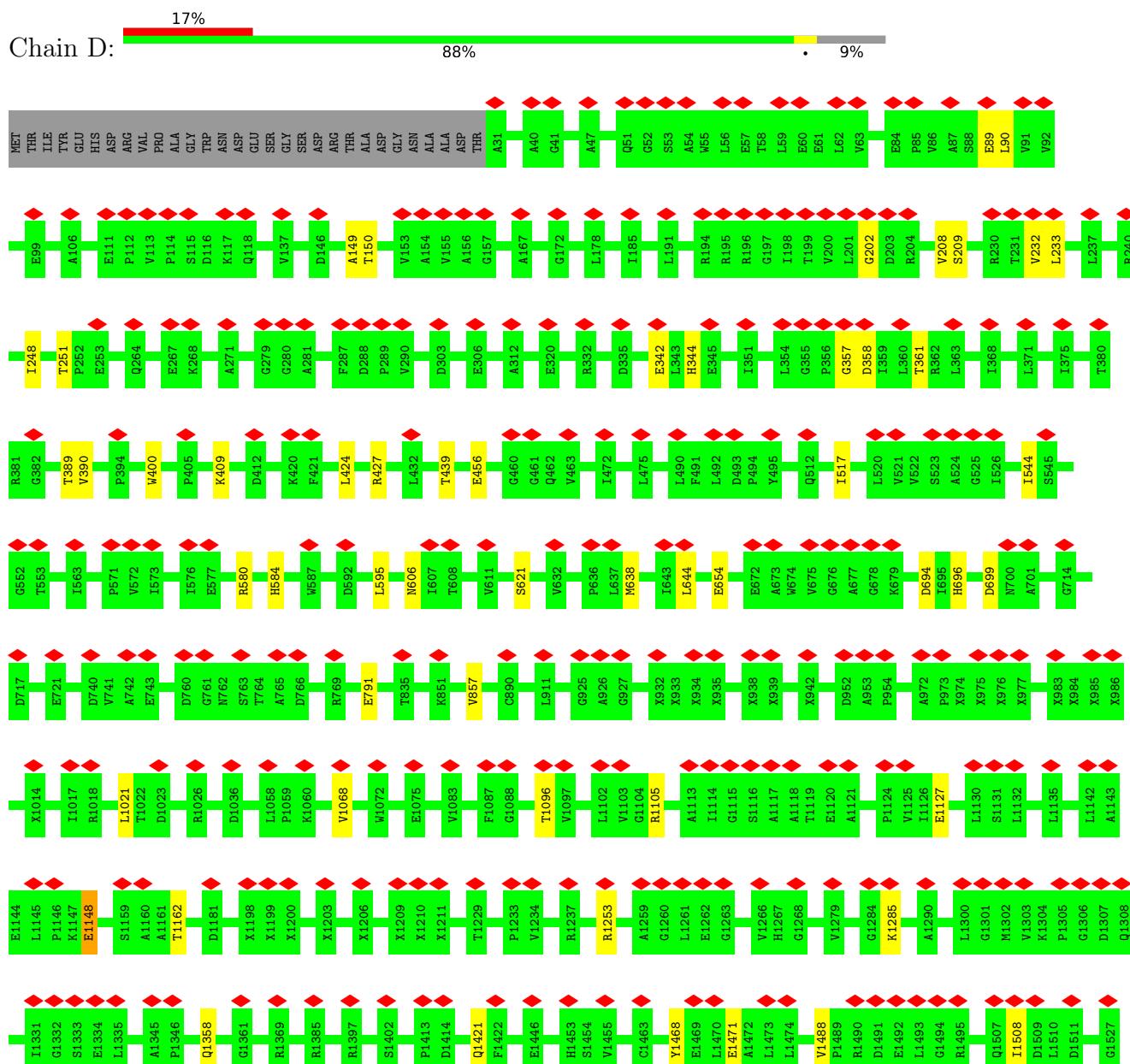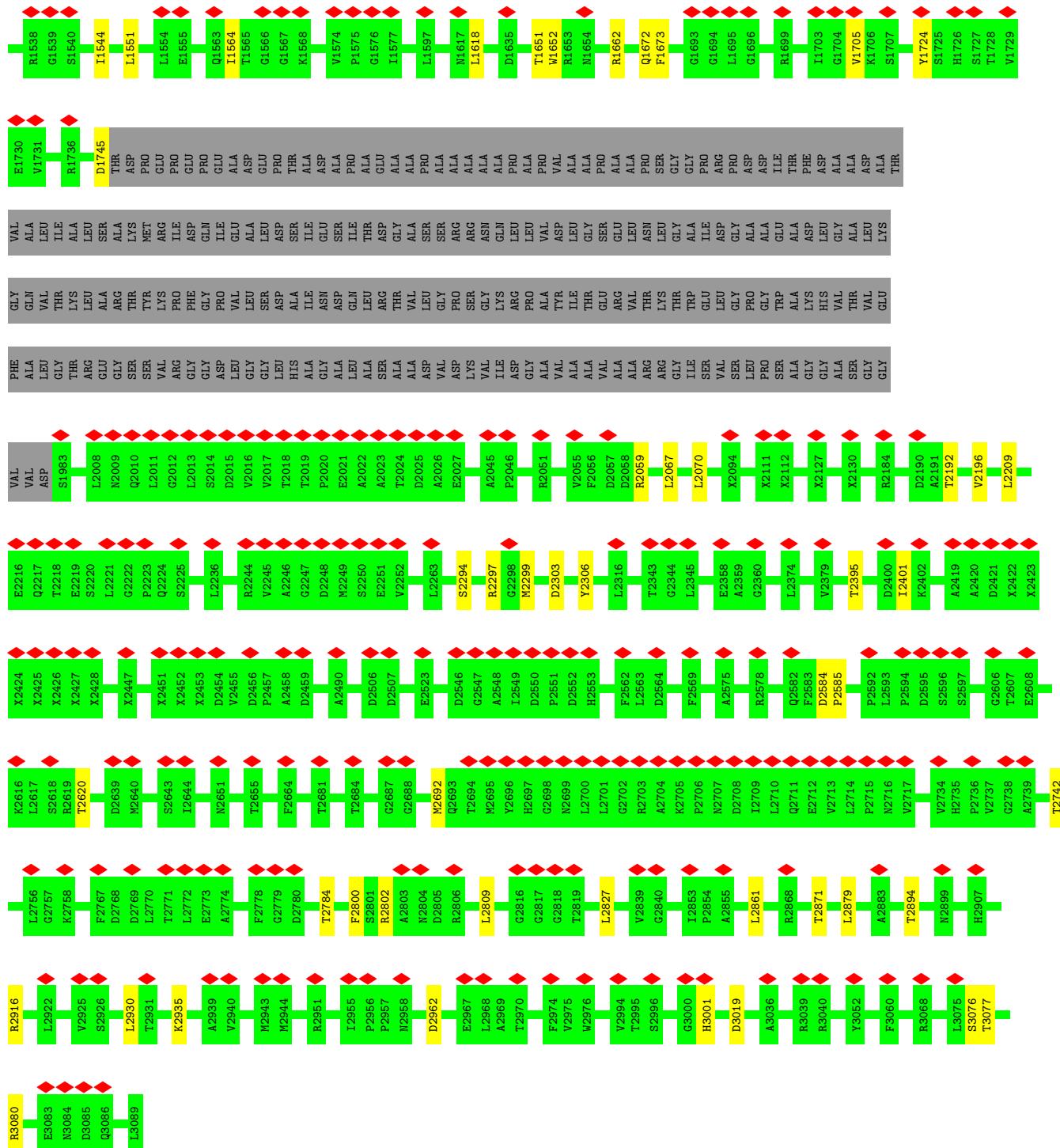
● Molecule 1: FATTY ACID SYNTHASE

Chain E:
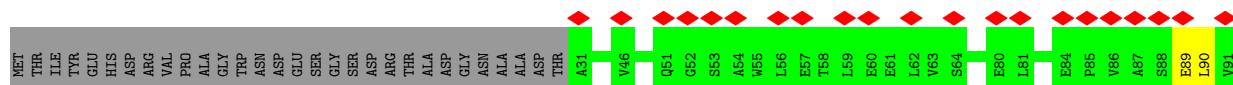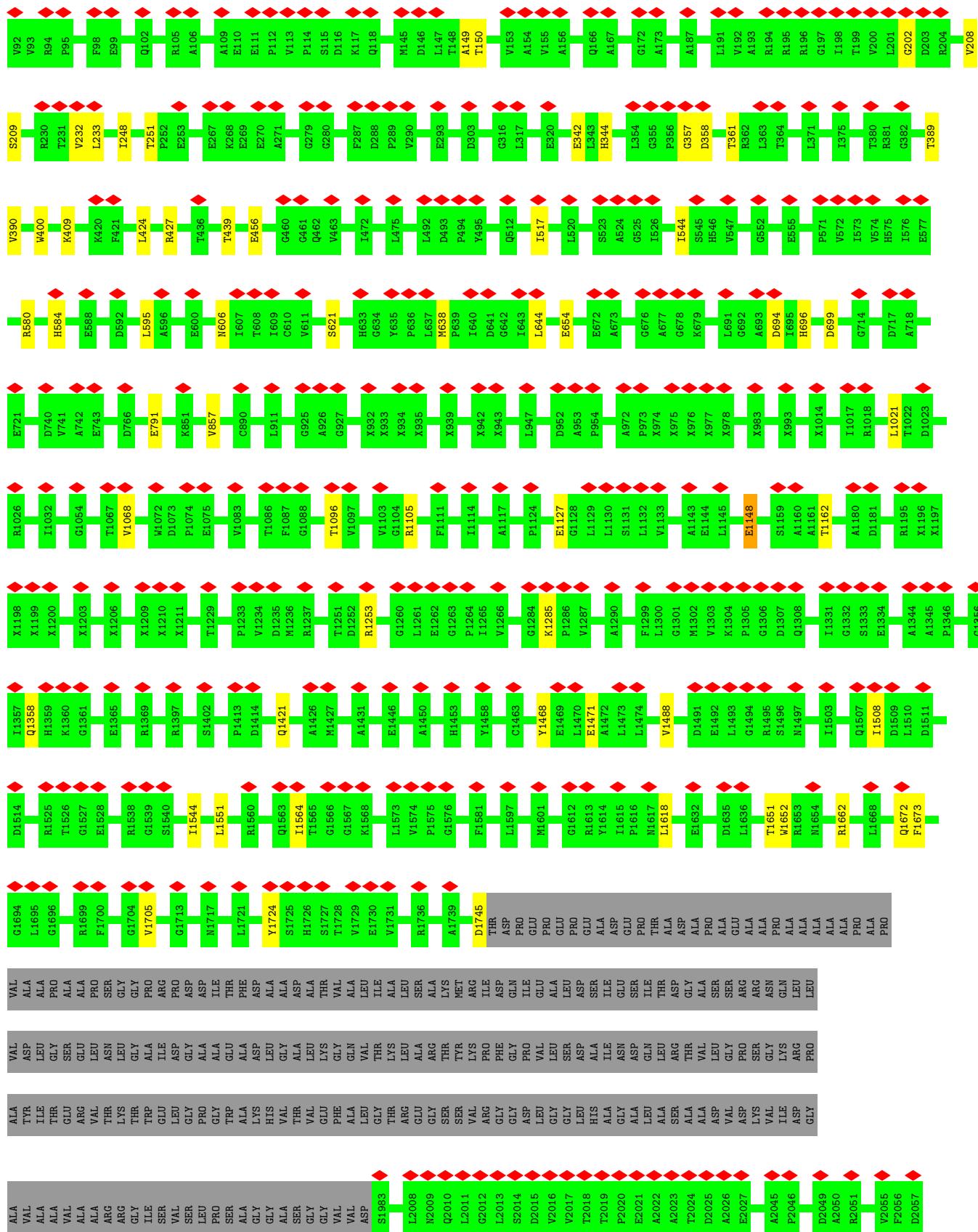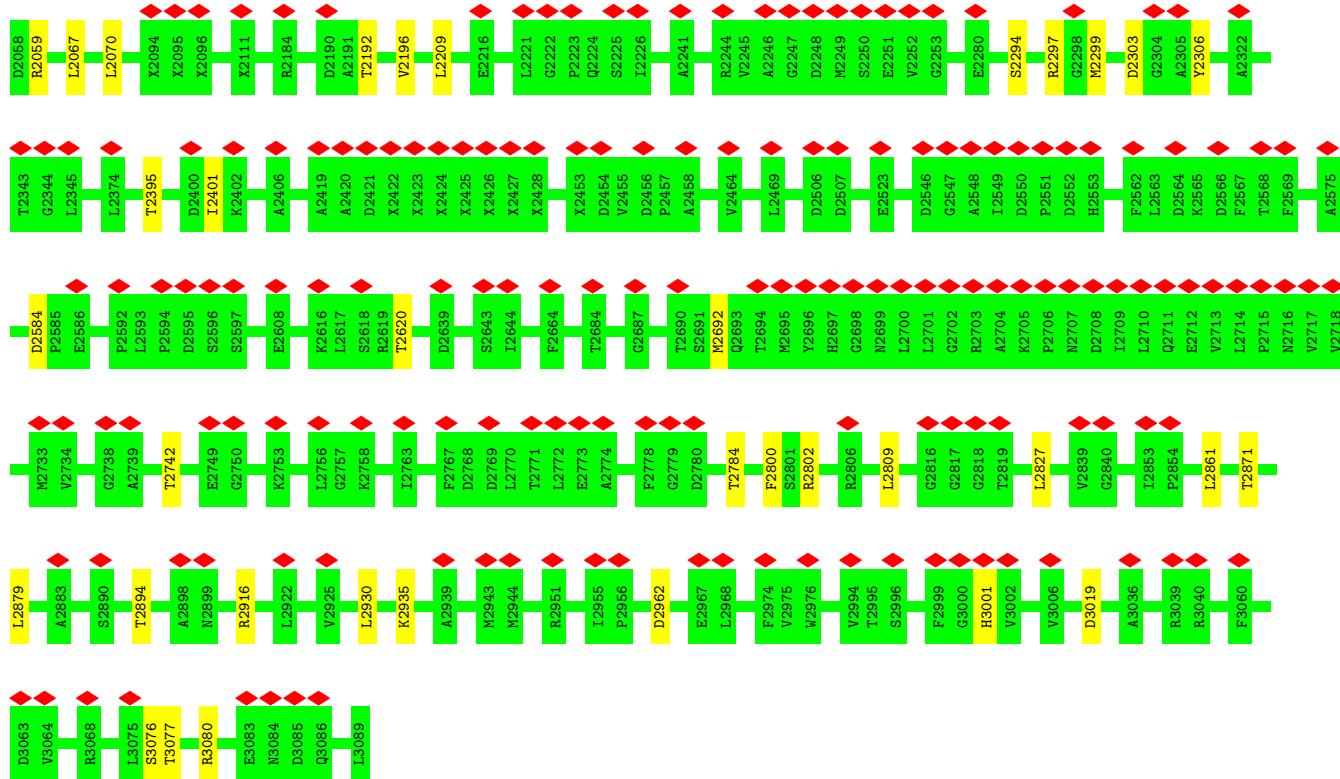
• Molecule 1: FATTY ACID SYNTHASE

