



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 18, 2026 – 06:11 AM UTC

PDB ID : 4V59 / pdb_00004v59
Title : Crystal structure of fatty acid synthase complexed with nadp+ from thermomyces lanuginosus at 3.1 angstrom resolution.
Authors : Jenni, S.; Leibundgut, M.; Boehringer, D.; Frick, C.; Mikolasek, B.; Ban, N.
Deposited on : 2007-03-09
Resolution : 3.10 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

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A user guide is available at

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

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:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

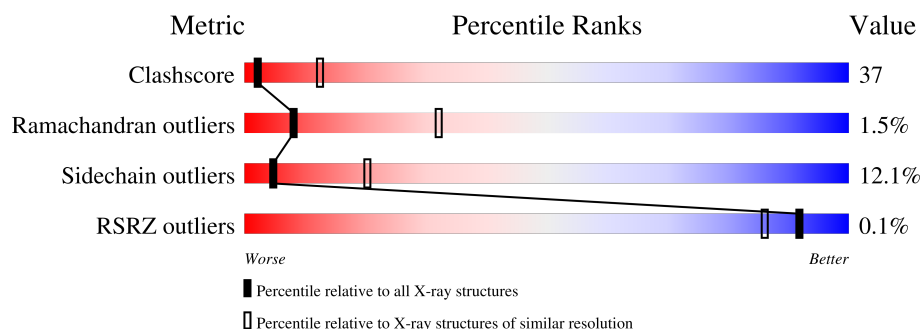
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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.



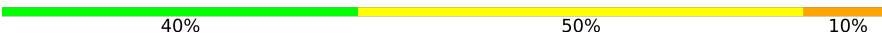
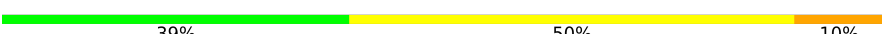
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1878	
1	B	1878	
1	C	1878	
1	D	1878	
1	E	1878	
1	F	1878	
2	G	2060	

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Mol	Chain	Length	Quality of chain
2	H	2060	
2	I	2060	
2	J	2060	
2	K	2060	
2	L	2060	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	FMN	G	2101	-	-	X	-
4	FMN	H	2101	-	-	X	-
4	FMN	I	2101	-	-	X	-
4	FMN	J	2101	-	-	X	-
4	FMN	K	2101	-	-	X	-
4	FMN	L	2101	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 167247 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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.

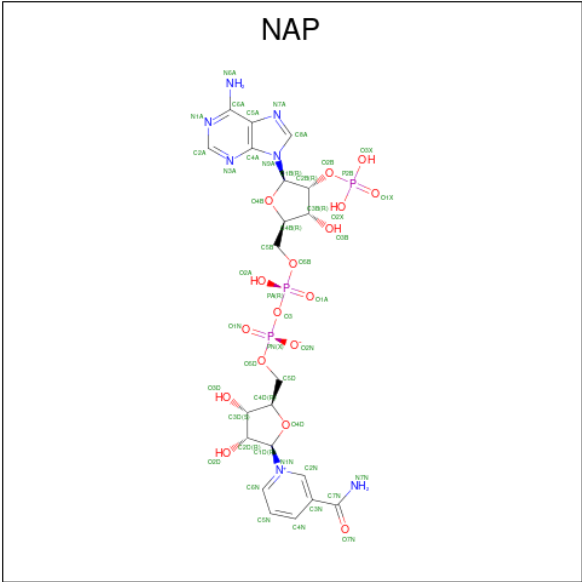
- Molecule 1 is a protein called FATTY ACID SYNTHASE ALPHA SUBUNITS.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1457	Total	C	N	O	S	0	0	0
			11514	7290	2005	2170	49			
1	B	1464	Total	C	N	O	S	0	0	0
			11571	7323	2015	2183	50			
1	C	1462	Total	C	N	O	S	0	0	0
			11555	7312	2012	2181	50			
1	D	1467	Total	C	N	O	S	0	0	0
			11593	7336	2021	2186	50			
1	E	1456	Total	C	N	O	S	0	0	0
			11506	7285	2004	2169	48			
1	F	1461	Total	C	N	O	S	0	0	0
			11546	7307	2010	2179	50			

- Molecule 2 is a protein called FATTY ACID SYNTHASE BETA SUBUNITS.

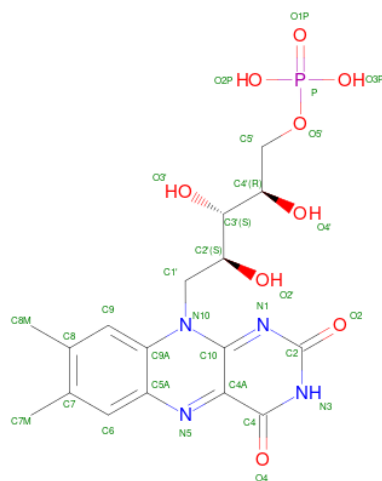
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	G	2060	Total	C	N	O	S	0	0	0
			16200	10314	2781	3051	54			
2	H	2060	Total	C	N	O	S	0	0	0
			16200	10314	2781	3051	54			
2	I	2060	Total	C	N	O	S	0	0	0
			16200	10314	2781	3051	54			
2	J	2060	Total	C	N	O	S	0	0	0
			16200	10314	2781	3051	54			
2	K	2060	Total	C	N	O	S	0	0	0
			16200	10314	2781	3051	54			
2	L	2060	Total	C	N	O	S	0	0	0
			16200	10314	2781	3051	54			

- Molecule 3 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (CCD ID: NAP) (formula: C₂₁H₂₈N₇O₁₇P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
3	B	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
3	C	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
3	D	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
3	E	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
3	F	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
3	G	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
3	H	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
3	I	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
3	J	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
3	K	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
3	L	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

- Molecule 4 is FLAVIN MONONUCLEOTIDE (CCD ID: FMN) (formula: C₁₇H₂₁N₄O₉P).

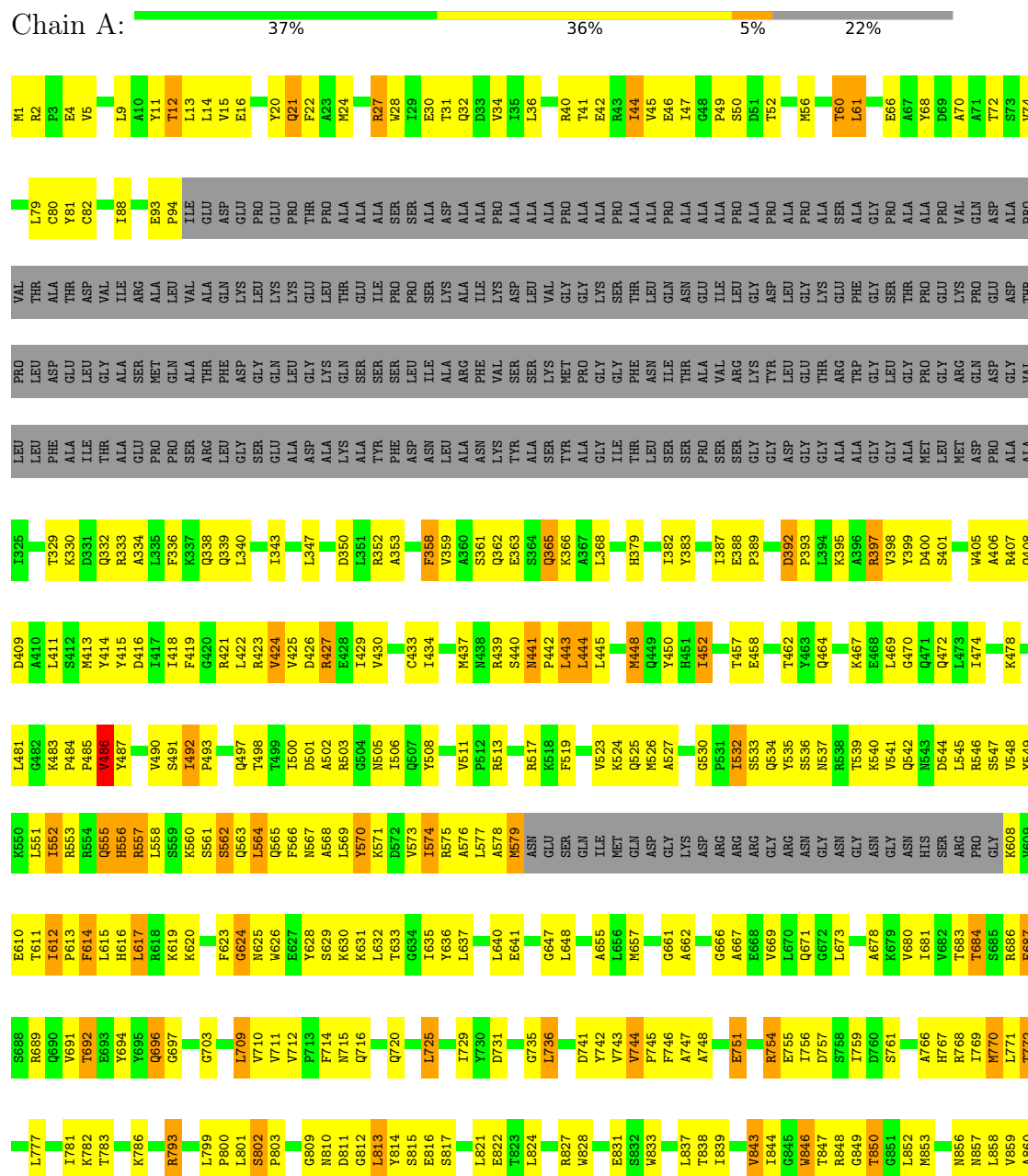


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	G	1	Total 31	C 17	N 4	O 9	P 1	0	0
4	H	1	Total 31	C 17	N 4	O 9	P 1	0	0
4	I	1	Total 31	C 17	N 4	O 9	P 1	0	0
4	J	1	Total 31	C 17	N 4	O 9	P 1	0	0
4	K	1	Total 31	C 17	N 4	O 9	P 1	0	0
4	L	1	Total 31	C 17	N 4	O 9	P 1	0	0

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 electron 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 dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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 ALPHA SUBUNITS



Y1210	R1121	S1048	P959	N879	P803	V712	S629	S562	L481	M413	ALA	GLY	ASP	ALA	S73
K1211	I1129	G1049	R960	L880	F808	F713	K630	Q563	G482	M413	ALA	VAL	THR	PRO	V74
Y1212	I1130	W1050	A961	L881	F809	F714	K631	L564	K483	Y414	THR	LEU	PRO	VAL	L79
H1214	F1131	Y1051	N962	G882	G809	N715	L632	Q565	P484	Y415	ALA	PHE	ASP	ALA	C80
L1215	I1132	D1052	L963	L883	N810	Q716	T633	F566	P485	D416	THR	GLY	ASP	THR	Y81
S1216	I1133	K964	N965	M884	D811	G717	G634	G634	Y486	G812	ALA	ALA	LEU	ASP	C82
E1217	T1055	T1055	Y965	G885	G812	S718	I635	A568	Y487	I418	ILE	THR	GLY	VAL	I88
V1218	G1056	G1056	P966	I888	L813	L725	Y636	L569	V490	G420	ALA	THR	GLY	ALA	E93
G1223	E1057	E1057	F967	V889	Y814	L726	Y637	Y570	S491	L422	PRO	GLN	GLY	ALA	P94
T1224	P1058	P1058	P968	N890	E816	V726	L640	V573	I492	R421	GLY	THR	ASP	ARG	E93
S1225	V1059	V1059	G969	L891	E816	I729	G647	I574	P493	R423	ALA	ALA	LEU	ALA	I88
G1226	D1060	D1060	Q892	Q892	S817	I730	L648	R575	T498	V424	THR	THR	VAL	VAL	I88
V1228	D1063	D1063	Q893	Q893	S817	I730	L648	A576	T499	V425	THR	THR	VAL	VAL	I88
T1229	V1064	V1064	F898	F898	E822	G735	A655	M579	T499	V425	THR	THR	VAL	VAL	I88
L1232	T1147	T1147	D900	D900	L824	L736	L656	M579	T499	V425	THR	THR	VAL	VAL	I88
R1233	Y1068	Y1068	Q983	Q983	Q834	F746	G666	L584	T499	V425	THR	THR	VAL	VAL	I88
G1234	E1069	E1069	R985	R985	G834	A747	A667	M585	T499	V425	THR	THR	VAL	VAL	I88
M1235	K1070	K1070	G986	G986	G834	A747	A667	Q886	T499	V425	THR	THR	VAL	VAL	I88
K1236	Y1071	Y1071	Q987	Q987	G834	A747	A667	Q886	T499	V425	THR	THR	VAL	VAL	I88
K1237	I1072	I1072	Y988	Y988	G834	A747	A667	Q886	T499	V425	THR	THR	VAL	VAL	I88
D1238	H1075	H1075	N989	N989	G834	A747	A667	Q886	T499	V425	THR	THR	VAL	VAL	I88
I1249	F1156	F1156	L990	L990	G834	A747	A667	Q886	T499	V425	THR	THR	VAL	VAL	I88
L1250	D1157	D1157	L990	L990	G834	A747	A667	Q886	T499	V425	THR	THR	VAL	VAL	I88
Q1251	R1158	R1158	V994	V994	G834	A747	A667	Q886	T499	V425	THR	THR	VAL	VAL	I88
E1252	L1159	L1159	Y995	Y995	G834	A747	A667	Q886	T499	V425	THR	THR	VAL	VAL	I88
S1253	A1160	A1160	Y996	Y996	G834	A747	A667	Q886	T499	V425	THR	THR	VAL	VAL	I88
F1254	I1081	I1081	T997	T997	G834	A747	A667	Q886	T499	V425	THR	THR	VAL	VAL	I88
T1257	G1162	G1162	G998	G998	G834	A747	A667	Q886	T499	V425	THR	THR	VAL	VAL	I88
A1260	Q1163	Q1163	L999	L999	G834	A747	A667	Q886	T499	V425	THR	THR	VAL	VAL	I88
M1264	I1164	I1164	A1000	A1000	G834	A747	A667	Q886	T499	V425	THR	THR	VAL	VAL	I88
L1265	E1085	E1085	I1001	I1001	G834	A747	A667	Q886	T499	V425	THR	THR	VAL	VAL	I88
L1266	F1086	F1086	E1001	E1001	G834	A747	A667	Q886	T499	V425	THR	THR	VAL	VAL	I88
L1267	Y1089	Y1089	G1003	G1003	G834	A747	A667	Q886	T499	V425	THR	THR	VAL	VAL	I88
S1268	D1090	D1090	P1004	P1004	G834	A747	A667	Q886	T499	V425	THR	THR	VAL	VAL	I88
S1269	P1091	P1091	W1005	W1005	G834	A747	A667	Q886	T499	V425	THR	THR	VAL	VAL	I88
T1270	R1092	R1092	G1006	G1006	G834	A747	A667	Q886	T499	V425	THR	THR	VAL	VAL	I88
I1273	R1093	R1093	N1007	N1007	G834	A747	A667	Q886	T499	V425	THR	THR	VAL	VAL	I88
K1274	K1094	K1094	A1008	A1008	G834	A747	A667	Q886	T499	V425	THR	THR	VAL	VAL	I88
T1275	Q1095	Q1095	L1009	L1009	G834	A747	A667	Q886	T499	V425	THR	THR	VAL	VAL	I88
P1276	L1096	L1096	R1011	R1011	G834	A747	A667	Q886	T499	V425	THR	THR	VAL	VAL	I88
P1277	E1177	E1177	W1012	W1012	G834	A747	A667	Q886	T499	V425	THR	THR	VAL	VAL	I88
G1278	D1178	D1178	E1013	E1013	G834	A747	A667	Q886	T499	V425	THR	THR	VAL	VAL	I88
A1279	I1179	I1179	M1014	M1014	G834	A747	A667	Q886	T499	V425	THR	THR	VAL	VAL	I88
C1280	T1180	T1180	N1017	N1017	G834	A747	A667	Q886	T499	V425	THR	THR	VAL	VAL	I88
D1281	V1183	V1183	Y1017	Y1017	G834	A747	A667	Q886	T499	V425	THR	THR	VAL	VAL	I88
T1282	L1186	L1186	L1022	L1022	G834	A747	A667	Q886	T499	V425	THR	THR	VAL	VAL	I88
D1288	T1187	T1187	E1023	E1023	G834	A747	A667	Q886	T499	V425	THR	THR	VAL	VAL	I88
Y1291	L1191	L1191	M1031	M1031	G834	A747	A667	Q886	T499	V425	THR	THR	VAL	VAL	I88
D1292	L1199	L1199	N1037	N1037	G834	A747	A667	Q886	T499	V425	THR	THR	VAL	VAL	I88
E1293	Y1207	Y1207	H1038	H1038	G834	A747	A667	Q886	T499	V425	THR	THR	VAL	VAL	I88
T1293	E1208	E1208	F1209	F1209	G834	A747	A667	Q886	T499	V425	THR	THR	VAL	VAL	I88

W1510	Y1442	G1356	G1278	L1191	E1117	L1042	Y952	Q873	T798	V710	G624	K560	Q482	S412
G1511	L1443	C1357	A1279	L1191	E1117	L1042	Y952	Q874	L798	V711	N625	S561	K483	M413
T1512	Q1444	Q1360	C1280	L1198	F1118	K1043	I956	M876	P800	V712	W626	S562	P484	Y414
T1513	E1445	Q1361	T1282	L1199	F1119	S1048	P959	M877	P801	F713	E627	S563	P485	Y415
T1514	V1446	T1362	T1282	L1200	R1121	S1049	P960	A877	S802	F714	W628	L564	D416	Y466
H1523	A1448	M1363	D1288	S1200	R1121	W1050	A961	F878	G809	W715	S629	Q565	Y467	I417
G1524	A1449	Q1366	T1293	Y1207	T1129	W1051	A961	L881	G809	Q716	K630	F566	I418	I418
T1525	I1450	Q1367	I1294	E1208	F1130	D1052	N962	G882	D811	Q720	L632	A568	S491	F419
S1526	K1451	A1368	I1294	F1209	I1131	K964	N963	L883	D812	Q721	L633	A569	S492	Q420
T1527	R1454	Q1369	I1294	Y1210	I1132	T1055	Y965	M884	L813	L725	G634	Y570	P493	L422
V1528	R1454	K1298	K1211	K1211	Q1137	E1056	P966	Y814	Y814	W726	I635	V573	Q497	R423
D1531	E1457	M1371	A1299	V1212	Y1138	E1057	P967	S815	S815	I729	Y636	I574	T498	W424
K1532	D1458	G1372	R1300	V1213	Y1138	P1058	P968	V889	S816	Y730	L637	R575	T499	V425
N1533	G1459	V1373	V1301	H1214	T1139	P1059	P968	M890	S817	Y731	L640	A576	T499	D426
E1534	L1460	P1374	C1302	L1215	Y1140	Y1059	Y973	L891	L821	Q735	G647	L577	D501	E428
E1535	L1375	I1375	L1303	S1216	R1141	C892	K892	L891	E822	L736	L648	M579	R503	I429
E1536	E1461	Y1376	E1312	E1217	L1142	D1063	K892	Q893	E822	Q736	L648	M580	G504	V430
D1462	D1462	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1463	E1463	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1464	E1464	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1465	E1465	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1466	E1466	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1467	E1467	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1468	E1468	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1469	E1469	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1470	E1470	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1471	E1471	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1472	E1472	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1473	E1473	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1474	E1474	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1475	E1475	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1476	E1476	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1477	E1477	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1478	E1478	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1479	E1479	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1480	E1480	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1481	E1481	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1482	E1482	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1483	E1483	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1484	E1484	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1485	E1485	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1486	E1486	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1487	E1487	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1488	E1488	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1489	E1489	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1490	E1490	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1491	E1491	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1492	E1492	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1493	E1493	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1494	E1494	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1495	E1495	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1496	E1496	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1497	E1497	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1498	E1498	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1499	E1499	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1500	E1500	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1501	E1501	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1502	E1502	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1503	E1503	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1504	E1504	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1505	E1505	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1506	E1506	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1507	E1507	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1508	E1508	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1509	E1509	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1510	E1510	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1511	E1511	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1512	E1512	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1513	E1513	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1514	E1514	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1515	E1515	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1516	E1516	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1517	E1517	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1518	E1518	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1519	E1519	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1520	E1520	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1521	E1521	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1522	E1522	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1523	E1523	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1524	E1524	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1525	E1525	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1526	E1526	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1527	E1527	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1528	E1528	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1529	E1529	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1530	E1530	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1531	E1531	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1532	E1532	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1533	E1533	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1534	E1534	M1381	G1306	V1218	L1142	Y1064	K892	Q893	E822	Q736	L648	M580	G504	V430
E1535	E													

- Molecule 1: FATTY ACID SYNTHASE ALPHA SUBUNITS

Chain E:



P1091	M1007	K934	K865	K782	T692	K619	R557	Y487	Y415	P381	ILE	LEU	ASP	Y81	M1
M1092	A1008	E935	L866	T783	E993	K619	L558	Y490	D416	Q332	THR	GLY	VAL	C82	R2
R1093	R1011	N940	G867	K786	E993	K620	S559	Y491	T417	R333	ALA	ALA	ILE	I88	P3
Q1094	M1012	N940	G868	K786	E993	K620	S559	Y492	T418	A334	GLU	SER	ARG	I88	E4
L1095	E1013	V943	R870	T792	E993	K621	S561	Y493	F419	L335	PRO	MET	ALA	I88	V5
L1097	M1014	R871	R871	T793	E993	K622	S562	Y494	G420	F336	PRO	GLN	VAL	P94	E8
Q1098	E1017	S872	S872	T794	E993	K623	S563	Y495	R421	K387	ILE	ALA	VAL	P94	L9
E1099	Y1017	Q873	Q873	L799	E993	K624	S564	Y496	L422	Q338	ARG	THR	ALA	GLU	A10
H948	H948	Q874	Q874	P800	E993	K625	S565	Y497	V424	Q339	LEU	PHE	GLN	GLU	T11
E949	E949	E875	E875	L801	E993	K626	S566	Y498	V425	L340	GLY	GLY	LYS	GLU	T12
A950	L1022	E876	E876	S802	E993	K627	S567	Y499	V426	L341	GLY	GLY	LYS	GLU	L13
E1031	M1031	A951	A951	S803	E993	K628	S568	Y500	D427	L342	GLY	GLY	LYS	PRO	L14
E1103	M1032	A952	A952	S804	E993	K629	S569	Y501	R428	L343	GLY	GLY	LYS	PRO	V15
Q1104	M1032	A953	A953	S805	E993	K630	S570	Y502	E429	L344	GLY	GLY	LYS	PRO	E16
L1105	M1037	V955	V955	S810	E993	K631	S571	Y503	V430	D350	GLY	GLY	LYS	PRO	L17
E1106	H1038	I956	I956	G812	E993	K632	S572	Y504	V431	L345	GLY	GLY	LYS	PRO	L18
E1107	E1107	T957	T957	G813	E993	K633	S573	Y505	V432	A353	GLY	GLY	LYS	PRO	A19
E1108	P1041	E958	E958	S814	E993	K634	S574	Y506	C433	F388	TYR	SER	ILE	ALA	Q21
E1109	L1042	R960	R960	S815	E993	K635	S575	Y507	I434	V359	PHE	SER	PRO	ALA	M24
E1110	K1043	R961	R961	S816	E993	K636	S576	Y508	M437	F389	ASP	LEU	PRO	ALA	R27
E1111	K1043	R962	R962	S817	E993	K637	S577	Y509	M438	V359	ASN	LEU	PRO	ALA	V28
E1112	P1046	N962	N962	S818	E993	K638	S578	Y510	M439	A360	ASN	LEU	PRO	ALA	I29
F1119	Y1047	L963	L963	E821	E993	K639	S579	Y511	R439	S361	GLY	GLY	LYS	PRO	E30
K1120	S1048	K964	K964	E822	E993	K640	S580	Y512	S440	Q362	GLY	GLY	LYS	PRO	T31
R1121	G1049	Y965	Y965	E823	E993	K641	S581	Y513	P442	E363	GLY	GLY	LYS	PRO	L36
V1127	V1050	P966	P966	E824	E993	K642	S582	Y514	L443	S364	GLY	GLY	LYS	PRO	R40
E1128	D1052	P967	P967	E825	E993	K643	S583	Y515	L444	Q365	GLY	GLY	LYS	PRO	T41
I1129	E969	E969	E969	E826	E993	K644	S584	Y516	L445	K366	GLY	GLY	LYS	PRO	E42
E1130	T1055	L970	L970	E827	E993	K645	S585	Y517	M448	A367	GLY	GLY	LYS	PRO	R43
E1131	G1056	L971	L971	E828	E993	K646	S586	Y518	Q449	E368	GLY	GLY	LYS	PRO	I44
E1132	E1057	W973	W973	E829	E993	K647	S587	Y519	Q450	P369	GLY	GLY	LYS	PRO	V45
G1136	D1060	D974	D974	E830	E993	K648	S588	Y520	D453	A390	GLY	GLY	LYS	PRO	E46
Q1137	D1063	K978	K978	E831	E993	K649	S589	Y521	T457	I387	GLY	GLY	LYS	PRO	P49
Y1138	Y1064	P979	P979	E832	E993	K650	S590	Y522	E458	E388	GLY	GLY	LYS	PRO	S50
T1139	K1065	L980	L980	E833	E993	K651	S591	Y523	Y462	P391	GLY	GLY	LYS	PRO	I51
L1140	E1066	Q983	Q983	E834	E993	K652	S592	Y524	T463	D392	GLY	GLY	LYS	PRO	T52
R1141	L1142	R984	R984	E835	E993	K653	S593	Y525	Q464	P393	GLY	GLY	LYS	PRO	R59
G1146	A1146	R985	R985	E836	E993	K654	S594	Y526	K467	L394	GLY	GLY	LYS	PRO	L61
T1147	K1070	G986	G986	E837	E993	K655	S595	Y527	E468	K395	GLY	GLY	LYS	PRO	E66
L1148	L11072	V988	V988	E838	E993	K656	S596	Y528	Y469	A396	GLY	GLY	LYS	PRO	A67
L1149	H1075	N989	N989	E839	E993	K657	S597	Y529	Q470	V399	GLY	GLY	LYS	PRO	Y69
T1150	E1075	L990	L990	E840	E993	K658	S598	Y530	Q471	D400	GLY	GLY	LYS	PRO	A71
A1153	I1078	V995	V995	E841	E993	K659	S599	Y531	Q472	A401	GLY	GLY	LYS	PRO	T72
L1154	E1079	V996	V996	E842	E993	K660	S600	Y532	L473	D401	GLY	GLY	LYS	PRO	S73
Q1155	L1080	T997	T997	E843	E993	K661	S601	Y533	L474	S401	GLY	GLY	LYS	PRO	V74
F1156	E1081	E998	E998	E844	E993	K662	S602	Y534	Y464	W405	GLY	GLY	LYS	PRO	L79
D1157	E1082	L999	L999	E845	E993	K663	S603	Y535	K478	A406	GLY	GLY	LYS	PRO	C80
R1158	P1083	A1000	A1000	E846	E993	K664	S604	Y536	Y465	W406	GLY	GLY	LYS	PRO	
L1159	E1084	E1001	E1001	E847	E993	K665	S605	Y537	K479	R407	GLY	GLY	LYS	PRO	
V1160	L1085	T1002	T1002	E848	E993	K666	S606	Y538	Y470	R408	GLY	GLY	LYS	PRO	
A1161	F1086	G1003	G1003	E849	E993	K667	S607	Y539	Q471	D409	GLY	GLY	LYS	PRO	
L1162	P1004	W1004	W1004	E850	E993	K668	S608	Y540	Q472	M413	GLY	GLY	LYS	PRO	
Q1163	Q1163	W1005	W1005	E851	E993	K669	S609	Y541	L473	T329	GLY	GLY	LYS	PRO	
I1164	I1164	G1006	G1006	E852	E993	K670	S610	Y542	L474	K330	GLY	GLY	LYS	PRO	