Chain F:

15%

88%　　　　9%
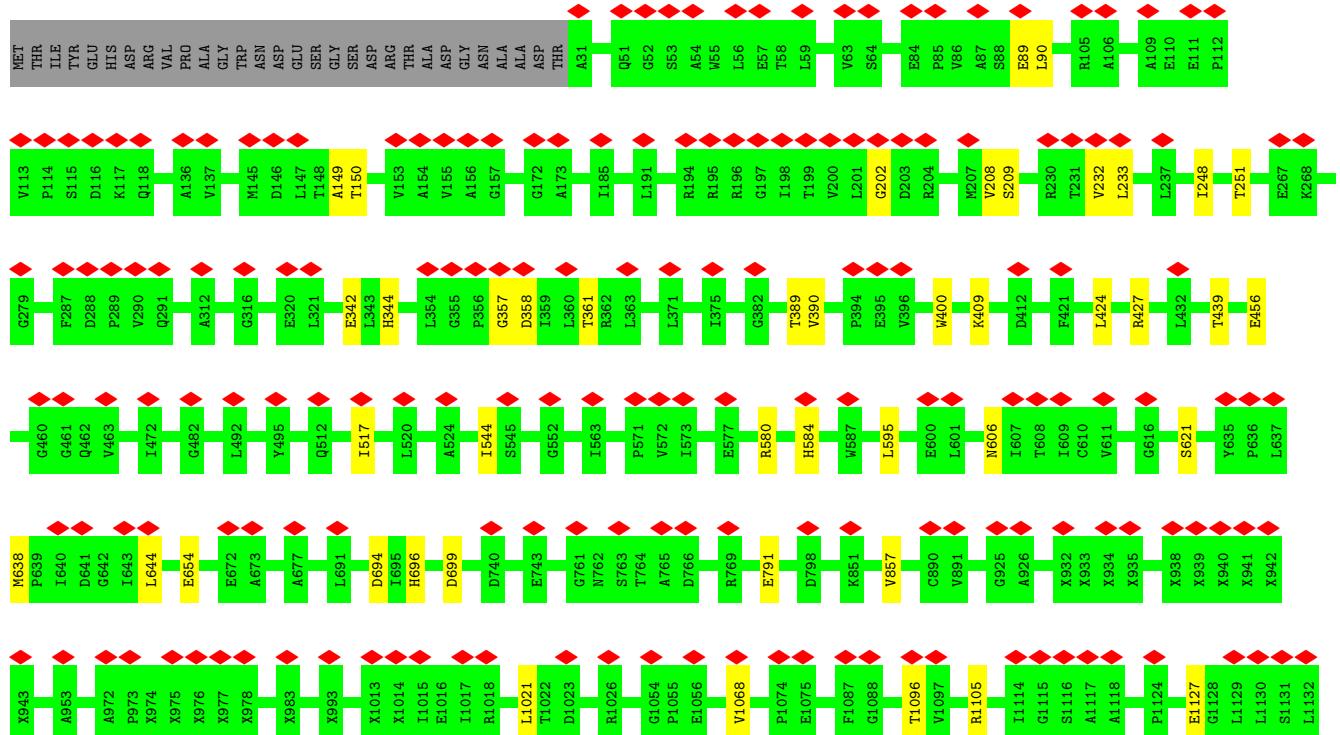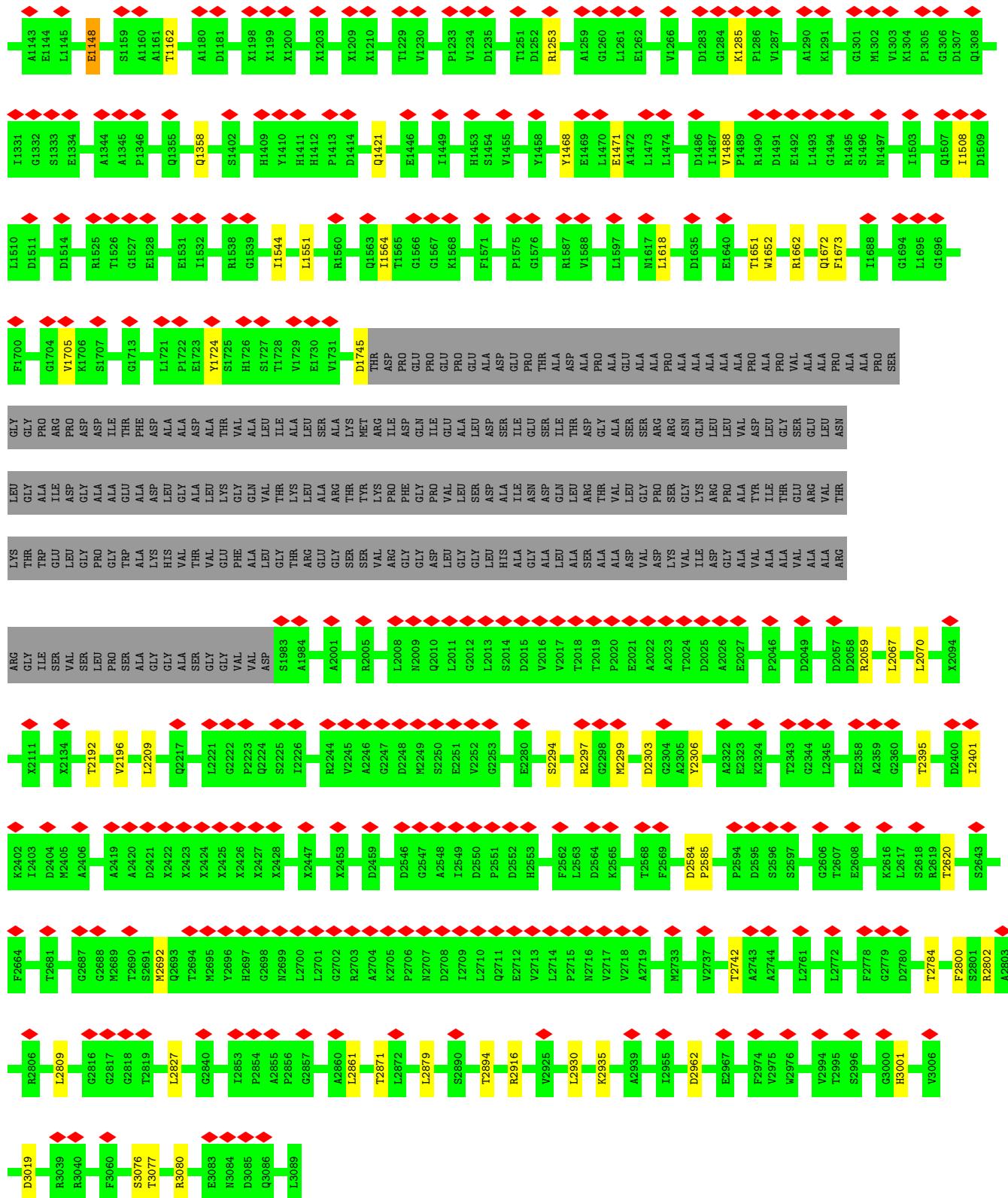
● Molecule 1: FATTY ACID SYNTHASE

Chain A:

20%

56%   33%   ·   9%

• Molecule 1: FATTY ACID SYNTHASE

Chain B:

17%

56% 33% 9%
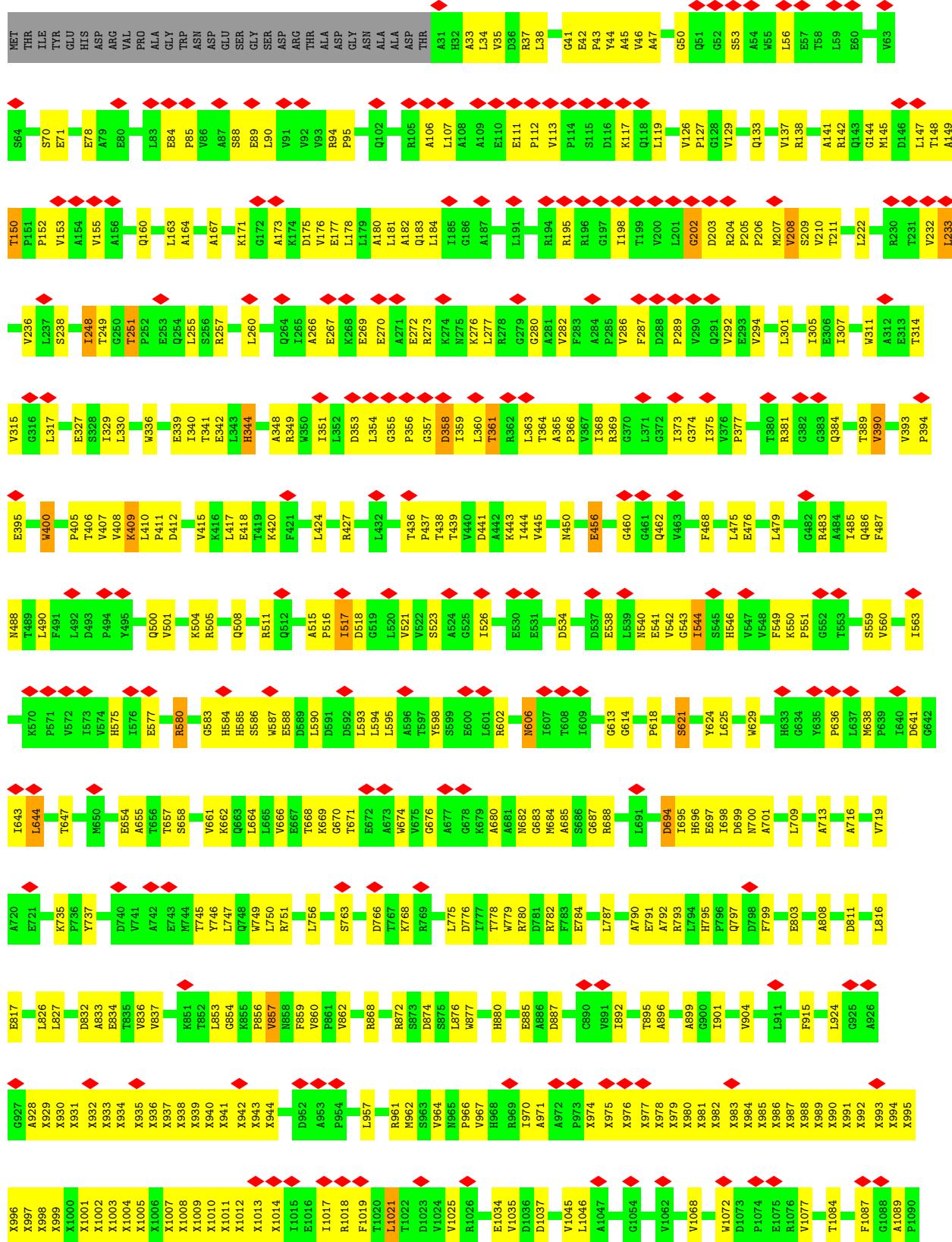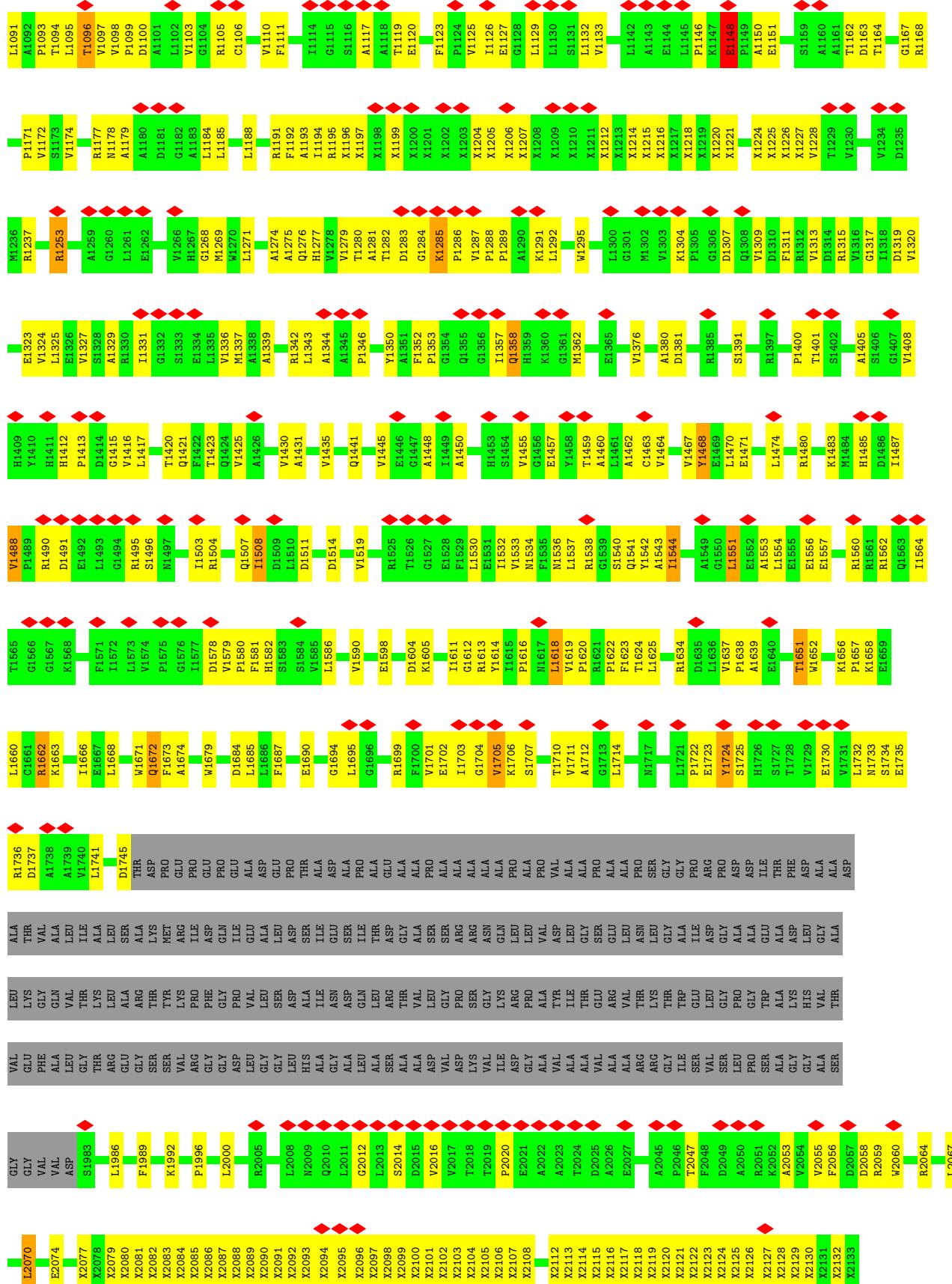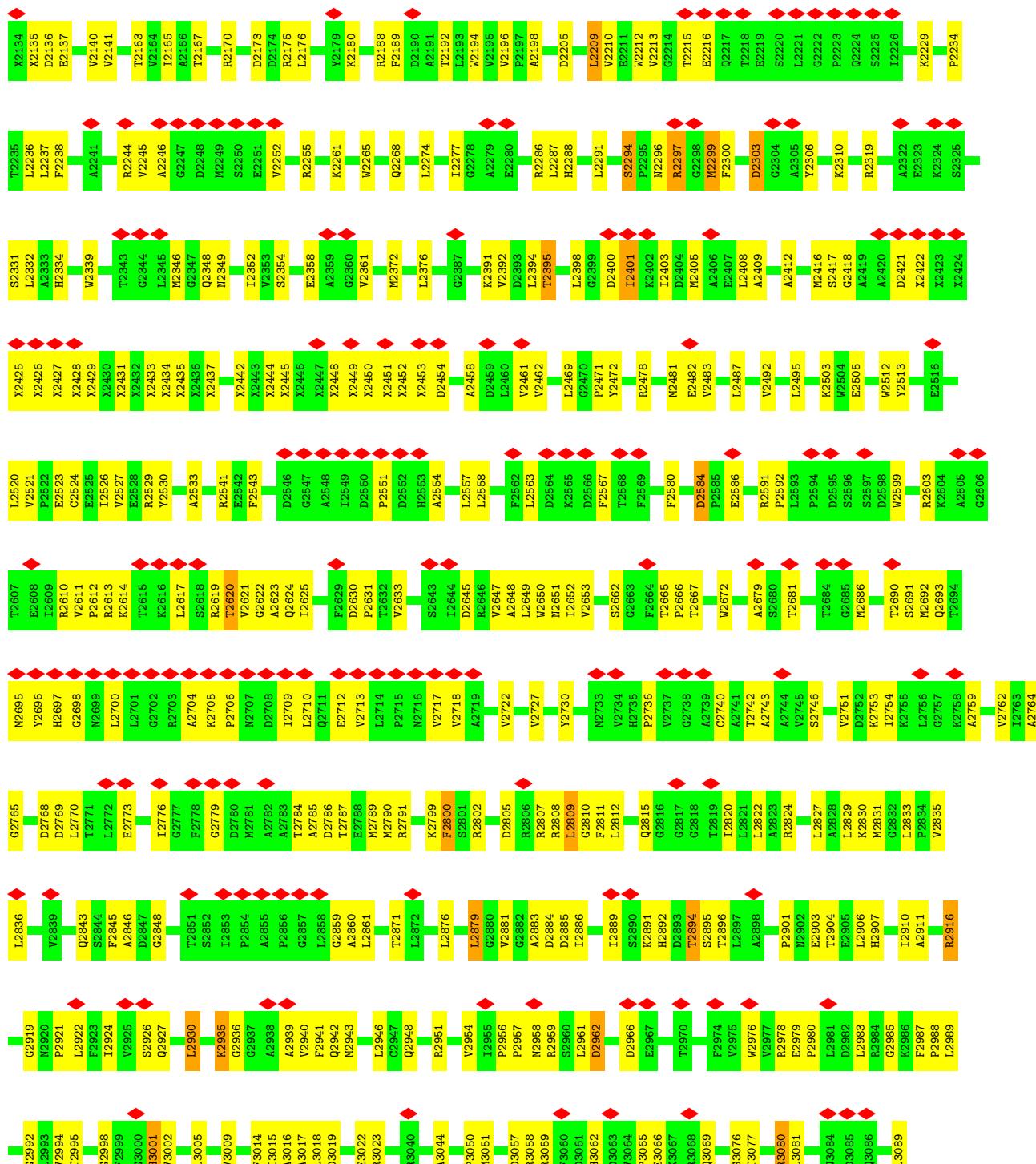
• Molecule 1: FATTY ACID SYNTHASE

Chain C:

18%

56% 33% 9%
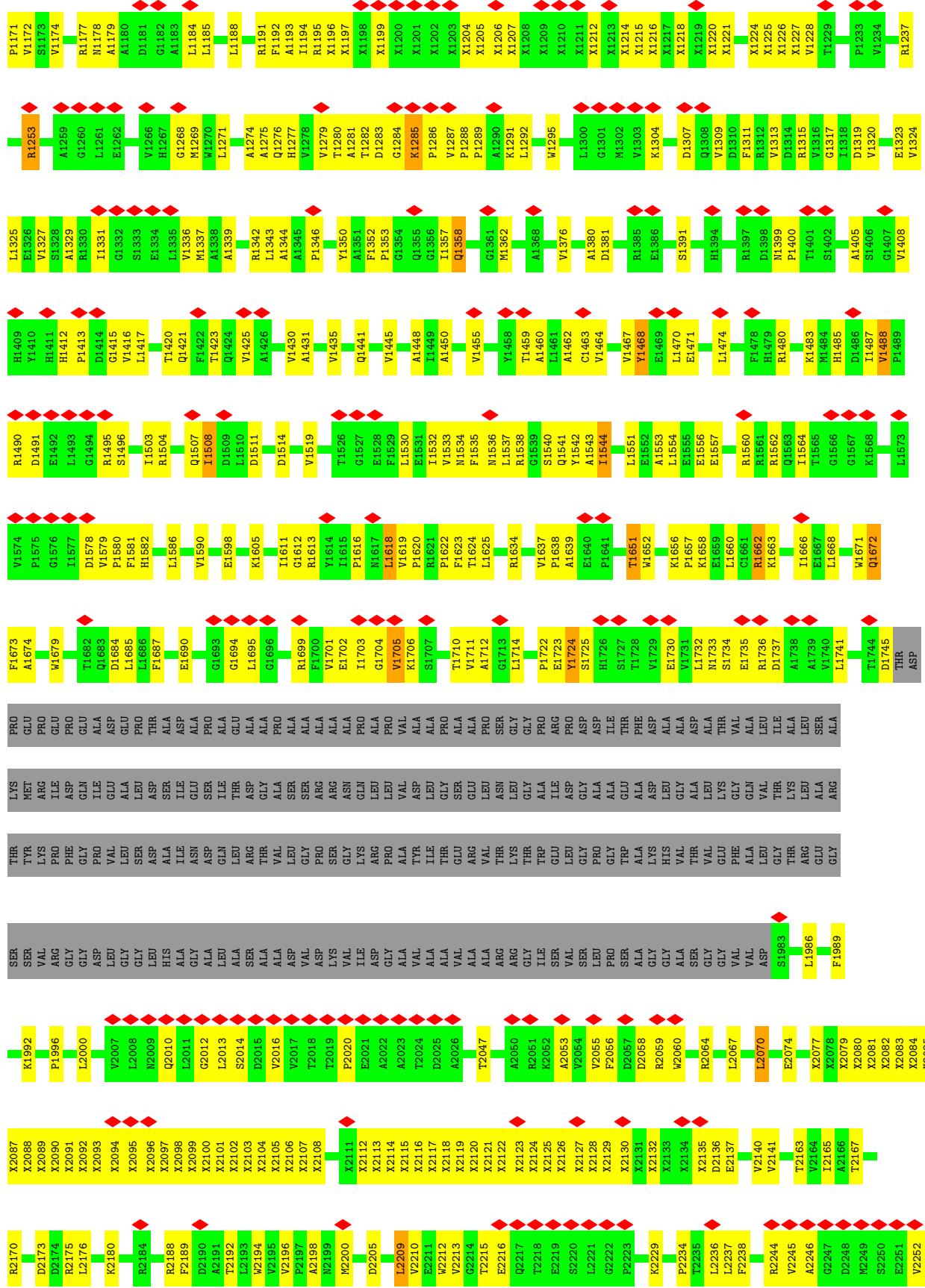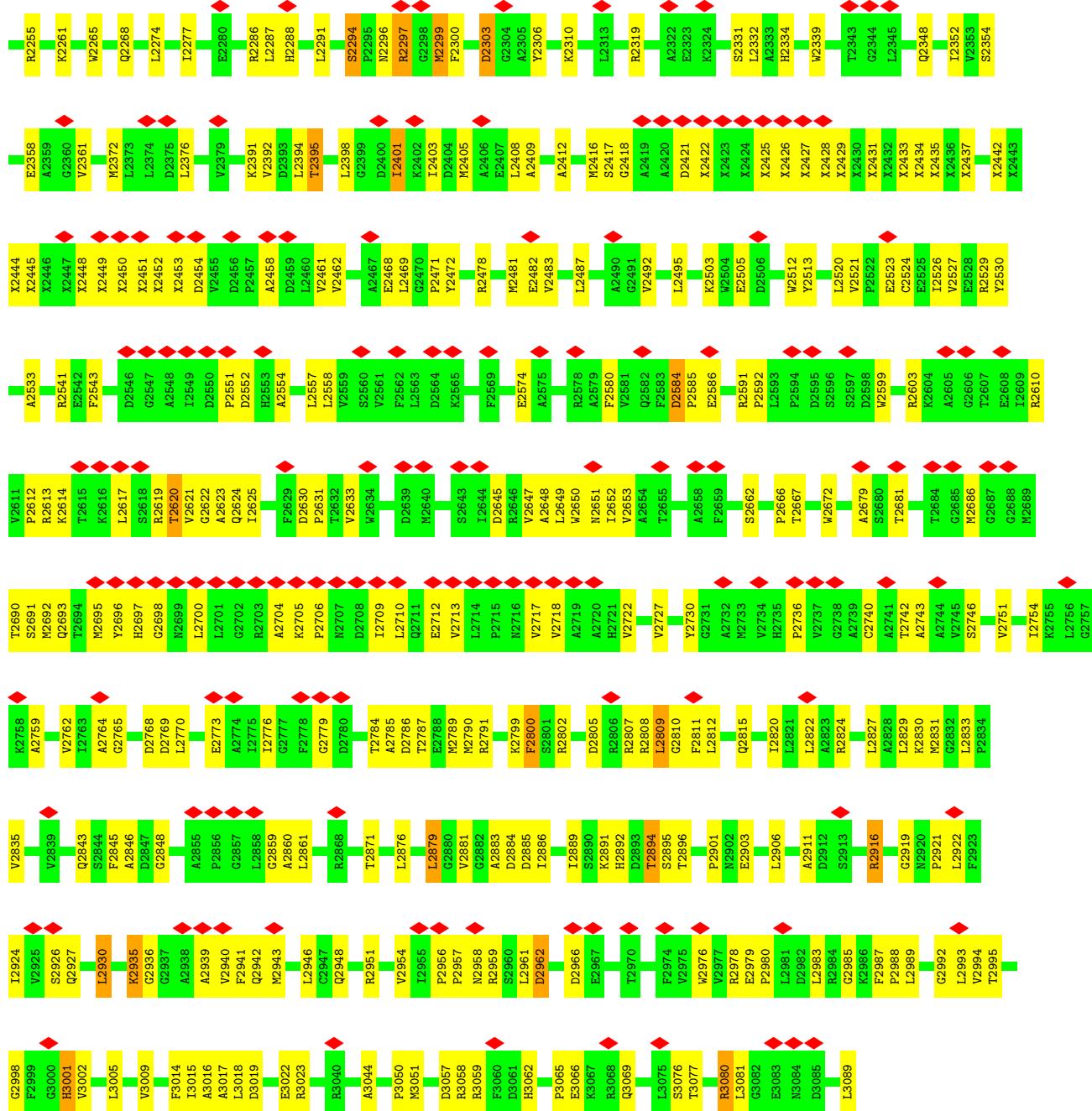
4 Experimental information ⓘ

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 $(e^-/\text{Å}^2)$	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 (Å)	392.0, 392.0, 392.0	wwPDB
Map dimensions	160, 160, 160	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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	0.24	0/20319	0.48	0/27667
1	B	0.24	0/20319	0.48	0/27667
1	C	0.24	0/20319	0.48	0/27667
1	D	0.24	0/20319	0.48	0/27667
1	E	0.24	0/20319	0.48	0/27667
1	F	0.24	0/20319	0.48	0/27667
All	All	0.24	0/121914	0.48	0/166002

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.

There are no bond angle outliers.

There are no chirality outliers.

5 of 30 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	1148	GLU	Peptide

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Mol	Chain	Res	Type	Group
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	1056	0
1	B	21020	0	20990	1067	0
1	C	21020	0	20990	1051	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	5	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	3117	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 3117 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 ⓘ

5.3.1 Protein backbone ⓘ

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%)	41	77
1	B	2637/3089 (85%)	2489 (94%)	140 (5%)	8 (0%)	41	77
1	C	2637/3089 (85%)	2489 (94%)	139 (5%)	9 (0%)	41	77
1	D	2637/3089 (85%)	2488 (94%)	140 (5%)	9 (0%)	41	77
1	E	2637/3089 (85%)	2488 (94%)	141 (5%)	8 (0%)	41	77
1	F	2637/3089 (85%)	2488 (94%)	140 (5%)	9 (0%)	41	77
All	All	15822/18534 (85%)	14931 (94%)	840 (5%)	51 (0%)	44	77

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%)	1987 (96%)	89 (4%)	29	53
1	B	2076/2264 (92%)	1986 (96%)	90 (4%)	29	53
1	C	2076/2264 (92%)	1987 (96%)	89 (4%)	29	53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	2076/2264 (92%)	1987 (96%)	89 (4%)	29	53
1	E	2076/2264 (92%)	1987 (96%)	89 (4%)	29	53
1	F	2076/2264 (92%)	1987 (96%)	89 (4%)	29	53
All	All	12456/13584 (92%)	11921 (96%)	535 (4%)	33	53

5 of 535 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	439	THR
1	C	696	HIS
1	C	427	ARG
1	C	2809	LEU
1	F	427	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 71 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	1582	HIS
1	C	1672	GLN
1	C	2699	ASN
1	B	486	GLN
1	B	386	ASN

5.3.3   RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5   Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6　Ligand geometry　ⓘ

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	E	4000	-	33,33,33	1.07	2 (6%)	48,50,50	1.26	8 (16%)
2	FMN	B	4000	-	33,33,33	1.08	2 (6%)	48,50,50	1.26	8 (16%)
2	FMN	F	4000	-	33,33,33	1.07	2 (6%)	48,50,50	1.26	7 (14%)
2	FMN	D	4000	-	33,33,33	1.07	2 (6%)	48,50,50	1.26	8 (16%)
2	FMN	C	4000	-	33,33,33	1.07	2 (6%)	48,50,50	1.26	7 (14%)
2	FMN	A	4000	-	33,33,33	1.07	2 (6%)	48,50,50	1.26	8 (16%)

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	E	4000	-	-	5/18/18/18	0/3/3/3
2	FMN	B	4000	-	-	5/18/18/18	0/3/3/3
2	FMN	F	4000	-	-	5/18/18/18	0/3/3/3
2	FMN	D	4000	-	-	5/18/18/18	0/3/3/3
2	FMN	C	4000	-	-	5/18/18/18	0/3/3/3
2	FMN	A	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	4.13	1.38	1.30
2	E	4000	FMN	C4A-N5	4.11	1.38	1.30
2	F	4000	FMN	C4A-N5	4.08	1.38	1.30
2	C	4000	FMN	C4A-N5	4.08	1.38	1.30
2	D	4000	FMN	C4A-N5	4.08	1.38	1.30

The worst 5 of 46 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	4000	FMN	C4-N3-C2	-3.01	120.08	125.64
2	F	4000	FMN	C4-N3-C2	-3.00	120.09	125.64
2	E	4000	FMN	C4-N3-C2	-2.99	120.11	125.64
2	B	4000	FMN	C4-N3-C2	-2.98	120.13	125.64
2	D	4000	FMN	C4-N3-C2	-2.97	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 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	4000	FMN	5	0
2	C	4000	FMN	4	0
2	A	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 then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand FMN E 4000