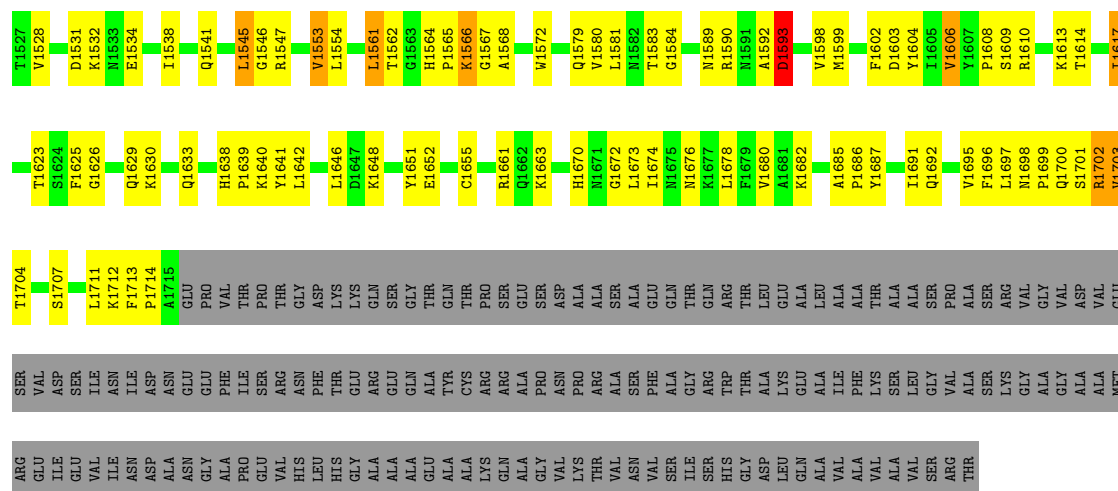
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T1166	S1253	E1333	P1414	F1493	L1578	Y1654	SER	GLU	ALA
W1167	F1254	R1333		W1494	Q1579	C1655	GLY	GLN	ALA
D1169	T1257	G1335	T1418	R1496	V1580	V1656	ALA	ALA	GLU
A1170	M1258	R1335	K1419	R1499	W1581	K1658	GLN	ALA	ALA
R1171	A1259	E1336	Y1420	T1500	N1582	R1661	THR	CYS	ALA
R1172	A1260	P1337	R1421	R1499	G1583	Q1661	ARG	ARG	LYS
Y1173		G1338	R1422	A1501	T1584	K1663	PRO	ALA	GLN
	M1264	M1340	R1423	R1504	P1587	H1670	SER	PRO	VAL
E1177	L1267	M1341	Q1424	G1505		N1671	ASN	PRO	LYS
D1178	S1268	R1342	L1425	G1509	R1590	G1672	ALA	ARG	THR
T1179	S1269	P1343	L1427	T1509	N1591	L1673	SER	ALA	VAL
T1180	T1270	T1344	E1426	W1510	A1592	N1674	ALA	ASN	VAL
V1183	P1272	S1345	Q1430	G1511	D1593	N1675	PHE	GLU	VAL
P1184	P1272	S1345	Q1431	L1512	V1598	N1676	ALA	GLY	ILE
P1185	L1273	T1346		T1513	M1599	K1677	THR	ARG	SER
T1186	K1274	T1347	L1441	I1514		L1678	GLN	TRP	HIS
V1187	T1275	F1351	Y1442	F1522	F1602	K1682	ARG	THR	GLY
L1188	T1276	M1352	L1443	G1524	D1603	Y1604	THR	ALA	GLY
L1191	G1278	E1353	E1446	G1524	T1604	P1686	ALA	LYS	ASP
L1199	A1279	S1354	V1447	G1524	I1605	Y1687	GLU	LYS	LEU
	C1280	Q1355	A1448	T1527	Y1606		ALA	ALA	GLN
	A1281	G1356	A1449	V1528	Y1607		LEU	ALA	ALA
	T1282	C1357	A1450	A1529	P1608	T1691	ALA	ILE	VAL
D1205	T1282	Q1360	K1451	D1531	Q1692	Q1692	PHE	ALA	ALA
F1206	D1288	T1361	K1451	D1531	R1610	V1695	LYS	VAL	VAL
V1207		I1362		D1531		F1696	SER	ALA	ALA
E1208		M1363	R1454	N1533	K1613	L1697	GLY	VAL	SER
F1209	T1293		E1457	E1534	T1614	N1698	PRO	VAL	ARG
T1210		Q1366			I1617	P1699	ALA	ALA	THR
K1211	Q1296	A1367	D1462	T1538	F1620	Q1700	SER	GLY	ALA
Y1212	K1297	L1367	E1463	Q1541		S1701	ARG	GLY	ALA
H1214	A1299	A1368	T1464	L1542		R1702	VAL	VAL	ALA
L1215	R1300	M1371	A1465	L1545	T1623	V1703	GLY	VAL	GLY
S1216	V1301	G1372	Y1466	L1545	S1624	T1704	ALA	ALA	ALA
E1217	G1302	P1373	R1467	G1546	F1625	Q1705	ASP	ALA	ALA
V1218	L1303	P1374	R1468	R1547	G1626	E1706	VAL	MET	GLU
G1219		T1375	E1469			S1707	SER	ARG	SER
	G1306		R1470		Q1629	N1708	VAL	GLU	VAL
G1223	F1307	M1381		V1553	K1630	G1709	ASP	ILE	ASP
S1224	D1308	T1386	H1473	L1554		E1710	SER	GLU	GLU
G1225	D1309	D1387	I1474	G1555	Q1633	K1711	GLY	ILE	GLU
V1226	Q1310	K1388	E1475	T1556		F1712	ILE	ASN	VAL
	Q1311	T1389	R1476	F1557	H1638	P1713	ILE	ASN	F1713
T1229	E1312				P1639	P1714	ASP	ASP	ASP
	E1313				K1640	A1715	ALA	ALA	ASN
L1232	G1314	V1393	R1480	L1561	Y1641	GLU	GLU	ASN	GLY
A1233	S1315	P1394	E1481	T1562	L1642	PRU	GLY	GLY	GLY
G1234	Y1316	A1395	A1482	G1563		VAL	ALA	ALA	VAL
M1235	E1317	P1396	A1483	H1564	L1646	THR	PHE	ALA	THR
Y1236			E1484	P1565	D1647	THR	ILE	PRO	ILE
G1237	M1321	V1400	A1485	K1566	G1567	THR	SER	GLU	SER
D1238	G1322	L1401	Q1486	G1567	A1568	THR	ARG	VAL	VAL
	A1323	T1402	T1487	A1568		GLY	ASN	HTS	HTS
T1249	T1324	T1403	S1488		Q1650	ASP	PHE	LEU	THR
L1250		A1404	F1489		Y1651	LYS	THR	HTS	GLY
Q1251	A1327		N1491		E1652		GLU		

● Molecule 1: FATTY ACID SYNTHASE ALPHA SUBUNITS

Chain F:  38% 34% 5% 22%

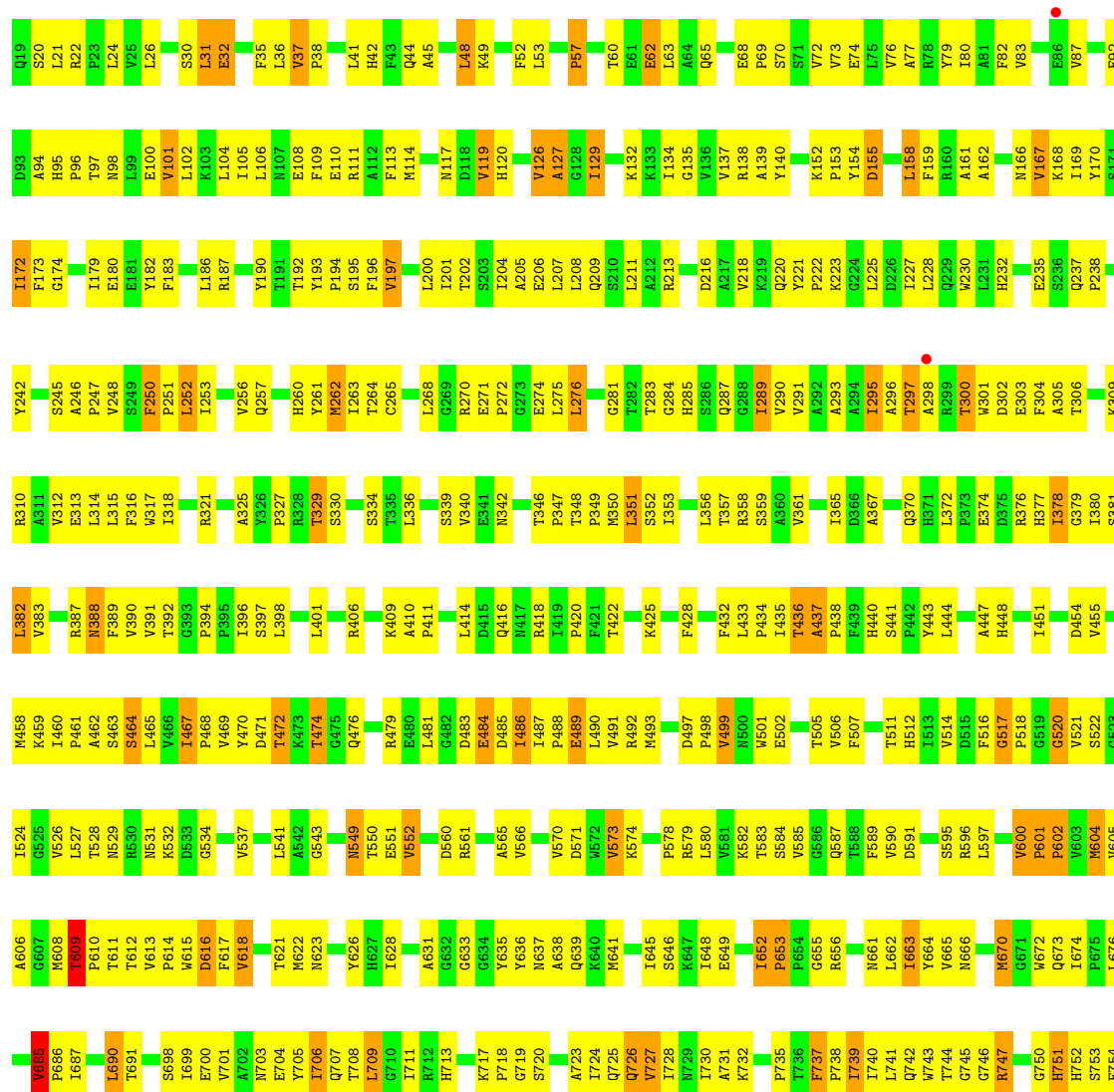
K1	S73	PRO	THR	VAL	ALA	THR	VAL	ALA	ALA
R2	V74	LEU	LEU	THR	ALA	THR	ALA	ALA	ALA
V5	L79	ASP	ASP	ALA	GLU	ASP	ALA	GLU	ALA
E6	C80	THR	THR	ALA	THR	THR	ALA	THR	ALA
L9	Y81	ASP	THR	VAL	ILE	GLY	VAL	THR	ALA
A10	C82	VAL	THR	ALA	ALA	ALA	ALA	ALA	ALA
Y11	T88	ARG	ALA	ILE	ALA	ALA	ALA	ALA	ALA
T12	P94	ALA	THR	VAL	VAL	VAL	VAL	VAL	VAL
L13		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
L14		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
V15		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
E16		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
L17		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
Y20		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
Q21		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
F22		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
A23		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
A24		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
P25		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
V26		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
R27		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
Y28		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
T29		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
E30		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
T31		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
Q32		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
Q33		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
Y34		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
I35		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
L36		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
R40		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
T41		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
E42		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
R43		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
L44		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
V45		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
E46		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
L47		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
G48		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
P49		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
S50		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
P51		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
T52		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
M56		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
T60		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
L61		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
Q62		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
S63		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
E66		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
L67		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
Y68		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
T72		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY

A1449	A1450	K1451	R1454	E1457	D1462	E1463	T1464	A1465	Y1466	L1467	R1468	E1469	R1470	H1473	I1474	E1475	R1476	Q1480	E1481	E1482	A1483	A1484	A1485	Q1486	T1487	S1488	F1489	G1490	N1491	R1495	R1496	R1499	I1500	A1501	R1504	G1505	A1506	L1507	A1508	T1509	V1510	G1511	L1512	I1513	I1514	F1522	H1523	G1524	T1525	S1526					
Q1360	V1361	I1362	M1363	Q1366	L1367	A1368	M1371	G1372	V1373	P1374	M1381	T1386	D1387	K1388	I1389	V1393	P1394	A1395	P1396	V1400	L1401	Q1402	T1403	A1404	I1418	K1419	Y1420	R1421	R1422	L1425	E1426	L1427	R1428	Q1430	Q1431	I1432	M1435	L1441	Y1442	L1443	E1446	G1447	S1448	T1449	S1450	S1451	S1452	S1453	S1454						
A1281	T1282	D1288	V1289	T1293	I1294	K1298	A1299	R1300	V1301	C1302	L1303	G1306	F1307	D1308	F1310	Q1311	E1312	E1313	Y1316	E1317	M1321	G1322	A1323	T1324	A1330	R1333	G1334	E1335	P1337	G1338	E1339	M1340	R1341	P1342	P1343	T1344	S1345	T1346	T1347	F1351	M1352	E1353	S1354	Q1355	A1356	C1357									
Y1207	E1208	F1209	Y1210	E1211	F1212	V1213	H1214	L1215	S1216	E1217	V1218	G1219	G1223	S1224	G1225	V1226	T1229	L1232	R1233	G1234	M1235	Y1236	D1237	L1241	I1249	Q1250	P1251	E1252	S1253	F1254	T1257	A1260	M1264	L1265	L1266	L1267	S1268	S1269	T1270	G1271	P1272	I1273	K1274	T1275	P1276	V1277	G1278	A1279	C1280						
V1127	E1128	I1129	F1130	E1131	I1132	Q1137	Y1138	T1139	V1140	E1141	L1142	A1146	T1147	L1148	L1149	I1150	A1153	Q1155	Q1156	D1157	R1158	L1159	A1161	G1162	Q1163	I1164	T1165	G1167	V1168	D1169	A1170	R1171	R1172	Y1173	G1174	V1175	P1176	E1177	I1180	V1183	V1186	T1187	L1188	L1191	L1199	S1200	S1201								
S1048	G1049	W1050	V1051	D1052	T1055	G1056	E1057	P1058	D1063	F1064	K1065	Y1068	E1069	K1070	Y1071	I1072	H1075	I1078	R1079	L1080	I1081	P1082	V1083	E1084	L1085	F1086	Y1089	D1090	P1091	M1092	R1093	K1094	Q1095	L1096	E1099	V1100	V1101	I1102	E1103	Q1104	D1105	L1106	E1107	P1108	K1113	E1117	E1118	F1119	K1120	R1121					
A961	N962	L963	K964	A965	P966	F967	P968	E969	P971	D972	R973	K978	A999	P997	L980	Q983	L984	R985	G986	N987	V988	N989	L990	V995	L996	T997	G998	L999	A1000	E1001	G1003	P1004	H1005	G1006	N1007	A1008	R1011	H1012	E1013	M1014	Y1017	L1022	E1023	M1031	M1032	Y952	N1037	H1038	L1042	R960					
L881	G882	L883	M884	A885	L888	R889	N890	L891	C892	Q893	F898	D900	S901	L901	N902	G903	G904	L905	T888	F907	N908	P909	P910	L911	T847	R848	C849	T850	G851	L852	M853	A855	N856	N857	L858	R859	A860	E861	G862	V863	E864	K865	V868	R869	T870	F871	S872	Q873	Q874	R875	M876	A877	F878	N879	L880
V726	I729	W730	D731	G735	L736	L740	D741	A578	W742	Y743	V744	F745	A747	A748	I749	F750	E751	R754	E755	I756	D757	S758	I759	A766	H767	R768	I769	M770	R696	L771	T772	L777	A780	I781	K782	T783	K786	R793	L799	P800	L801	S802	F808	G809	N810	D811	G812								
G634	I635	Y636	L637	L640	G647	L648	H654	A655	L656	M657	G661	A662	G666	A667	V669	L670	L673	L674	S675	G676	G677	A678	K679	V680	T683	I684	S685	N686	L687	V691	T692	E693	Y694	Y695	Q696	G697	G703	Q708	L709	V710	W711	W712	F713	F714	W715	Q716	L725								
Y486	Y487	V490	S491	I492	P493	T498	D501	A502	R503	G504	N505	I506	Y508	R513	R517	K518	F519	V523	K524	Q525	P526	A527	S533	Q534	Y535	S536	N537	R538	V541	S547	V548	Y549	K550	L551	I552	R553	R554	Q555	H556	R557	N560	S561	S562	S563	L564	Q565	F566	N567							
ALA	I325	T329	K330	D331	Q332	R333	A334	F336	K337	Q338	Q339	L340	I343	L347	D350	L351	R352	A353	F358	V359	A360	S361	Q362	E363	S364	Q365	K366	A367	L368	E378	I382	Y383	I387	E388	D392	K395	A396	R397	V398	Y399	D400	W405	A406	R407	Q408	M413									
Y414	Y415	I417	I418	F419	G420	R421	L422	R423	V424	V425	D426	R427	E428	V430	C433	Q434	Q435	I436	M437	N438	R439	S440	N441	P442	L443	L444	M448	Q449	Y450	H451	I452	D453	H454	C455	P456	T457	E458	T462	Y463	Q464	K467	E468	L469	Q470	Q471	L472	L473	I474	L481	A482	K483				
A568	L569	Y570	V573	I574	R575	A576	A578	M579	N580	G585	GLN	ASP	GLY	LYS	ASP	ARG	ARG	ASN	GLY	ASN	GLY	ASN	ASN	HIS	SER	ARG	PRO	GLY	LYS	VAL	E610	T611	P612	P613	P614	L615	H616	L617	K620	F623	G624	N625	W626	E627	K628	S629	K630	K631	L632	T633					

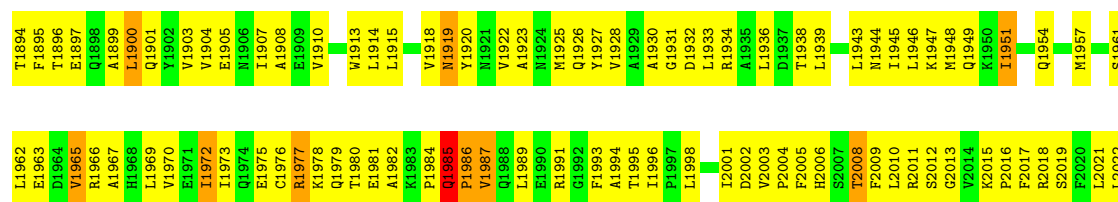


• Molecule 2: FATTY ACID SYNTHASE BETA SUBUNITS

Chain G: 41% 48% 10%

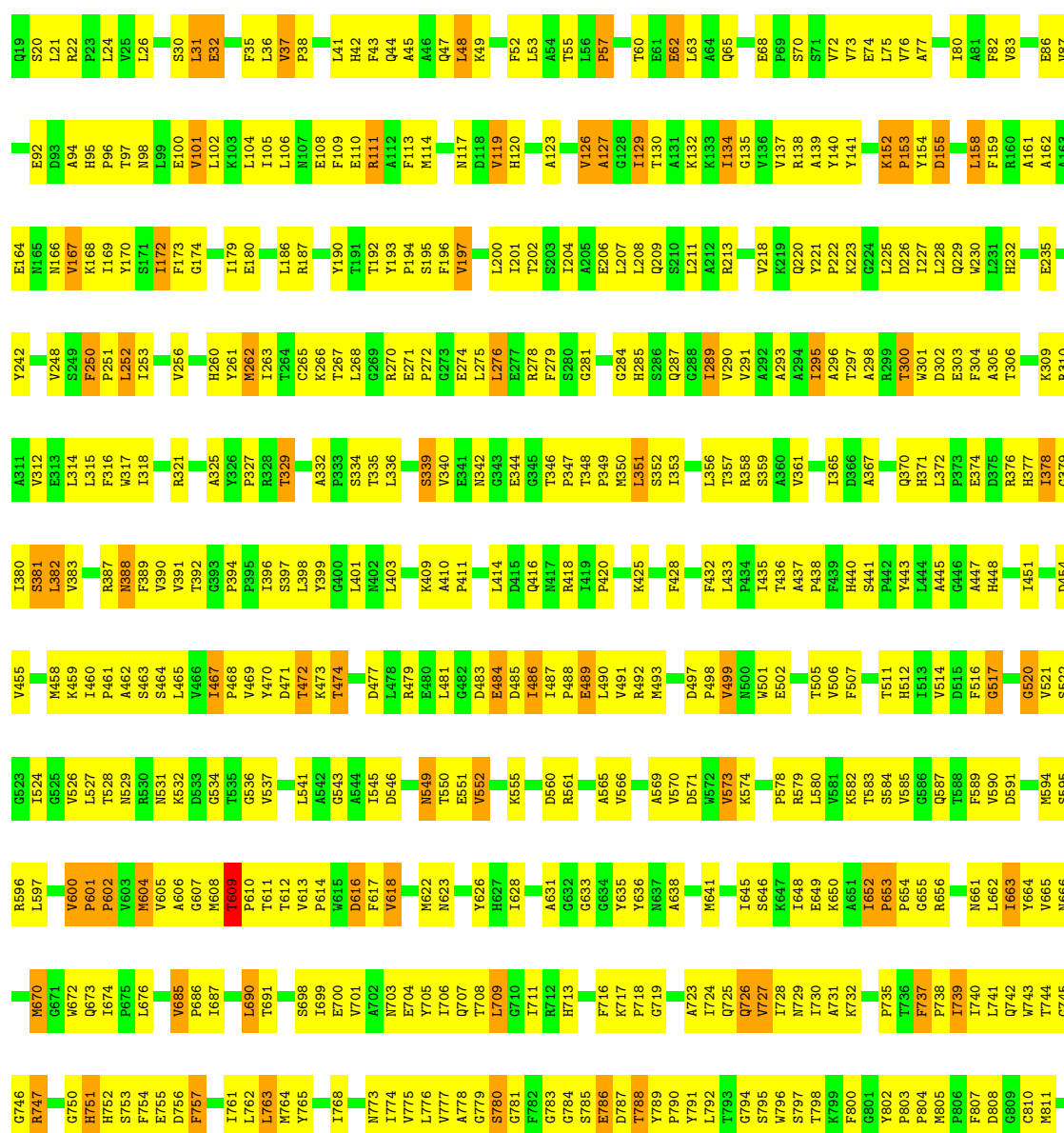






• Molecule 2: FATTY ACID SYNTHASE BETA SUBUNITS

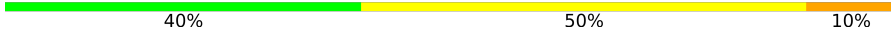
Chain H: 40% 49% 10%





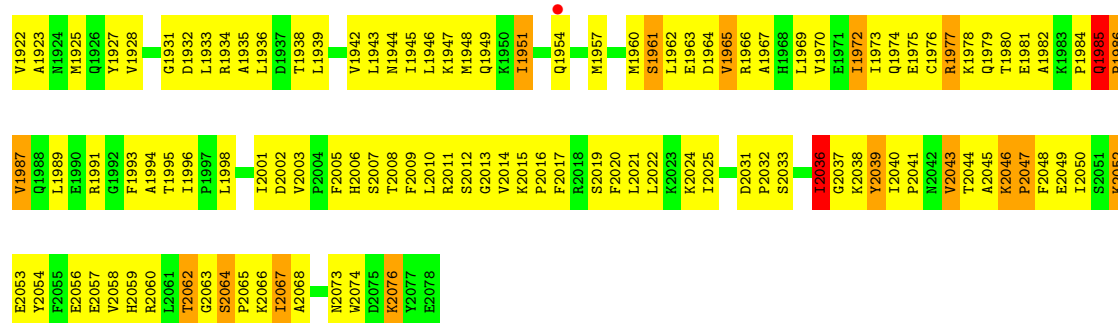
G746	R747	G750	H751	H752	S753	F754	F755	F756	F757	I761	L762	L763	M764	Y765	I768	N773	I774	V775	L776	V777	A778	G779	G780	H781	F782	G783	G784	S785	E786	T787	T788	Y789	P790	L791	L792	L793	G794	S795	V796	S797	T798	K799	F800	G801	Y802	P803	P804	M805	P806	F807	D808	G809	C810	M811	G1940	H1941	V1942	L1943	N1944	I1945	L1946	K1947	M1948	K1949	K1950	I1951	Q1954	M1957	M1960	S1961	L1962	E1963	D1964	V1965	R1966	A1967	H1968	L1969	V1970	E1971	I1972	I1973	Q1974	E1975	C1976	R1977	K1978	Q1979	T1980	E1981	A1982	K1983	P1984	Q1985	P1986	V1987	Q1988	E1989	Y2053	Y2054	E1990	F2055	E2056	E2057	V2058	H2059	R2060	T2061	G2062	S2063	S2064	P2065	K2066	P2004	F2005	H2006	L2007	T2008	F2009	L2010	R2011	S2012	G2013	V2014	K2015	P2016	F2017	T2018	S2019	F2020	L2021	L2022	I2025	T2028	D2031	P2032	S2033	K2034	L2035	R2036	K2037	G2038	Y2039	L2040	P2041	N2042	V2043	T2044	A2045	K2046	P2047	F2048	E2049	L2050	S2051	K2052	E2053	Y2054	F2055	E2056	E2057	V2058	H2059	R2060	T2061	G2062	S2063	S2064	P2065	K2066	I2067	A2068	N2073	W2074	D2075	K2076	Y2077	E2078
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● Molecule 2: FATTY ACID SYNTHASE BETA SUBUNITS

Chain I:  40% 50% 10%

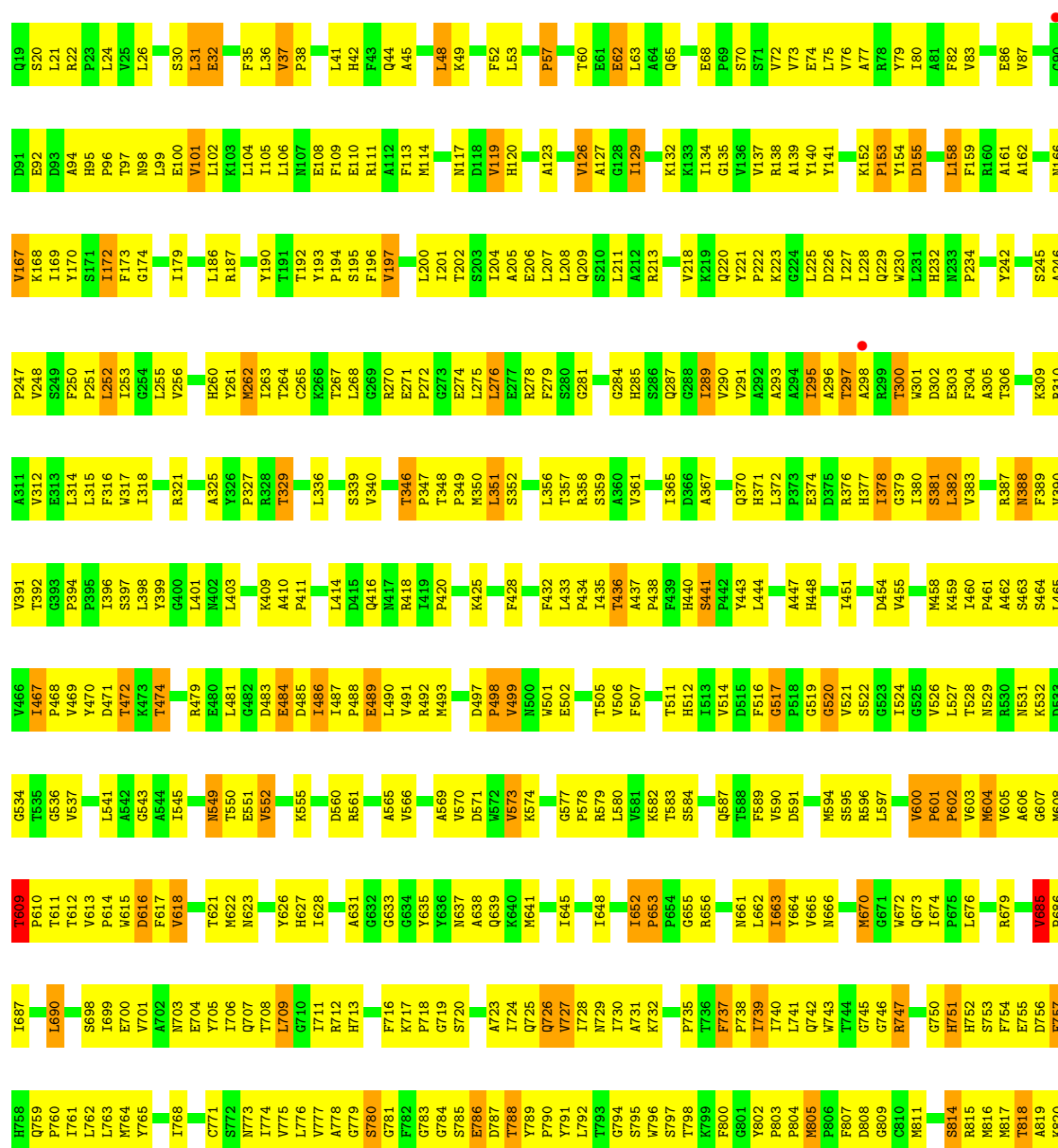
G746	G747	G750	G751	G752	G753	G754	G755	G756	G757	I761	L762	L763	M764	Y765	I768	N773	I774	V775	L776	V777	A778	G779	G780	H781	F782	G783	G784	S785	E786	T787	T788	Y789	P790	L791	L792	L793	G794	S795	V796	S797	T798	K799	F800	G801	Y802	P803	P804	M805	P806	F807	D808	G809	C810	M811																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
Q671	W672	M604	V605	G606	M608	T609	P610	V611	P612	V613	W615	A542	G543	A544	I545	T621	M622	M623	Y626	H627	I628	A631	G632	G633	G634	Y635	Y636	M637	A638	Q639	K640	V641	P645	S646	W647	L648	E649	T652	P653	P654	G655	R656	M661	L662	P663	V664	V665	L741	N666	P667	R668	A669	M670																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
M458	K459	I460	P461	A462	S463	S464	V466	I467	P468	V469	D471	L472	K473	T474	I545	R479	E480	L481	G482	D483	E484	D485	T486	L487	P488	E489	L490	V491	R492	M493	D497	P498	V499	N500	W501	E502	L505	V506	F507	T511	H512	L513	V514	D515	F516	G517	P518	M519	S520	R521	L522	T523	N524	K525	D526	G527	A528	V529	W530	L531	M532	S533	T534	P535	V536	I537	P538	G539	H540	K541	L542	M543	N544	T545	V546	W547	L548	M549	S550	E551	Y552	K553	D554	T555	R556	A557	G558	H559	I560	V561	W562	X563	Y564	Z565	A566	B567	C568	D569	E570	F571	G572	H573	I574	J575	K576	L577	M578	N579	O580	P581	Q582	R583	S584	T585	U586	V587	W588	X589	Y590	Z591	A592	B593	C594	D595	E596	F597	G598	H599	I600	J601	K602	L603	M604	N605	O606	P607	Q608	R609	S610	T611	U612	V613	W614	X615	Y616	Z617	A618	B619	C620	D621	E622	F623	G624	H625	I626	J627	K628	L629	M630	N631	O632	P633	Q634	R635	S636	T637	U638	V639	W640	X641	Y642	Z643	A644	B645	C646	D647	E648	F649	G650	H651	I652	J653	K654	L655	M656	N657	O658	P659	Q660	R661	S662	T663	U664	V665	W666	X667	Y668	Z669	A670	B671	C672	D673	E674	F675	G676	H677	I678	J679	K680	L681	M682	N683	O684	P685	Q686	R687	S688	T689	U690	V691	W692	X693	Y694	Z695	A696	B697	C698	D699	E700	F701	G702	H703	I704	J705	K706	L707	M708	N709	O710	P711	Q712	R713	S714	T715	U716	V717	W718	X719	Y720	Z721	A722	B723	C724	D725	E726	F727	G728	H729	I730	J731	K732	L733	M734	N735	O736	P737	Q738	R739	S740	T741	U742	V743	W744	X745	Y746	Z747	A748	B749	C750	D751	E752	F753	G754	H755	I756	J757	K758	L759	M760	N761	O762	P763	Q764	R765	S766	T767	U768	V769	W770	X771	Y772	Z773	A774	B775	C776	D777	E778	F779	G780	H781	I782	J783	K784	L785	M786	N787	O788	P789	Q790	R791	S792	T793	U794	V795	W796	X797	Y798	Z799	A800	B801	C802	D803	E804	F805	G806	H807	I808	J809	K810	L811	M812	N813	O814	P815	Q816	R817	S818	T819	U820	V821	W822	X823	Y824	Z825	A826	B827	C828	D829	E830	F831	G832	H833	I834	J835	K836	L837	M838	N839	O840	P841	Q842	R843	S844	T845	U846	V847	W848	X849	Y850	Z851	A852	B853	C854	D855	E856	F857	G858	H859	I860	J861	K862	L863	M864	N865	O866	P867	Q868	R869	S870	T871	U872	V873	W874	X875	Y876	Z877	A878	B879	C880	D881	E882	F883	G884	H885	I886	J887	K888	L889	M890	N891	O892	P893	Q894	R895	S896	T897	U898	V899	W900	X901	Y902	Z903	A904	B905	C906	D907	E908	F909	G910	H911	I912	J913	K914	L915	M916	N917	O918	P919	Q920	R921	S922	T923	U924	V925	W926	X927	Y928	Z929	A930	B931	C932	D933	E934	F935	G936	H937	I938	J939	K940	L941	M942	N943	O944	P945	Q946	R947	S948	T949	U950	V951	W952	X953	Y954	Z955	A956	B957	C958	D959	E960	F961	G962	H963	I964	J965	K966	L967	M968	N969	O970	P971	Q972	R973	S974	T975	U976	V977	W978	X979	Y980	Z981	A982	B983	C984	D985	E986	F987	G988	H989	I990	J991	K992	L993	M994	N995	O996	P997	Q998	R999	S1000																																																																																																																																																																																																																				
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● Molecule 2: FATTY ACID SYNTHASE BETA SUBUNITS

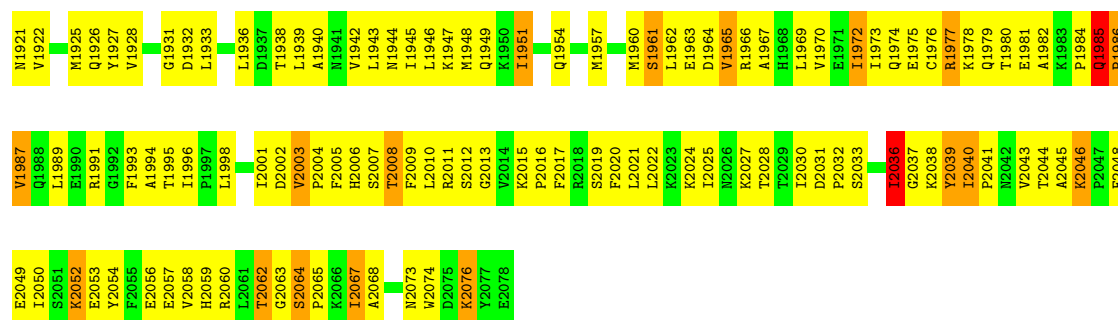
Chain J:  40%  50% 10%



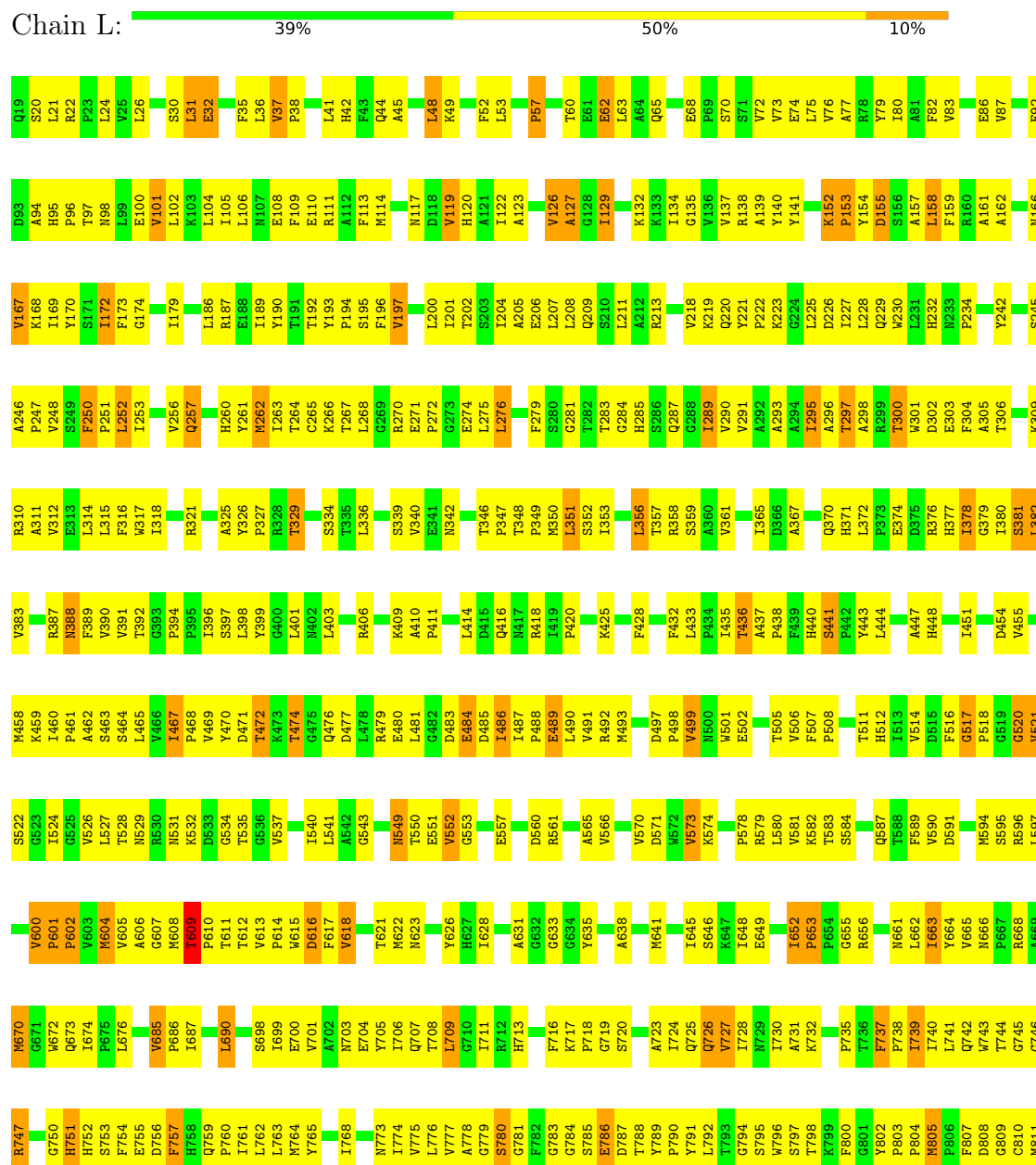




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G1533	G1534	G1535	G1536	G1537	G1538	G1539	G1540	G1541	G1542	G1543	G1544	G1545	G1546	G1547	G1548	G1549	G1550	G1551	G1552	G1553	G1554	G1555	G1556	G1557	G1558	G1559	G1560	G1561	G1562	G1563	G1564	G1565	G1566	G1567	G1568	G1569	G1570	G1571	G1572	G1573	G1574	G1575	G1576	G1577	G1578	G1579	G1580	G1581	G1582	G1583	G1584	G1585	G1586	G1587	G1588	G1589	G1590	G1591	G1592	G1593	G1594	G1595	G1596	G1597	G1598	G1599	G1600	G1601	G1602	G1603	G1604	G1605	G1606	G1607	G1608	G1609	G1610	G1611	G1612																																																																																											
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H1770	S1771	L1772	K1773	K1774	K1775	K1776	K1777	K1778	K1779	K1780	K1781	K1782	K1783	K1784	K1785	K1786	K1787	K1788	K1789	K1790	K1791	K1792	K1793	K1794	K1795	K1796	K1797	K1798	K1799	K1800	K1801	K1802	K1803	K1804	K1805	K1806	K1807	K1808	K1809	K1810	K1811	K1812	K1813	K1814	K1815	K1816	K1817	K1818	K1819	K1820	K1821	K1822	K1823	K1824	K1825	K1826	K1827	K1828	K1829	K1830	K1831	K1832	K1833	K1834	K1835	K1836	K1837	K1838	K1839	K1840	K1841	K1842	K1843	K1844	K1845	K1846	K1847	K1848	K1849	K1850	K1851	K1852																																																																																								
L1853	L1854	S1855	L1856	L1857	S1858	L1859	L1860	L1861	L1862	L1863	L1864	L1865	L1866	L1867	L1868	L1869	L1870	L1871	L1872	L1873	L1874	L1875	L1876	L1877	L1878	L1879	L1880	L1881	L1882	L1883	L1884	L1885	L1886	L1887	L1888	L1889	L1890	L1891	L1892	L1893	L1894	L1895	L1896	L1897	L1898	L1899	L1900	L1901	L1902	L1903	L1904	L1905	L1906	L1907	L1908	L1909	L1910	L1911	L1912	L1913	L1914	L1915	L1916	L1917	L1918	L1919	L1920																																																																																																							
P804	M805	P806	P807	P808	P809	P810	P811	P812	P813	P814	P815	P816	P817	P818	P819	P820	P821	P822	P823	P824	P825	P826	P827	P828	P829	P830	P831	P832	P833	P834	P835	P836	P837	P838	P839	P840	P841	P842	P843	P844	P845	P846	P847	P848	P849	P850	P851	P852	P853	P854	P855	P856	P857	P858	P859	P860	P861	P862	P863	P864	P865	P866	P867	P868	P869	P870																																																																																																								
L868	A869	T870	R871	Q872	G873	H874	F875	H876	K877	E878	K879	L880	L881	L882	L883	L884	L885	L886	L887	L888	L889	L890	L891	L892	L893	L894	L895	L896	L897	L898	L899	L900	L901	L902	L903	L904	L905	L906	L907	L908	L909	L910	L911	L912	L913	L914	L915	L916	L917	L918	L919	L920	L921	L922	L923	L924	L925	L926	L927	L928	L929	L930	L931	L932	L933	L934	L935	L936	L937																																																																																																					
M938	L941	M942	M943	M944	M945	M946	M947	M948	M949	M950	M951	M952	M953	M954	M955	M956	M957	M958	M959	M960	M961	M962	M963	M964	M965	M966	M967	M968	M969	M970	M971	M972	M973	M974	M975	M976	M977	M978	M979	M980	M981	M982	M983	M984	M985	M986	M987	M988	M989	M990	M991	M992	M993	M994	M995	M996	M997	M998	M999	P1000	E1001	E1002	E1003	E1004	E1005	E1006	E1007	E1008	E1009	E1010																																																																																																				
Q1011	D1012	Y1013	Q1014	H1015	F1016	L1017	L1018	L1019	Q1020	Q1021	R1022	K1023	P1024	Y1025	Y1026	Y1027	Y1028	Y1029	Y1030	Y1031	Y1032	Y1033	Y1034	Y1035	Y1036	Y1037	Y1038	Y1039	Y1040	Y1041	Y1042	Y1043	Y1044	Y1045	Y1046	Y1047	Y1048	Y1049	Y1050	Y1051	Y1052	Y1053	Y1054	Y1055	Y1056	Y1057	Y1058	Y1059	Y1060	Y1061	Y1062	Y1063	Y1064	Y1065	Y1066	Y1067	Y1068	Y1069	Y1070	Y1071	Y1072	Y1073	Y1074	Y1075	Y1076	Y1077	Y1078	Y1079	Y1080																																																																																																					
E1081	P1082	I1083	K1084	I1085	I1086	L1087	D1088	G1089	H1090	H1091	H1092	D1093	H1094	I1095	K1096	F1097	L1098	L1099	L1100	L1101	L1102	L1103	L1104	L1105	L1106	L1107	L1108	L1109	L1110	L1111	L1112	L1113	L1114	L1115	L1116	L1117	L1118	L1119	L1120	L1121	L1122	L1123	L1124	L1125	L1126	L1127	L1128	L1129	L1130	L1131	L1132	L1133	L1134	L1135	L1136	L1137	L1138	L1139	L1140	L1141	L1142	L1143	L1144	L1145	L1146	L1147	L1148	L1149	L1150	L1151	L1152	L1153	L1154	L1155	L1156	L1157																																																																																														
P1158	S1159	F1160	L1161	L1162	L1163	L1164	L1165	L1166	L1167	L1168	L1169	L1170	L1171	L1172	L1173	L1174	L1175	L1176	L1177	L1178	L1179	L1180	L1181	L1182	L1183	L1184	L1185	L1186	L1187	L1188	L1189	L1190	L1191	L1192	L1193	L1194	L1195	L1196	L1197	L1198	L1199	L1200	L1201	L1202	L1203	L1204	L1205	L1206	L1207	L1208	L1209	L1210	L1211	L1212	L1213	L1214	L1215	L1216	L1217	L1218	L1219	L1220	L1221	L1222	L1223	L1224	L1225	L1226	L1227	L1228	L1229	L1230																																																																																																		
T1231	V1232	E1233	I1234	L1235	L1236	L1237	G1238	D1239	N1240	E1241	I1242	I1243	L1244	L1245	L1246	L1247	L1248	L1249	L1250	L1251	L1252	L1253	L1254	L1255	L1256	L1257	L1258	L1259	L1260	L1261	L1262	L1263	L1264	L1265	L1266	L1267	L1268	L1269	L1270	L1271	L1272	L1273	L1274	L1275	L1276	L1277	L1278	L1279	L1280	L1281	L1282	L1283	L1284	L1285	L12																																																																																																																			