Bond lengths

Bond angles

Torsions

Rings

Ligand FMN B 4000

Bond lengths

Bond angles

Torsions

Rings

Ligand FMN F 4000

Bond lengths

Bond angles

Torsions

Rings

Ligand FMN D 4000

Bond lengths

Bond angles

Torsions

Rings

Ligand FMN C 4000

Bond lengths

Bond angles

Torsions

Rings

Ligand FMN A 4000

Bond lengths

Bond angles

Torsions

Rings
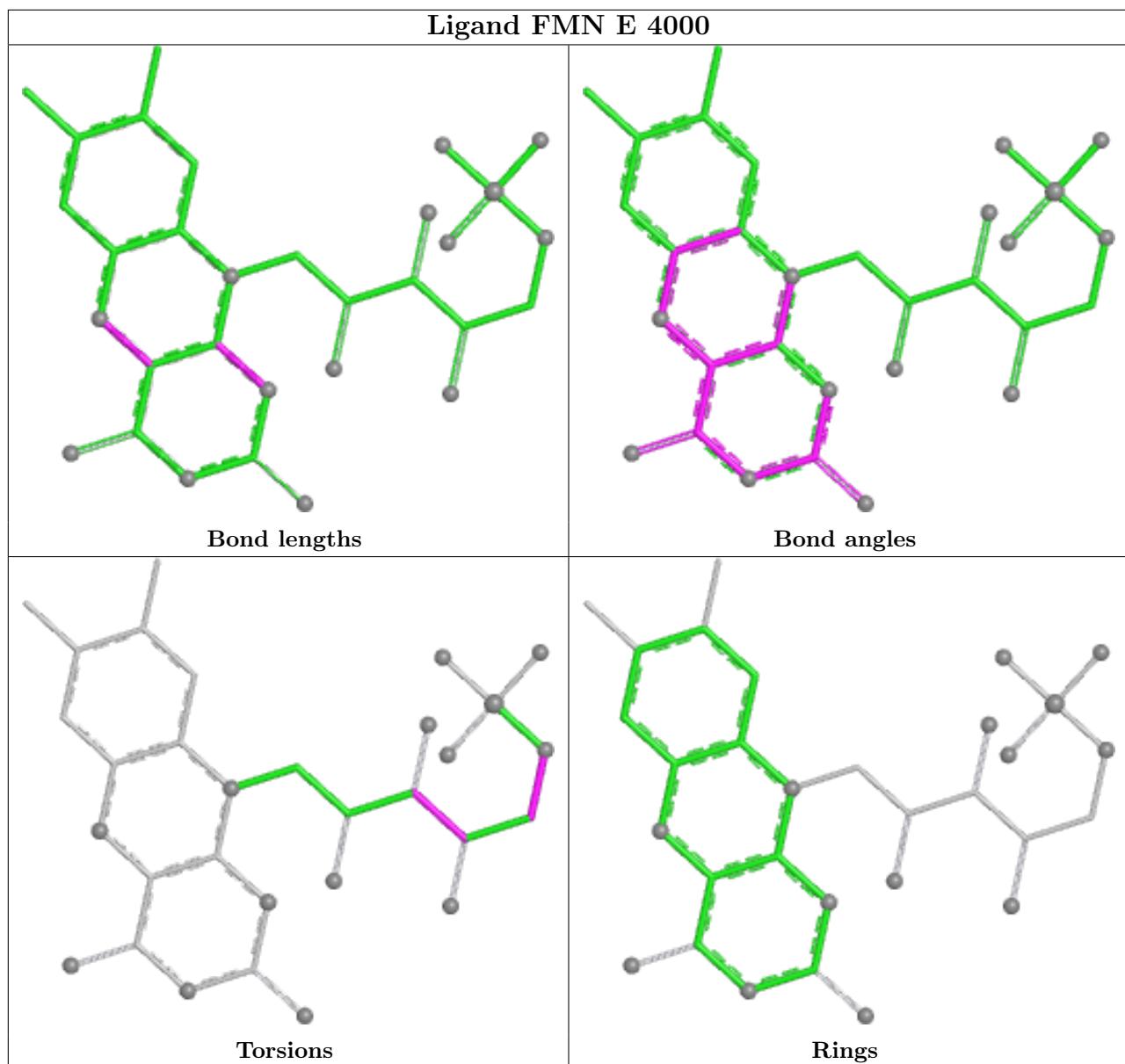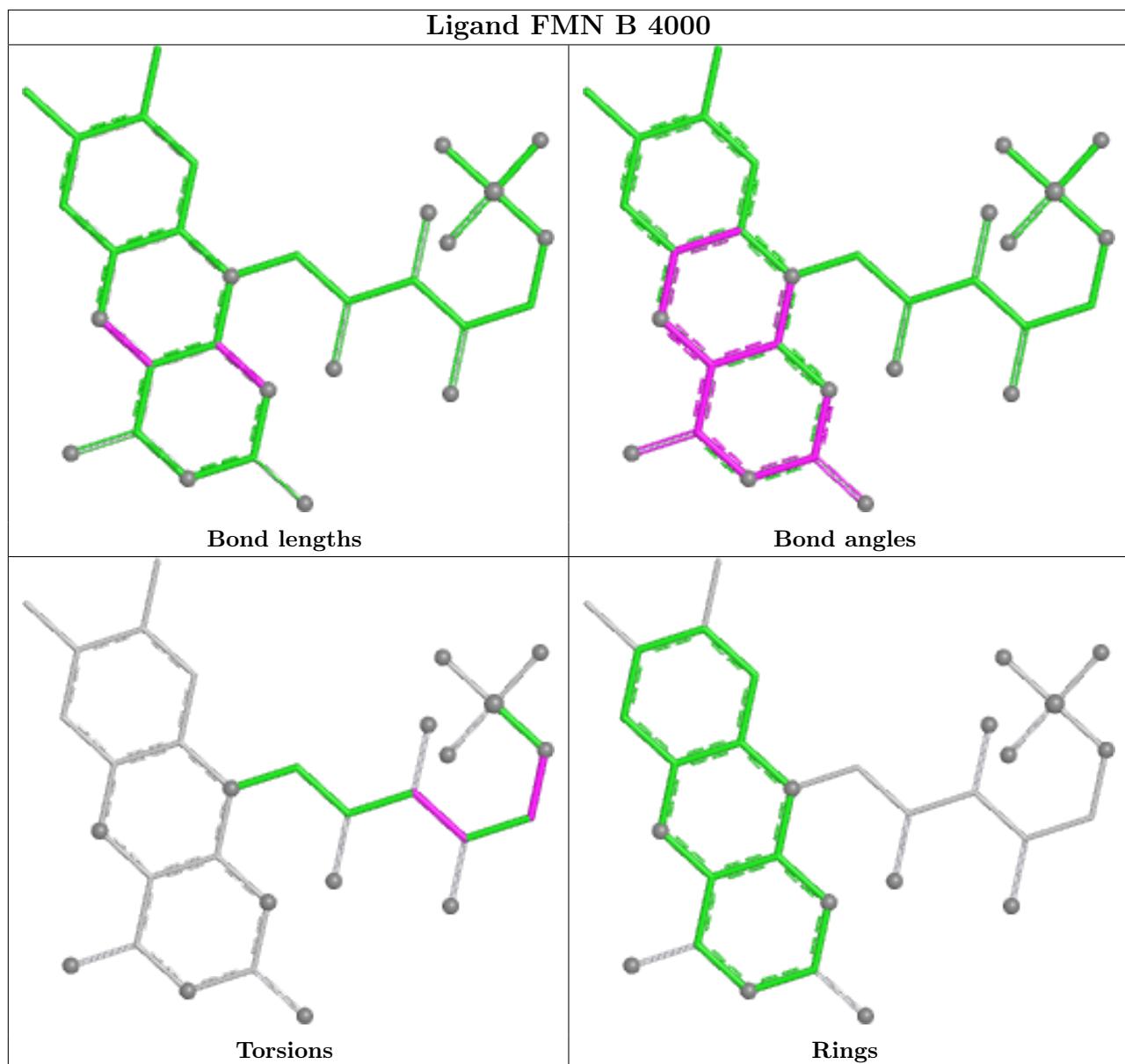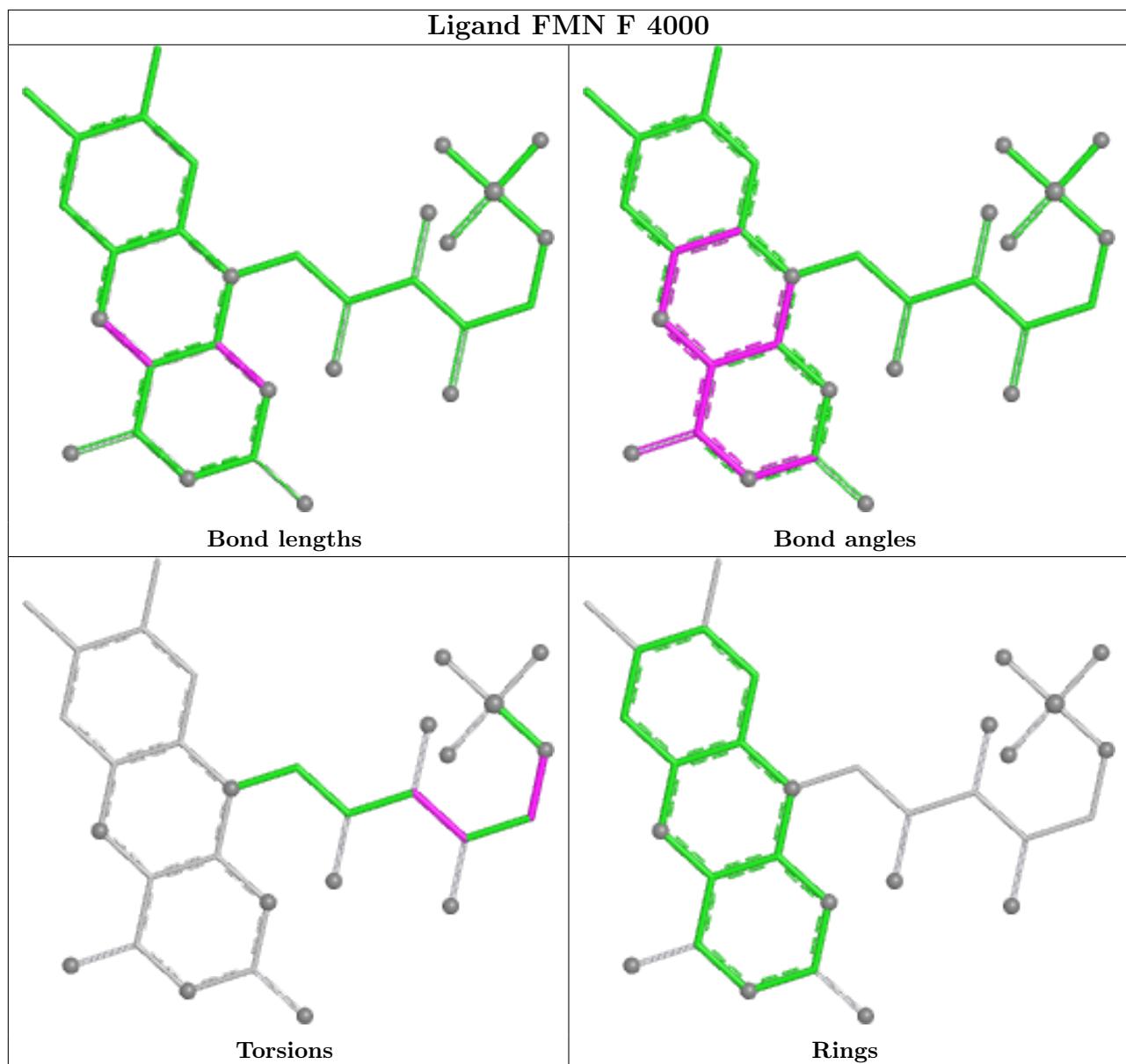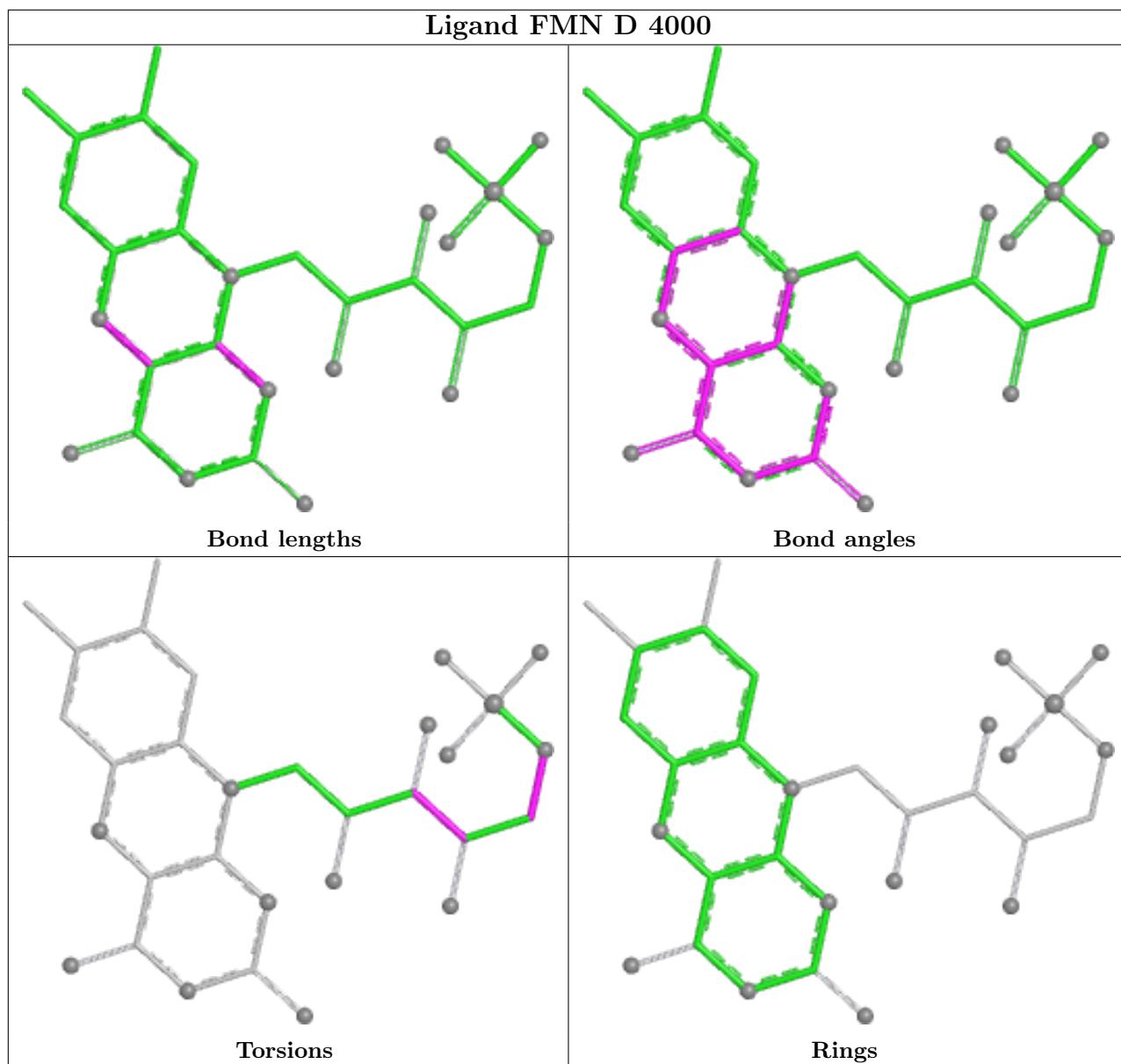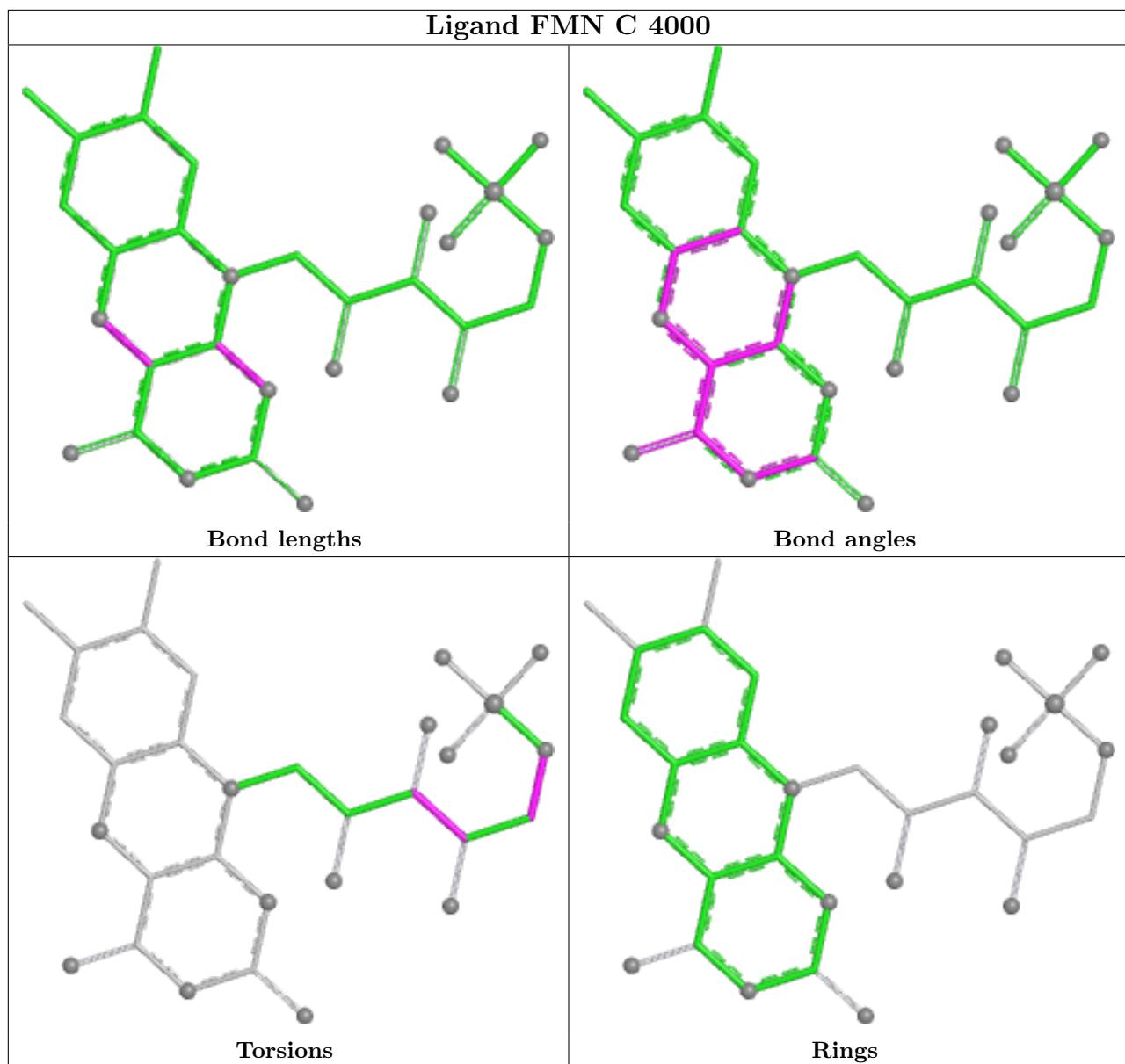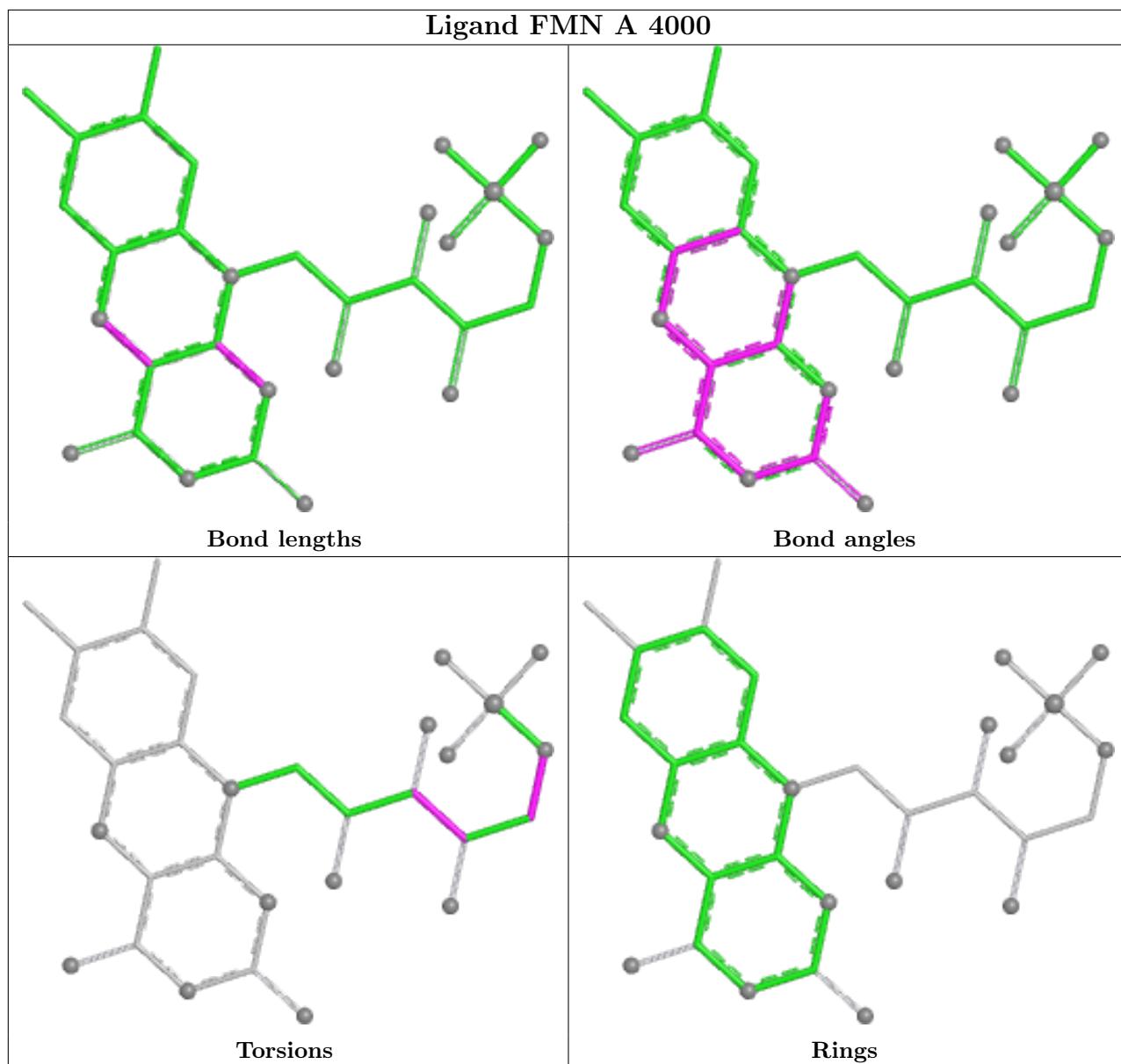
5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Map visualisation ⓘ