● Molecule 2: FATTY ACID SYNTHASE BETA SUBUNITS



A1846	T1768	P1688	M1610	D1529	M1454	P1384	V1237	M1167	I1086	L1018	V950	E878	S814
L1847	V1769	V1689	Y1611	Y1530	Q1455	P1388	G1238	S1168	L1087	L1019	Y951	K882	R815
A1848	M1770	L1690	T1612	G1533	L1456	L1389	N1239	V1169	D1088	Q1020	P952	I883	M816
M1851	S1774	Y1692	V1616	G1537	H1457	L1390	N1240	Y1171	G1089	Q1021	P953	T817	M818
P1852	K1776	Q1700	R1617	N1538	T1460	V1391	I1242	R1172	H1091	R1022	Y955	D887	M819
I1853	Q1701	V1701	V1620	P1539	P1461	G1392	A1243	H1173	D1092	R1023	K956	R888	A819
E1854	K1779	E1621	E1621	P1540	Q1462	D1393	L1244	A1174	D1093	K1026	T959	S889	K820
S1855	L1780	M1705	W1623	V1540	D1463	V1394	L1245	M1175	H1094	P1027	T959	R890	K821
L1856	F1781	G1704	W1623	I1541	L1464	L1395	F1247	F1176	I1095	V1028	F962	R891	A822
S1857	M1706	M1706	W1623	D1542	A1465	D1396	L1247	T1177	K1096	P1029	F962	E894	H823
E1783	D1707	Y1543	A1624	Y1543	V1466	T1397	E1248	T1178	F1097	F1030	Y963	T824	T824
V1859	L1708	S1550	A1624	Y1543	L1467	L1397	G1249	E1179	L1098	Y1031	R964	S825	S825
V1860	Y1709	I1551	R1468	S1550	R1468	Q1400	R1250	V1180	L1099	P1032	R965	K887	K826
F1861	K1716	E1552	S1469	I1551	S1469	I1401	T1251	F1181	R1100	A1033	V966	R898	Q827
L1865	R1721	E1552	W1472	E1552	W1472	N1402	V1257	R1186	Y1103	E1036	E967	R899	A828
M1867	A1722	Q1553	F1473	P1554	F1473	A1403	P1258	F1187	D1104	W1041	E968	D900	K829
Q1868	K1723	S1634	K1474	V1555	K1474	V1404	L1259	Q1188	G1105	K1044	R969	Y901	Q830
L1799	K1724	W1636	L1475	P1560	L1475	N1406	F1261	T1189	K1106	Y1048	S977	I902	A831
V1800	K1725	H1637	T1481	I1561	T1481	S1409	F1262	M1190	E1107	Q1049	L979	I903	I832
S1801	F1726	P1637	E1482	I1561	E1482	G1410	R1263	L1192	V1110	D1045	L979	K904	V833
L1802	R1727	M1638	L1483	L1563	L1483	M1411	Y1265	L1193	V1112	S1046	S977	K905	D834
T1803	E1728	M1639	L1484	G1565	L1484	M1412	Y1265	L1193	V1112	D1062	L979	I906	A835
R1873	N1729	M1642	T1487	K1566	T1487	V1413	H1266	L1195	I1113	E1051	L979	N907	P836
D1874	K1730	W1643	R1491	K1567	R1491	C1416	E1268	F1196	E1114	Q1050	L979	D908	G837
G1877	K1731	P1567	L1492	P1568	L1492	K1420	G1270	P1198	F1116	Y1050	L979	Q911	V838
F1805	I1735	M1645	L1492	P1568	L1492	K1420	G1270	P1198	F1116	E1051	L979	K912	D840
T1808	P1808	N1646	R1421	P1574	R1421	G1353	Y1271	R1200	R1119	I1062	L986	V913	Q842
L1809	K1738	W1646	V1496	M1577	V1496	K1424	A1272	R1200	R1119	I1063	D987	W914	W843
L1810	K1739	T1650	R1497	M1577	R1497	K1424	A1272	R1200	R1119	Y1057	D987	W914	W843
L1812	N1740	T1650	F1498	E1578	F1498	P1425	P1273	Y1203	A1123	G1068	E983	F915	E844
M1813	N1741	T1650	K1499	M1579	K1499	P1426	R1275	V1204	A1123	Q1059	P989	G916	N845
E1814	K1742	L1653	M1500	M1579	M1500	M1427	R1275	V1204	A1123	D1060	P991	R917	T846
A1885	K1743	L1653	V1503	V1583	V1503	K1359	M1278	T1207	D1125	V1061	A992	N918	Y847
V1886	E1744	H1654	V1503	S1584	V1503	K1359	M1278	T1207	D1125	G1062	D994	V924	T851
N1887	L1745	V1656	V1504	S1584	V1504	V1428	E1279	M1208	E1126	R1063	D994	D925	D925
P1888	T1746	G1657	S1505	D1586	S1505	V1429	G1280	P1209	E1127	T1066	R995	L926	V854
S1889	F1749	M1658	S1506	D1586	S1506	V1429	G1280	P1209	E1127	T1066	R995	E927	I855
R1890	G1750	I1659	V1507	N1588	V1507	K1362	R1281	P1212	L1133	T1067	L997	E927	T856
I1891	G1751	P1589	V1507	N1588	V1507	P1363	R1281	P1212	L1133	L1066	L997	M929	V857
T1894	G1752	P1589	V1507	N1588	V1507	P1363	R1281	P1212	L1133	L1066	L997	T930	L858
F1895	P1752	H1591	V1510	I1590	V1510	K1365	F1288	T1215	A1135	Q1068	Y1000	Y931	S859
L1896	G1753	H1591	V1510	I1590	V1510	K1365	F1288	T1215	A1135	Q1068	Y1000	A932	E860
E1897	K1754	V1592	V1513	V1592	V1513	G1437	R1290	I1217	D1138	P1070	E1002	A932	E860
Q1898	K1755	V1592	V1513	V1592	V1513	G1437	R1290	I1217	D1138	V1071	E1002	A932	E860
A1899	L1756	V1596	V1513	V1596	V1513	V1439	V1293	S1218	K1141	A1072	S1004	E933	M861
L1900	I1757	F1596	V1517	F1596	V1517	V1439	V1293	S1218	K1141	A1072	S1004	E933	M861
F1833	K1758	S1597	V1517	F1596	V1517	V1439	V1293	S1218	K1141	A1072	S1004	E933	M861
Q1901	Q1759	S1597	V1517	F1596	V1517	V1439	V1293	S1218	K1141	A1072	S1004	E933	M861
A1934	T1760	N1601	V1519	N1601	V1519	V1444	L1305	V1229	D1156	V1078	A1010	L941	L868
V1903	L1761	L1602	K1520	N1444	K1520	N1444	L1305	V1229	D1156	V1078	A1010	L941	L868
G1839	M1762	E1676	E1521	T1445	E1521	T1445	L1305	V1229	D1156	V1078	A1010	L941	L868
V1904	S1677	P1603	I1522	F1446	I1522	F1446	L1305	V1229	D1156	V1078	A1010	L941	L868
E1905	G1604	G1604	I1523	Q1447	I1523	Q1447	L1305	V1229	D1156	V1078	A1010	L941	L868
N1906	M1764	L1679	Q1524	R1448	Q1524	R1448	G1311	E1233	F1180	F1082	Q1014	K945	K871
I1907	T1765	L1684	V1525	V1452	V1525	V1452	E1314	I1234	I1164	I1083	F1015	H946	F875
A1908	F1766	E1684	V1525	V1452	V1525	V1452	E1314	I1234	I1164	I1083	F1015	H946	F875
E1909	E1767	V1528	V1528	P1453	V1528	P1453	L1315	L1236	L1164	D1085	L1017	E947	K877

Y2039	C1976	V1910
I2040	R1977	
P2041	K1978	W1913
N2042	Q1979	L1914
Z2043	T1980	L1915
T2044	E1981	
A2045	A1982	V1918
K2046	L1983	N1919
P2047	P1984	V1920
F2048	Q1985	N1921
E2049	P1986	V1922
I2050	V1987	A1923
S2051	Q1988	M1924
K2052	L1989	M1925
E2053	E1990	Q1926
Y2054	R1991	V1927
F2055	G1992	V1928
E2056	F1993	A1929
V2057	A1994	A1930
V2058	T1995	G1931
H2059	I1996	D1932
R2060	P1997	L1933
L2061	L1998	R1934
		A1935
T2062	T2001	A1936
G2063	D2002	D1937
S2064	V2003	T1938
P2065	P2004	L1939
K2066	F2005	A1940
I2067	H2006	
A2068	S2007	L1943
	T2008	M1944
N2073	F2009	I1945
D2074	L2010	L1946
D2075	R2011	K1947
K2076	G2012	M1948
Y2077	G2013	Q1949
E2078	V2014	K1950
	T2015	I1951
	P2016	
	F2017	Q1954
	R2018	
	S2019	M1957
	F2020	
	L2021	M1960
	L2022	S1961
		L1962
	T2025	E1963
	N2026	D1964
	K2027	V1965
		R1966
	T2030	A1967
	D2031	H1968
	P2032	L1969
	S2033	V1970
	K2034	E1971
	L2035	I1972
	L2036	L1973
	K2037	G1974
	V2038	V1975

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	215.78Å 412.67Å 220.90Å 90.00° 111.57° 90.00°	Depositor
Resolution (Å)	12.00 – 3.10 12.00 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.7 (12.00-3.10) 98.0 (12.00-3.10)	Depositor EDS
R_{merge}	0.24	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.89 (at 3.13Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.270 , 0.300 0.251 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	66.0	Xtriage
Anisotropy	0.182	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.20 , 0.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.39$, $\langle L^2 \rangle = 0.21$	Xtriage
Estimated twinning fraction	0.078 for l,-k,h	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	167247	wwPDB-VP
Average B, all atoms (Å ²)	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.40% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NAP, 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	0.55	0/11744	0.94	35/15873 (0.2%)
1	B	0.54	0/11801	0.93	33/15949 (0.2%)
1	C	0.55	0/11785	0.94	34/15928 (0.2%)
1	D	0.52	0/11824	0.94	29/15980 (0.2%)
1	E	0.53	0/11736	0.93	27/15863 (0.2%)
1	F	0.57	0/11776	0.95	46/15916 (0.3%)
2	G	0.47	0/16573	0.89	38/22516 (0.2%)
2	H	0.45	0/16573	0.90	29/22516 (0.1%)
2	I	0.45	0/16573	0.90	37/22516 (0.2%)
2	J	0.44	0/16573	0.90	33/22516 (0.1%)
2	K	0.48	0/16573	0.92	33/22516 (0.1%)
2	L	0.46	1/16573 (0.0%)	0.90	35/22516 (0.2%)
All	All	0.50	1/170104 (0.0%)	0.92	409/230605 (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	1
1	F	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L	1125	ASP	CA-C	-6.61	1.47	1.53

The worst 5 of 409 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	802	SER	CA-C-N	10.07	129.87	119.19
1	C	802	SER	C-N-CA	10.07	129.87	119.19
1	F	1107	GLU	CA-C-N	10.02	130.08	119.76
1	F	1107	GLU	C-N-CA	10.02	130.08	119.76
1	D	1107	GLU	CA-C-N	9.97	130.03	119.76

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	578	ALA	Peptide
1	F	613	PRO	Peptide

5.2 Too-close contacts [i](#)

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	11514	0	11476	783	1
1	B	11571	0	11529	740	1
1	C	11555	0	11507	744	0
1	D	11593	0	11552	763	0
1	E	11506	0	11467	790	0
1	F	11546	0	11499	733	0
2	G	16200	0	16081	1344	1
2	H	16200	0	16081	1373	1
2	I	16200	0	16081	1393	0
2	J	16200	0	16081	1385	0
2	K	16200	0	16081	1449	0
2	L	16200	0	16081	1424	0
3	A	48	0	25	5	0
3	B	48	0	25	5	0
3	C	48	0	25	4	0
3	D	48	0	25	6	0
3	E	48	0	25	4	0
3	F	48	0	25	4	0
3	G	48	0	25	4	0
3	H	48	0	25	5	0
3	I	48	0	25	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	J	48	0	25	4	0
3	K	48	0	25	4	0
3	L	48	0	25	4	0
4	G	31	0	19	14	0
4	H	31	0	19	13	0
4	I	31	0	19	14	0
4	J	31	0	19	15	0
4	K	31	0	19	13	0
4	L	31	0	19	14	0
All	All	167247	0	165930	12268	2

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 37.