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 ⓘ

6.1.1 Primary map

| X | Y | Z |
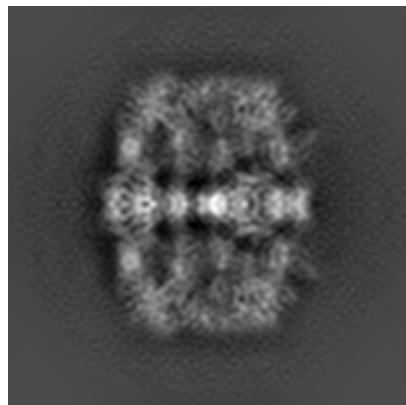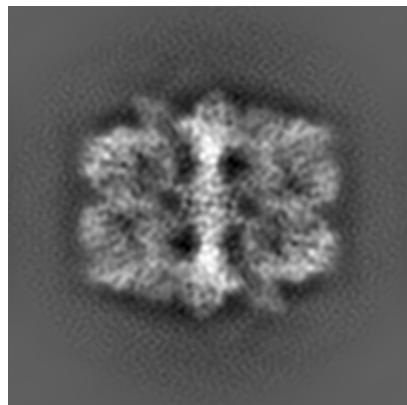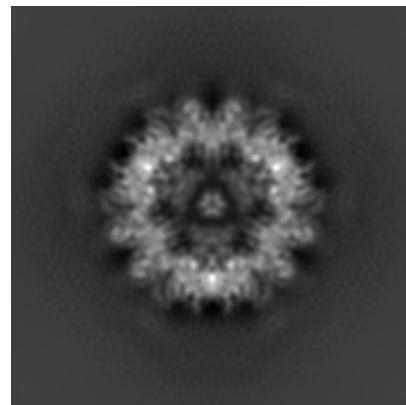
The images above show the map projected in three orthogonal directions.

6.2 Central slices ⓘ
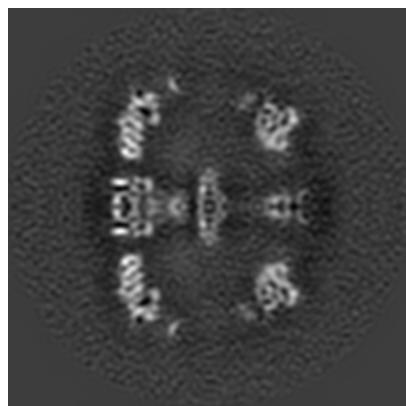
6.2.1 Primary map
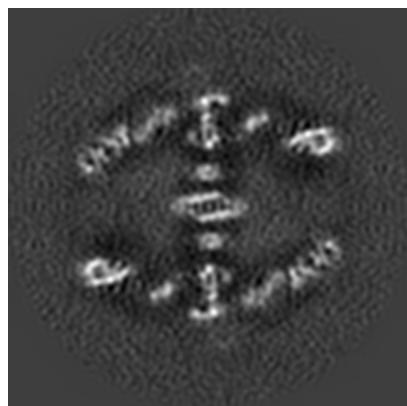
| X Index: 80 | Y Index: 80 | Z Index: 80 |
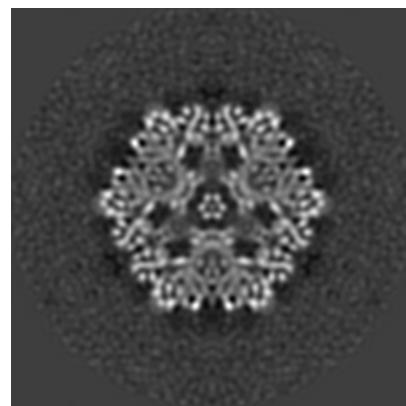
The images above show central slices of the map in three orthogonal directions.