The worst 5 of 12268 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:F:1443:LEU:HD21	1:F:1470:ARG:HB3	1.18	1.17
1:B:1268:SER:HB3	1:D:1389:ILE:HG13	1.23	1.16
1:D:1504:ARG:HG3	1:D:1504:ARG:HH11	1.02	1.15
1:F:1504:ARG:HH11	1:F:1504:ARG:HG3	1.04	1.15
1:C:1443:LEU:HD21	1:C:1470:ARG:HB3	1.18	1.14

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:575:ARG:NH1	2:H:164:GLU:O[2_555]	2.01	0.19
1:B:1452:SER:O	2:G:1092:ASN:ND2[1_556]	2.18	0.02

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 X-ray entries followed by that with respect to entries of similar resolution.

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	1451/1878 (77%)	1270 (88%)	164 (11%)	17 (1%)	10	37
1	B	1458/1878 (78%)	1278 (88%)	160 (11%)	20 (1%)	9	34
1	C	1456/1878 (78%)	1283 (88%)	156 (11%)	17 (1%)	10	37
1	D	1461/1878 (78%)	1276 (87%)	161 (11%)	24 (2%)	7	30
1	E	1450/1878 (77%)	1276 (88%)	155 (11%)	19 (1%)	9	35
1	F	1455/1878 (78%)	1282 (88%)	153 (10%)	20 (1%)	9	34
2	G	2058/2060 (100%)	1789 (87%)	237 (12%)	32 (2%)	7	30
2	H	2058/2060 (100%)	1791 (87%)	230 (11%)	37 (2%)	6	28
2	I	2058/2060 (100%)	1787 (87%)	238 (12%)	33 (2%)	7	30
2	J	2058/2060 (100%)	1784 (87%)	240 (12%)	34 (2%)	7	30
2	K	2058/2060 (100%)	1785 (87%)	239 (12%)	34 (2%)	7	30
2	L	2058/2060 (100%)	1780 (86%)	241 (12%)	37 (2%)	6	28
All	All	21079/23628 (89%)	18381 (87%)	2374 (11%)	324 (2%)	8	32

5 of 324 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	614	PHE
1	A	1566	LYS
1	B	614	PHE
1	B	624	GLY
1	B	1566	LYS

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 X-ray entries followed by that with respect to entries of similar resolution.

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	1220/1527 (80%)	1089 (89%)	131 (11%)	6	25
1	B	1227/1527 (80%)	1093 (89%)	134 (11%)	6	24
1	C	1225/1527 (80%)	1091 (89%)	134 (11%)	6	24
1	D	1229/1527 (80%)	1093 (89%)	136 (11%)	6	24

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	1219/1527 (80%)	1084 (89%)	135 (11%)	6	24
1	F	1224/1527 (80%)	1094 (89%)	130 (11%)	6	26
2	G	1752/1752 (100%)	1527 (87%)	225 (13%)	4	18
2	H	1752/1752 (100%)	1522 (87%)	230 (13%)	4	17
2	I	1752/1752 (100%)	1528 (87%)	224 (13%)	4	18
2	J	1752/1752 (100%)	1523 (87%)	229 (13%)	4	17
2	K	1752/1752 (100%)	1526 (87%)	226 (13%)	4	18
2	L	1752/1752 (100%)	1525 (87%)	227 (13%)	4	18
All	All	17856/19674 (91%)	15695 (88%)	2161 (12%)	5	20

5 of 2161 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	K	1265	TYR
2	K	1803	THR
2	K	1250	ARG
2	L	1265	TYR
1	F	1462	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 518 such sidechains are listed below:

Mol	Chain	Res	Type
2	L	65	GLN
2	L	529	ASN
2	L	47	GLN
2	G	260	HIS
2	G	44	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

18 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
3	NAP	I	2102	-	50,52,52	1.15	5 (10%)	71,80,80	1.58	9 (12%)
3	NAP	H	2102	-	50,52,52	1.28	6 (12%)	71,80,80	1.54	8 (11%)
3	NAP	E	1901	-	50,52,52	1.22	4 (8%)	71,80,80	1.63	12 (16%)
3	NAP	B	1901	-	50,52,52	1.23	4 (8%)	71,80,80	1.54	12 (16%)
3	NAP	J	2102	-	50,52,52	1.28	5 (10%)	71,80,80	1.57	11 (15%)
4	FMN	G	2101	-	33,33,33	6.33	23 (69%)	48,50,50	1.35	9 (18%)
3	NAP	A	1901	-	50,52,52	1.27	4 (8%)	71,80,80	1.49	9 (12%)
3	NAP	D	1901	-	50,52,52	1.45	6 (12%)	71,80,80	1.58	11 (15%)
4	FMN	I	2101	-	33,33,33	6.26	23 (69%)	48,50,50	1.37	8 (16%)
4	FMN	K	2101	-	33,33,33	6.53	24 (72%)	48,50,50	1.45	11 (22%)
4	FMN	L	2101	-	33,33,33	6.31	21 (63%)	48,50,50	1.36	10 (20%)
3	NAP	K	2102	-	50,52,52	1.25	7 (14%)	71,80,80	1.58	9 (12%)
4	FMN	H	2101	-	33,33,33	6.34	23 (69%)	48,50,50	1.29	6 (12%)
3	NAP	C	1901	-	50,52,52	1.36	7 (14%)	71,80,80	1.57	11 (15%)
4	FMN	J	2101	-	33,33,33	6.62	24 (72%)	48,50,50	1.37	8 (16%)
3	NAP	G	2102	-	50,52,52	1.28	6 (12%)	71,80,80	1.59	11 (15%)
3	NAP	L	2102	-	50,52,52	1.21	5 (10%)	71,80,80	1.56	9 (12%)
3	NAP	F	1901	-	50,52,52	1.29	5 (10%)	71,80,80	1.50	14 (19%)

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
3	NAP	I	2102	-	-	11/35/67/67	0/5/5/5
3	NAP	H	2102	-	-	12/35/67/67	0/5/5/5
3	NAP	E	1901	-	-	11/35/67/67	0/5/5/5
3	NAP	B	1901	-	-	11/35/67/67	0/5/5/5
3	NAP	J	2102	-	-	13/35/67/67	0/5/5/5
4	FMN	G	2101	-	-	5/18/18/18	0/3/3/3
3	NAP	A	1901	-	-	11/35/67/67	0/5/5/5
3	NAP	D	1901	-	-	11/35/67/67	0/5/5/5
4	FMN	I	2101	-	-	5/18/18/18	0/3/3/3
4	FMN	K	2101	-	-	5/18/18/18	0/3/3/3
4	FMN	L	2101	-	-	5/18/18/18	0/3/3/3
3	NAP	K	2102	-	-	11/35/67/67	0/5/5/5
4	FMN	H	2101	-	-	5/18/18/18	0/3/3/3
3	NAP	C	1901	-	-	11/35/67/67	0/5/5/5
4	FMN	J	2101	-	-	5/18/18/18	0/3/3/3
3	NAP	G	2102	-	-	13/35/67/67	0/5/5/5
3	NAP	L	2102	-	-	10/35/67/67	0/5/5/5
3	NAP	F	1901	-	-	11/35/67/67	0/5/5/5

The worst 5 of 202 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	J	2101	FMN	C9-C8	13.60	1.58	1.39
4	J	2101	FMN	C6-C7	13.51	1.58	1.39
4	K	2101	FMN	C6-C7	13.45	1.57	1.39
4	H	2101	FMN	C6-C7	13.29	1.57	1.39
4	G	2101	FMN	C6-C7	12.86	1.57	1.39

The worst 5 of 178 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	I	2102	NAP	N3A-C2A-N1A	-6.06	119.41	128.58
3	D	1901	NAP	N3A-C2A-N1A	-6.03	119.45	128.58
3	G	2102	NAP	N3A-C2A-N1A	-5.81	119.78	128.58
3	J	2102	NAP	N3A-C2A-N1A	-5.80	119.80	128.58
3	L	2102	NAP	N3A-C2A-N1A	-5.75	119.88	128.58

There are no chirality outliers.

5 of 166 torsion outliers are listed below:

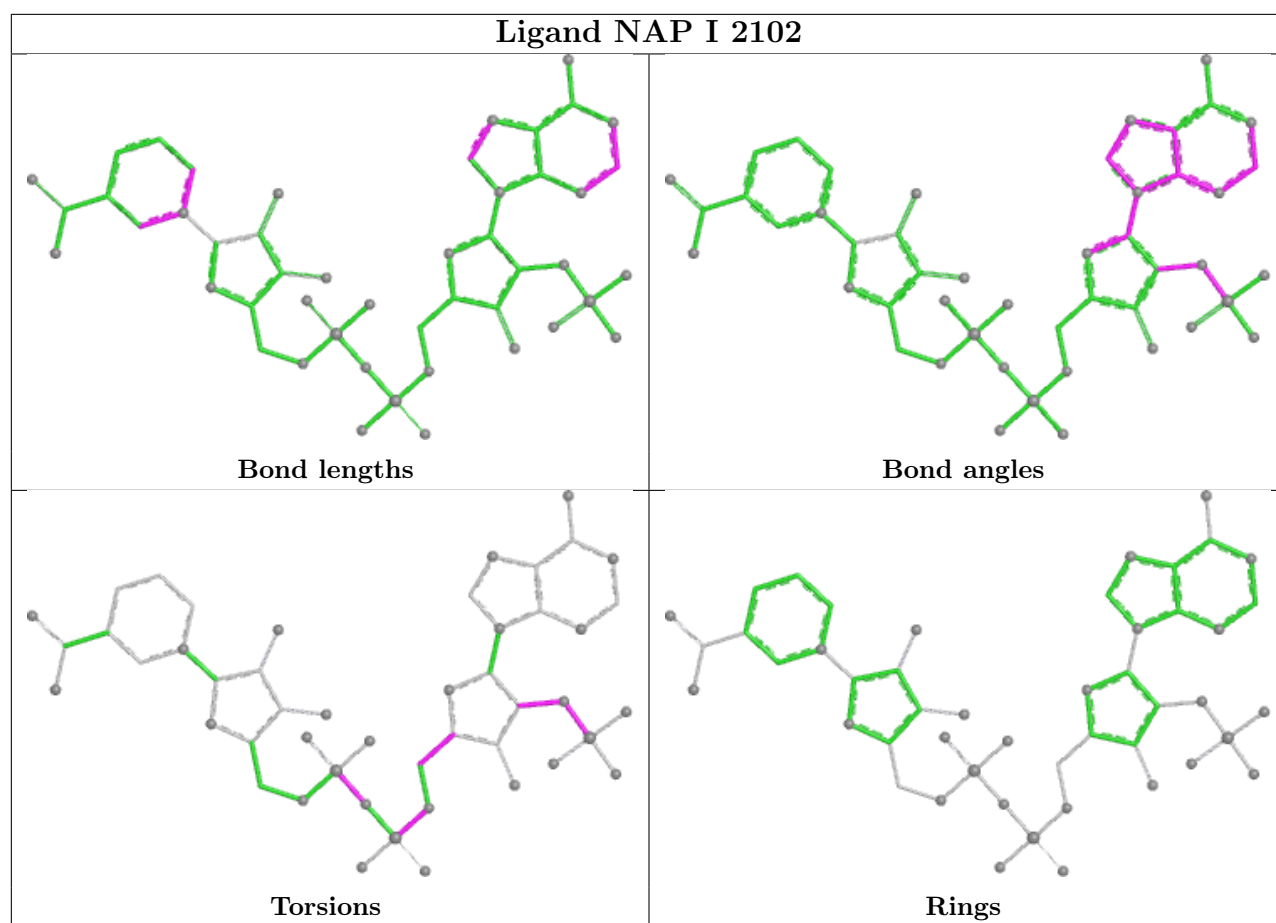
Mol	Chain	Res	Type	Atoms
3	A	1901	NAP	C5B-O5B-PA-O3
3	A	1901	NAP	PA-O3-PN-O5D
3	A	1901	NAP	C5D-O5D-PN-O3
3	A	1901	NAP	C5D-O5D-PN-O1N
3	A	1901	NAP	C5D-O5D-PN-O2N