6.3   Largest variance slices   (i)

6.3.1   Primary map
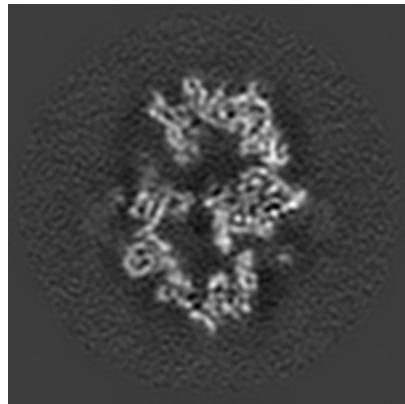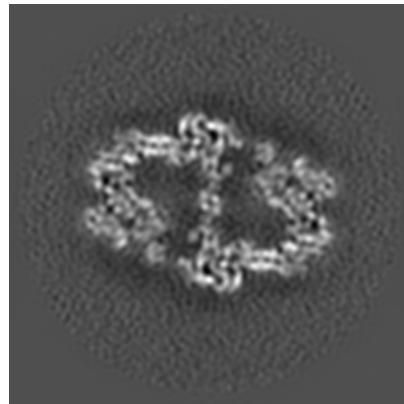
| X Index: 55 | Y Index: 105 | Z Index: 80 |
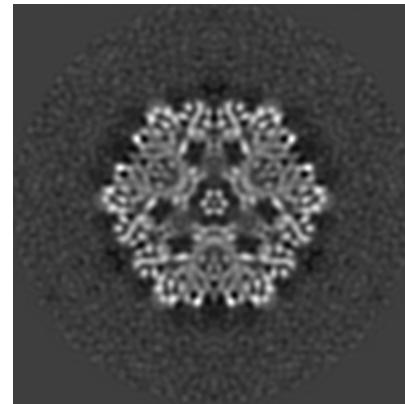
The images above show the largest variance slices of the map in three orthogonal directions.

6.4   Orthogonal surface views   (i)

6.4.1   Primary map

| X | Y | Z |
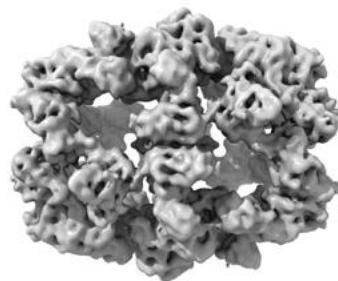
The images above show the 3D surface view of the map at the recommended contour level 2.7. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5 Mask visualisation ⓘ

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

7 Map analysis ⓘ

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

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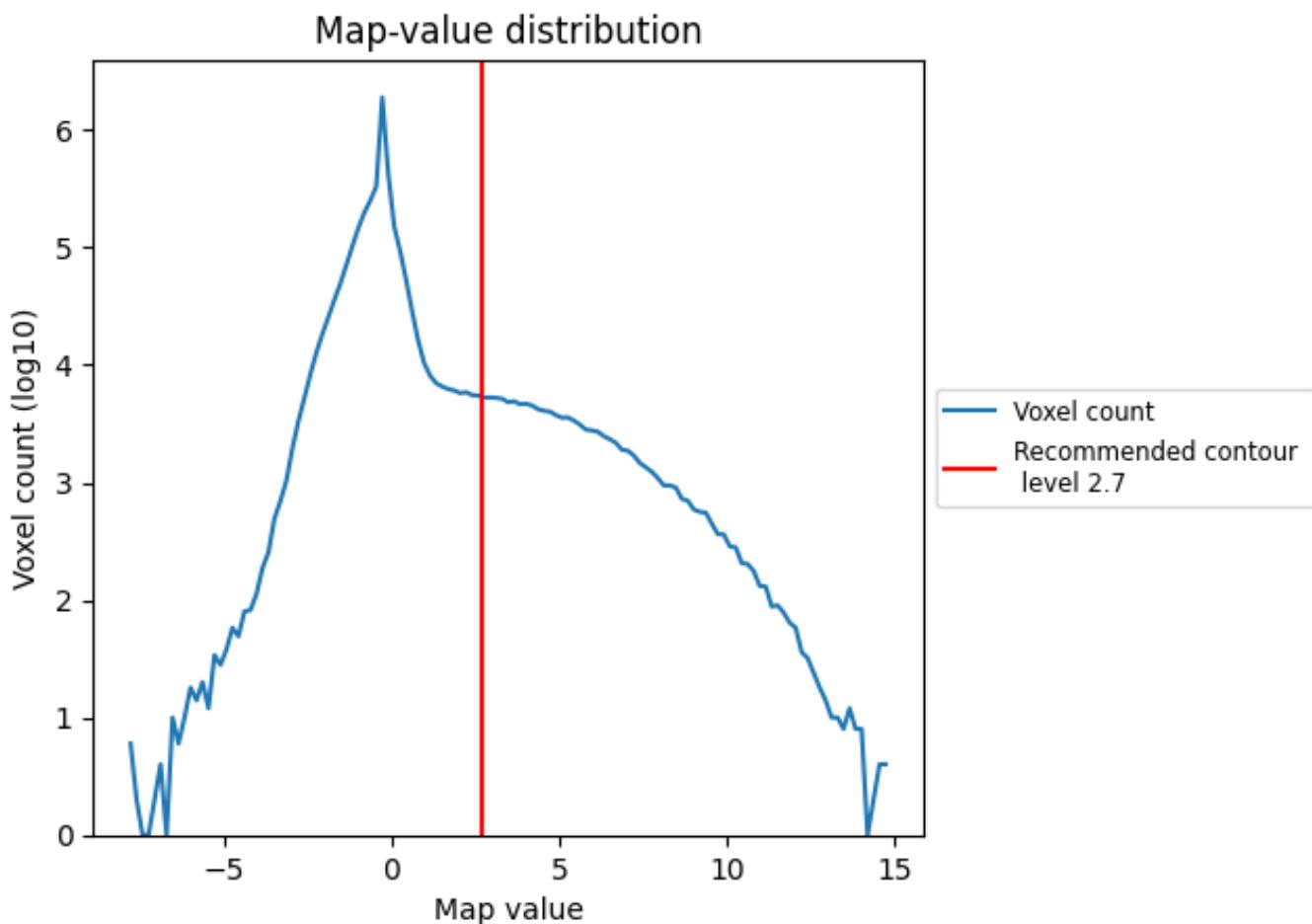
The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

7.2 Volume estimate ⓘ
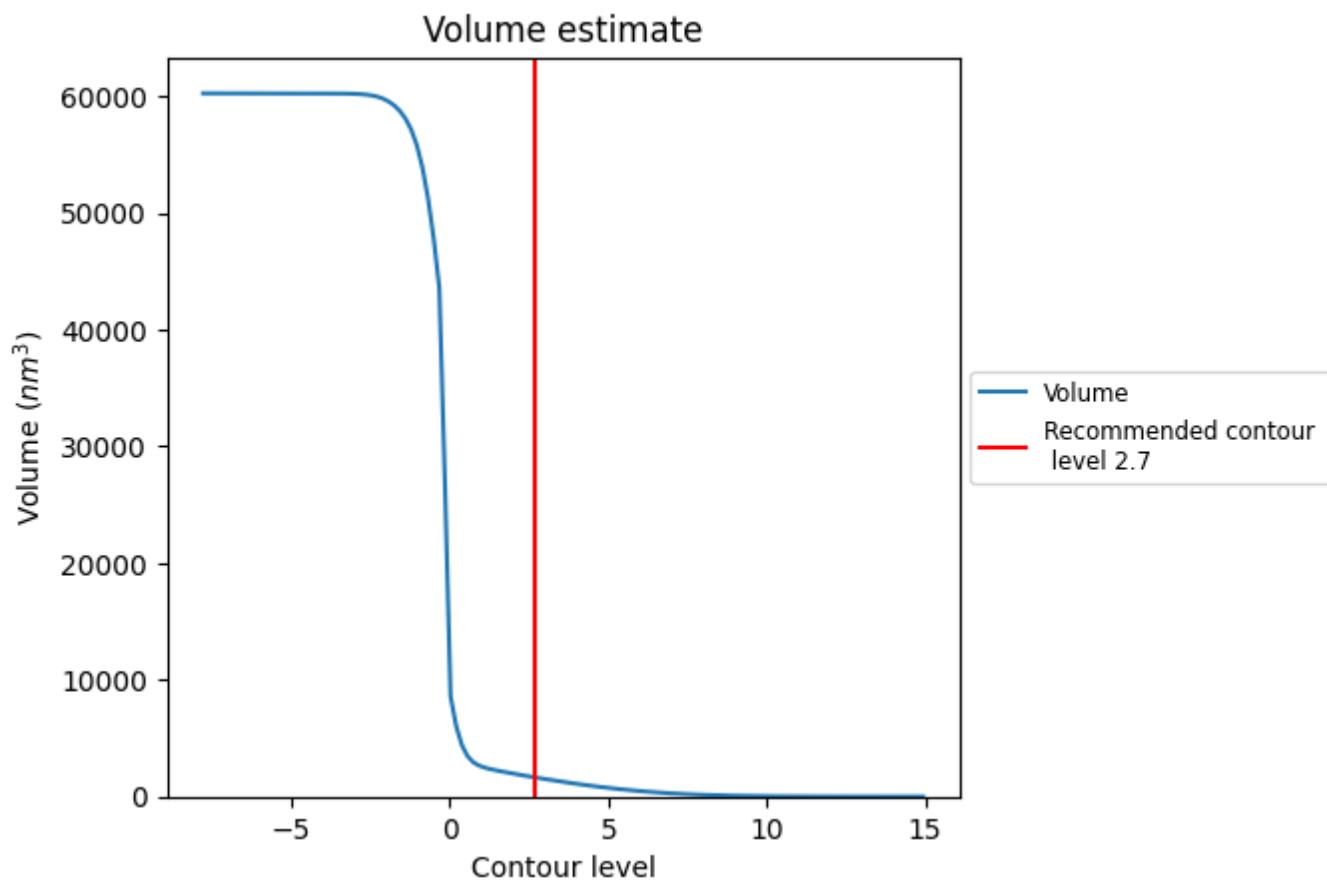
The volume at the recommended contour level is 1634 nm^3; this corresponds to an approximate mass of 1476 kDa.

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 ⓘ
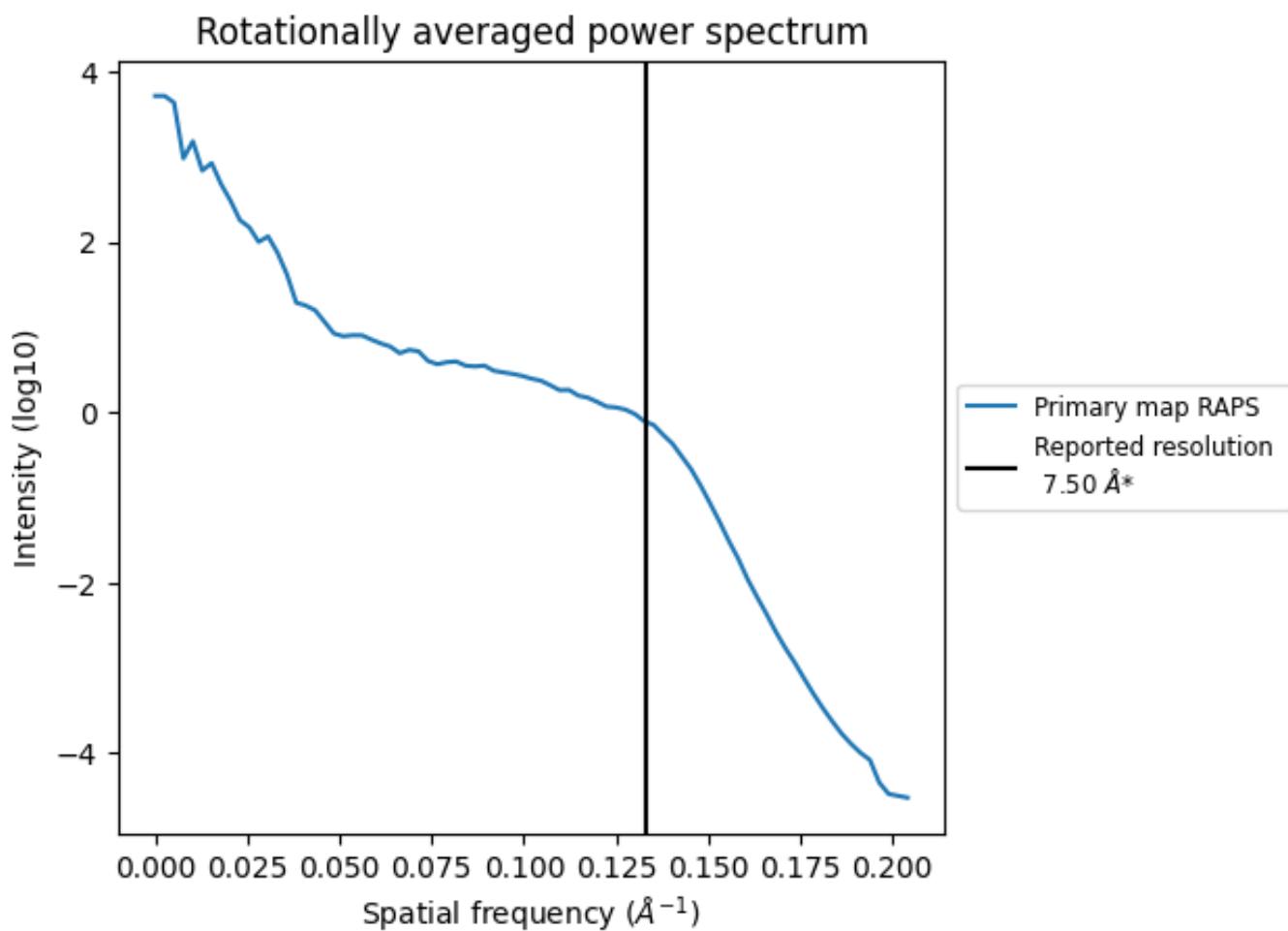
*Reported resolution corresponds to spatial frequency of 0.133 Å^{-1}

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 31.

9.1 Map-model overlay ⓘ

| X | Y | Z |
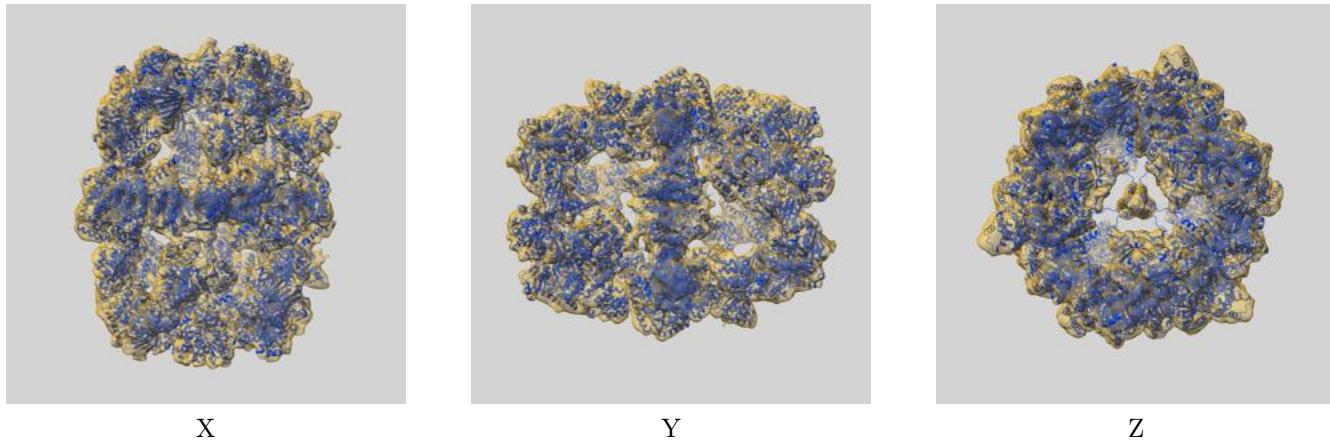
The images above show the 3D surface view of the map at the recommended contour level 2.7 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2   Q-score mapped to coordinate model ⓘ

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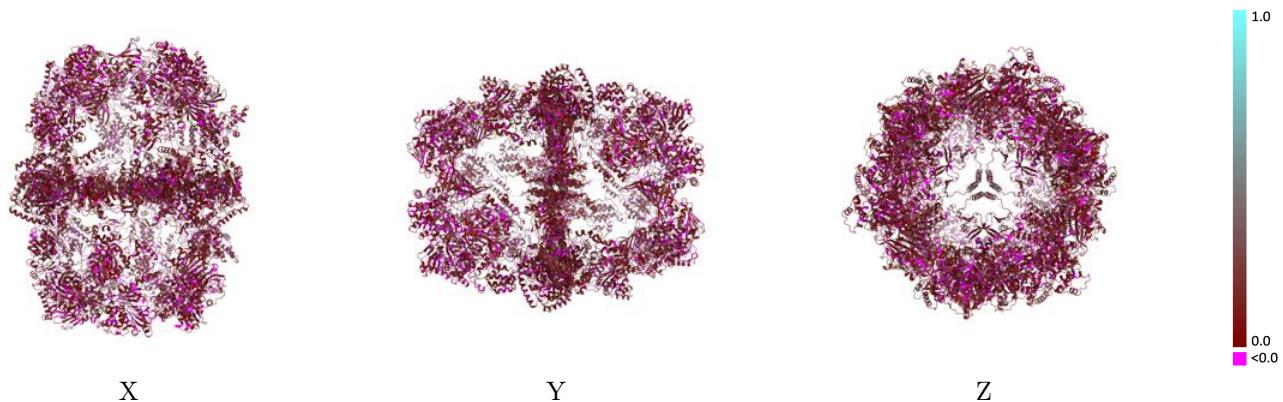
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3   Atom inclusion mapped to coordinate model ⓘ

X   Y   Z
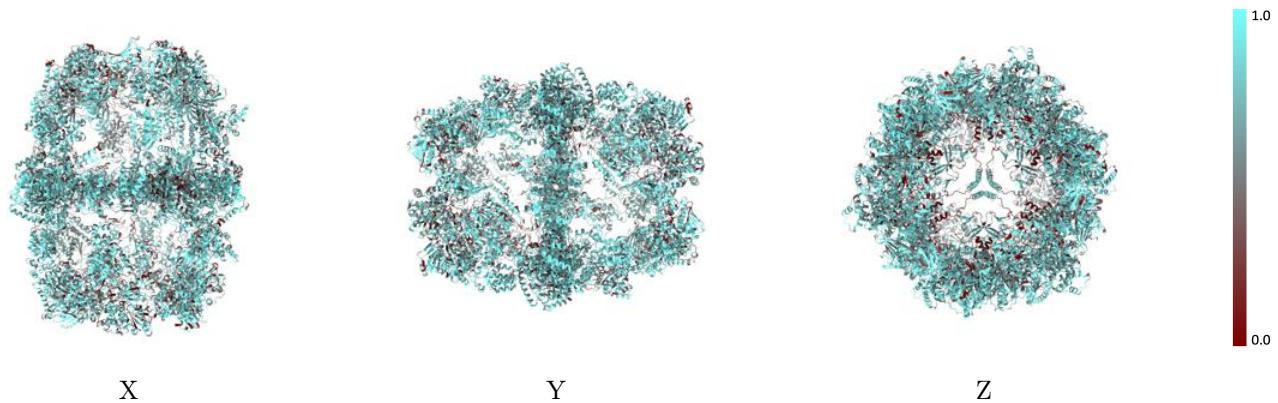
The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (2.7).

9.4　Atom inclusion ⓘ
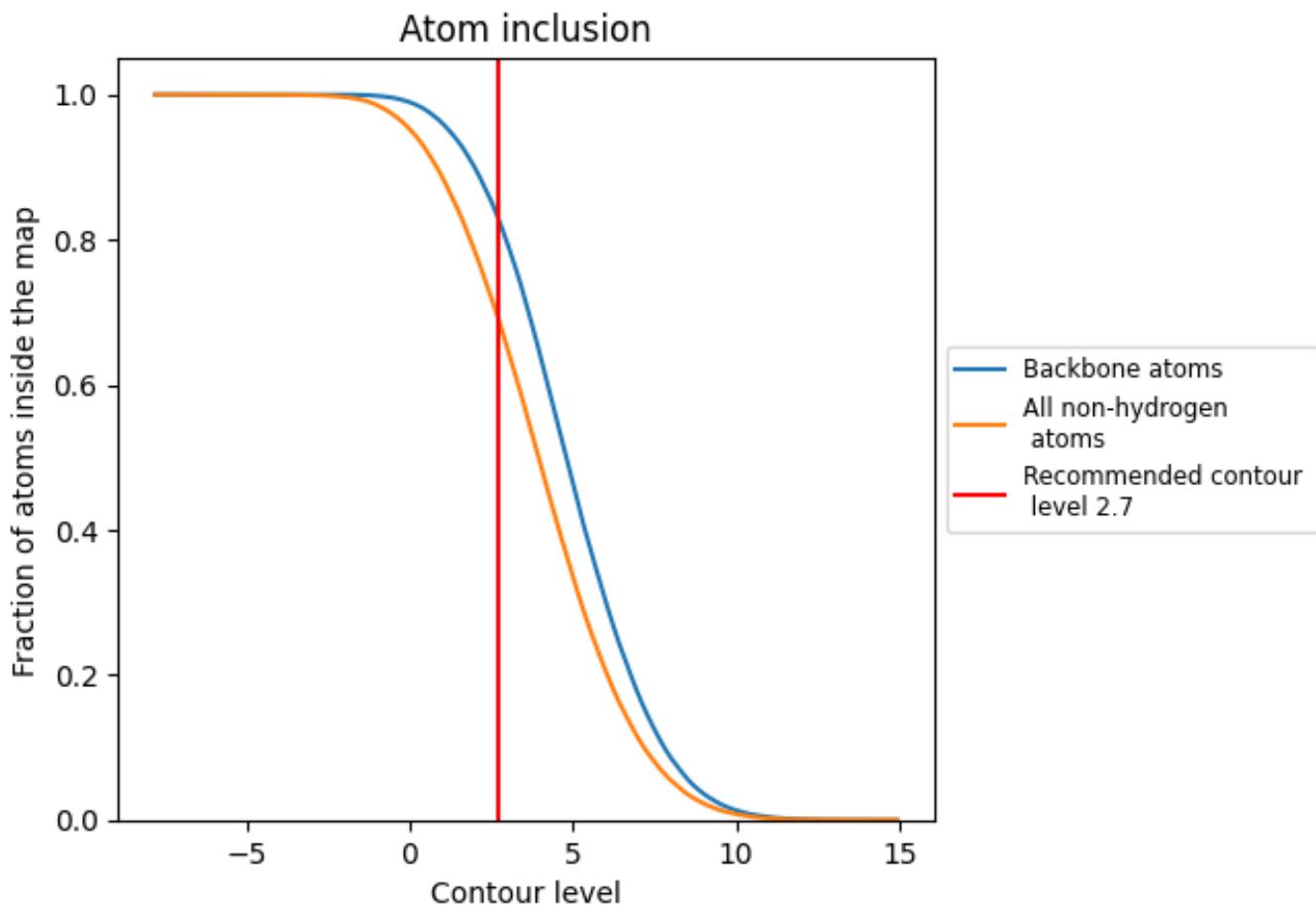
At the recommended contour level, 83% of all backbone atoms, 69% of all non-hydrogen atoms, are inside the map.

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	0.6932	0.1100
A	0.6749	0.1000
B	0.6945	0.1130
C	0.6892	0.1090
D	0.6976	0.1120
E	0.6908	0.1080
F	0.7121	0.1200

1.0

0.0

<0.0