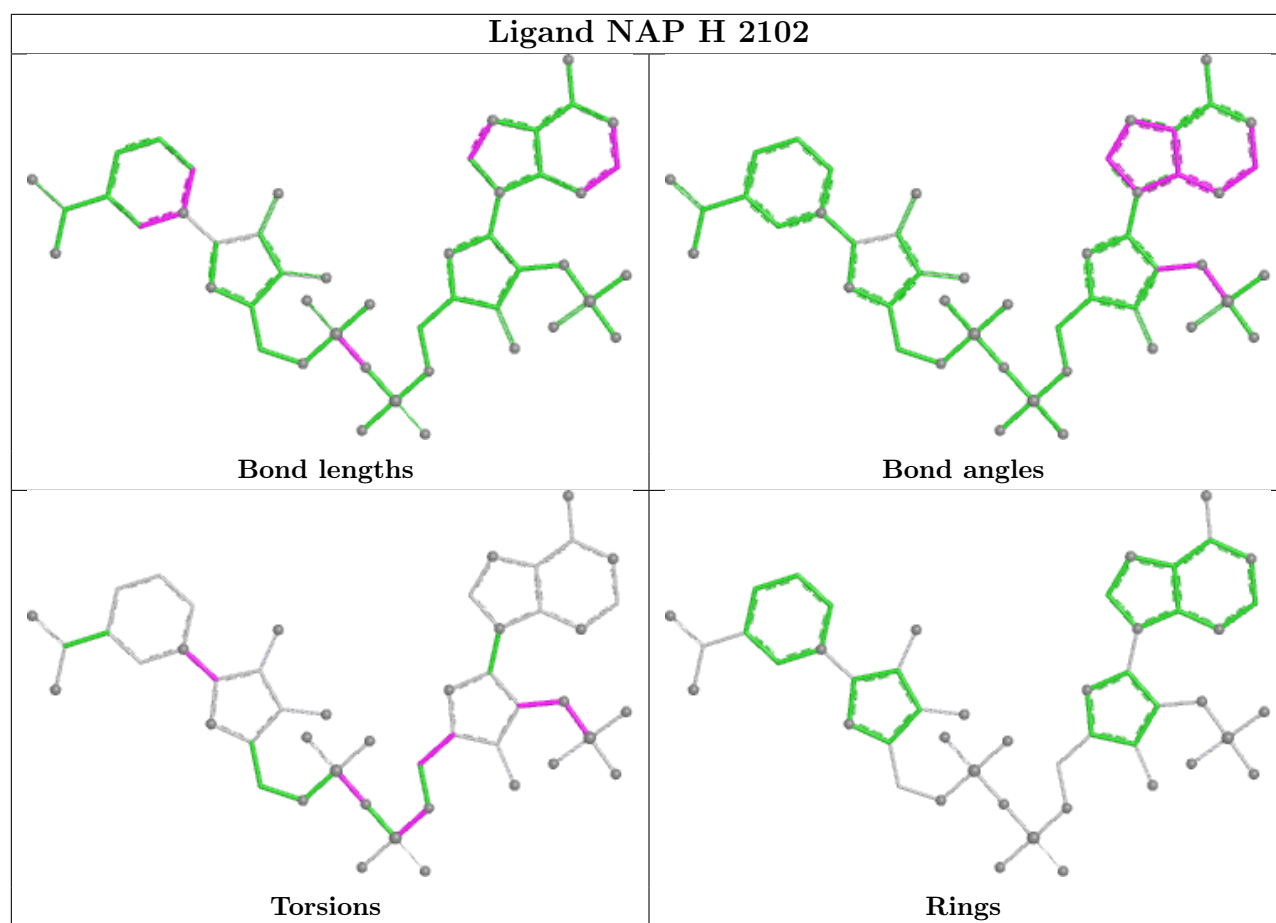
There are no ring outliers.

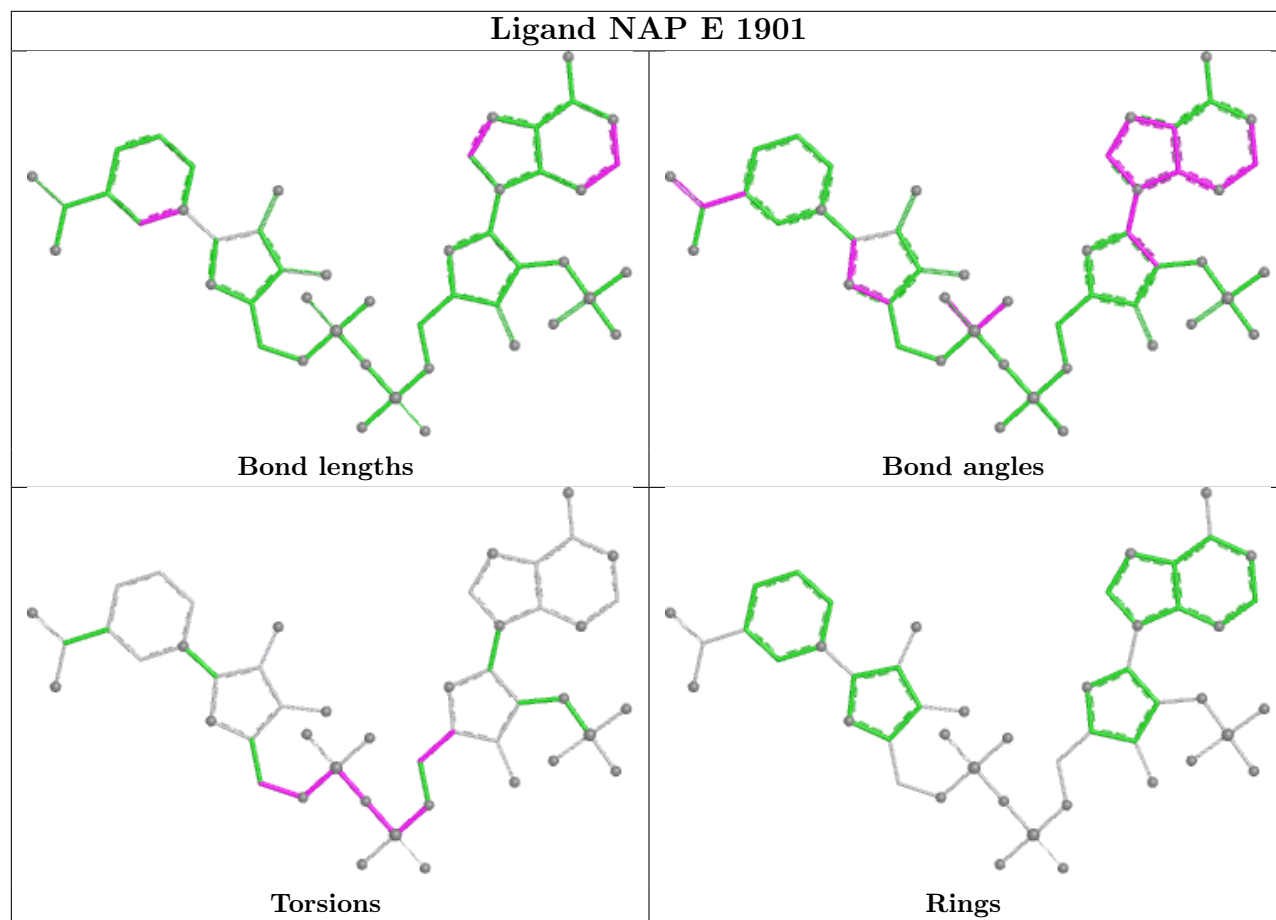
18 monomers are involved in 136 short contacts:

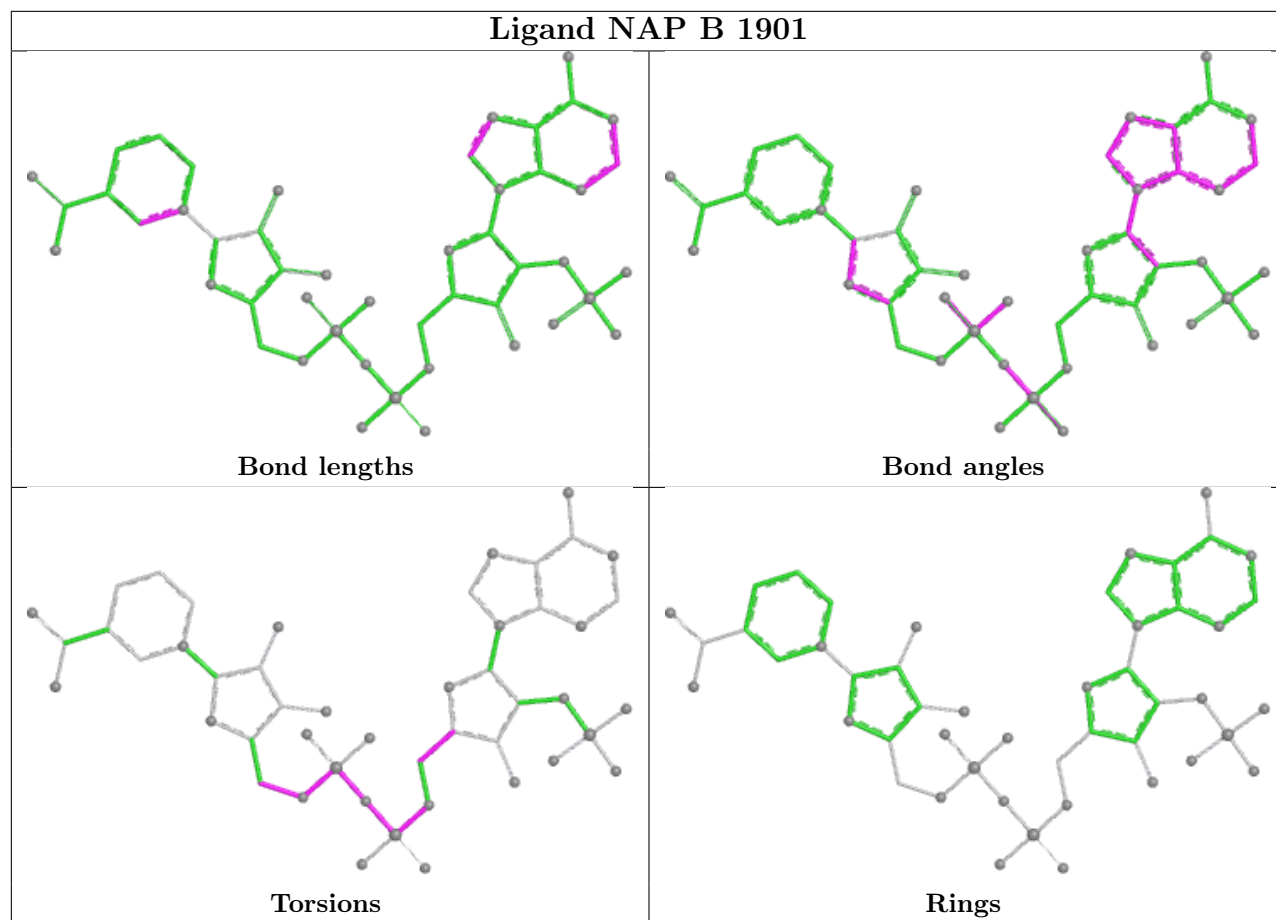
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	I	2102	NAP	4	0
3	H	2102	NAP	5	0
3	E	1901	NAP	4	0
3	B	1901	NAP	5	0
3	J	2102	NAP	4	0
4	G	2101	FMN	14	0
3	A	1901	NAP	5	0
3	D	1901	NAP	6	0
4	I	2101	FMN	14	0
4	K	2101	FMN	13	0
4	L	2101	FMN	14	0
3	K	2102	NAP	4	0
4	H	2101	FMN	13	0
3	C	1901	NAP	4	0
4	J	2101	FMN	15	0
3	G	2102	NAP	4	0
3	L	2102	NAP	4	0
3	F	1901	NAP	4	0

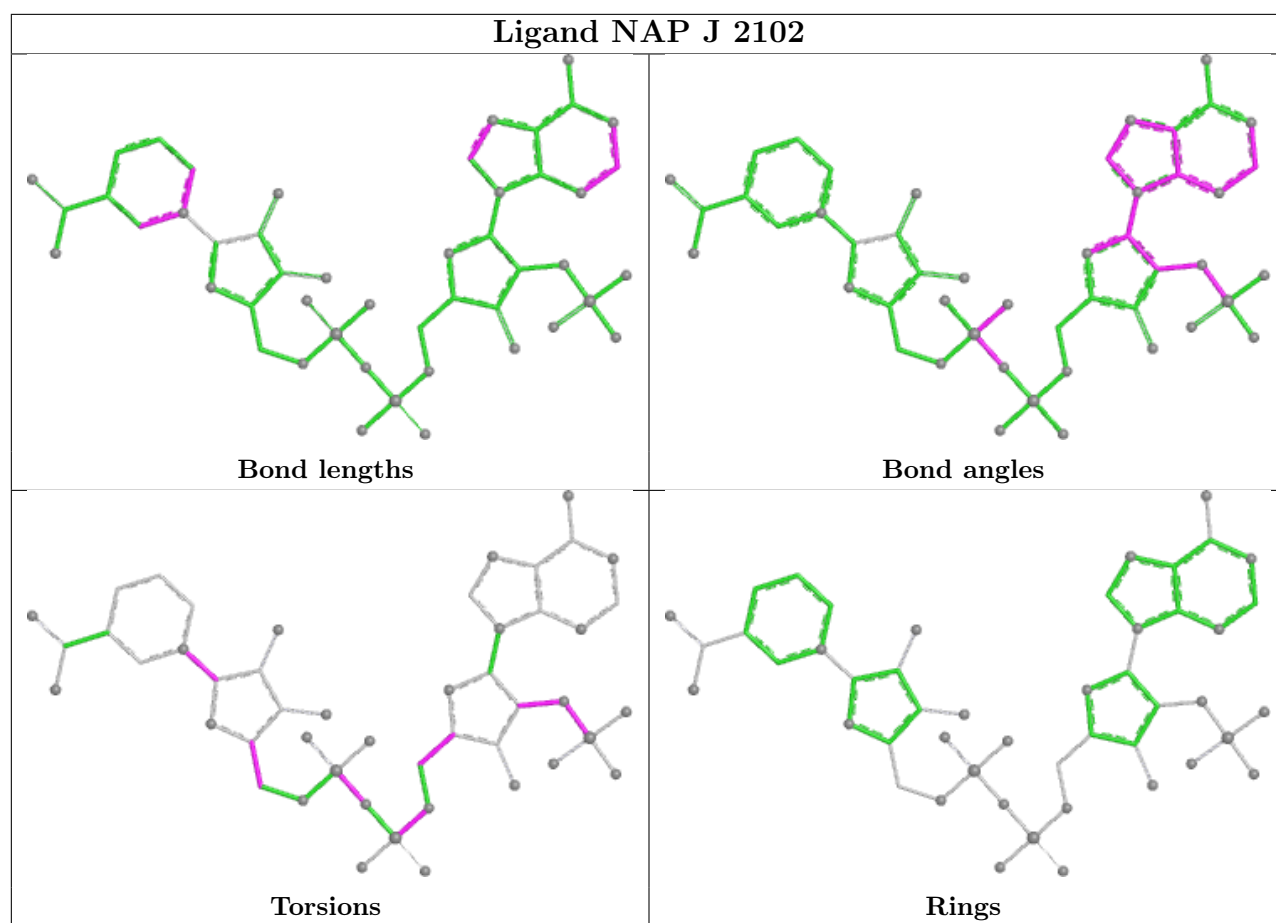
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



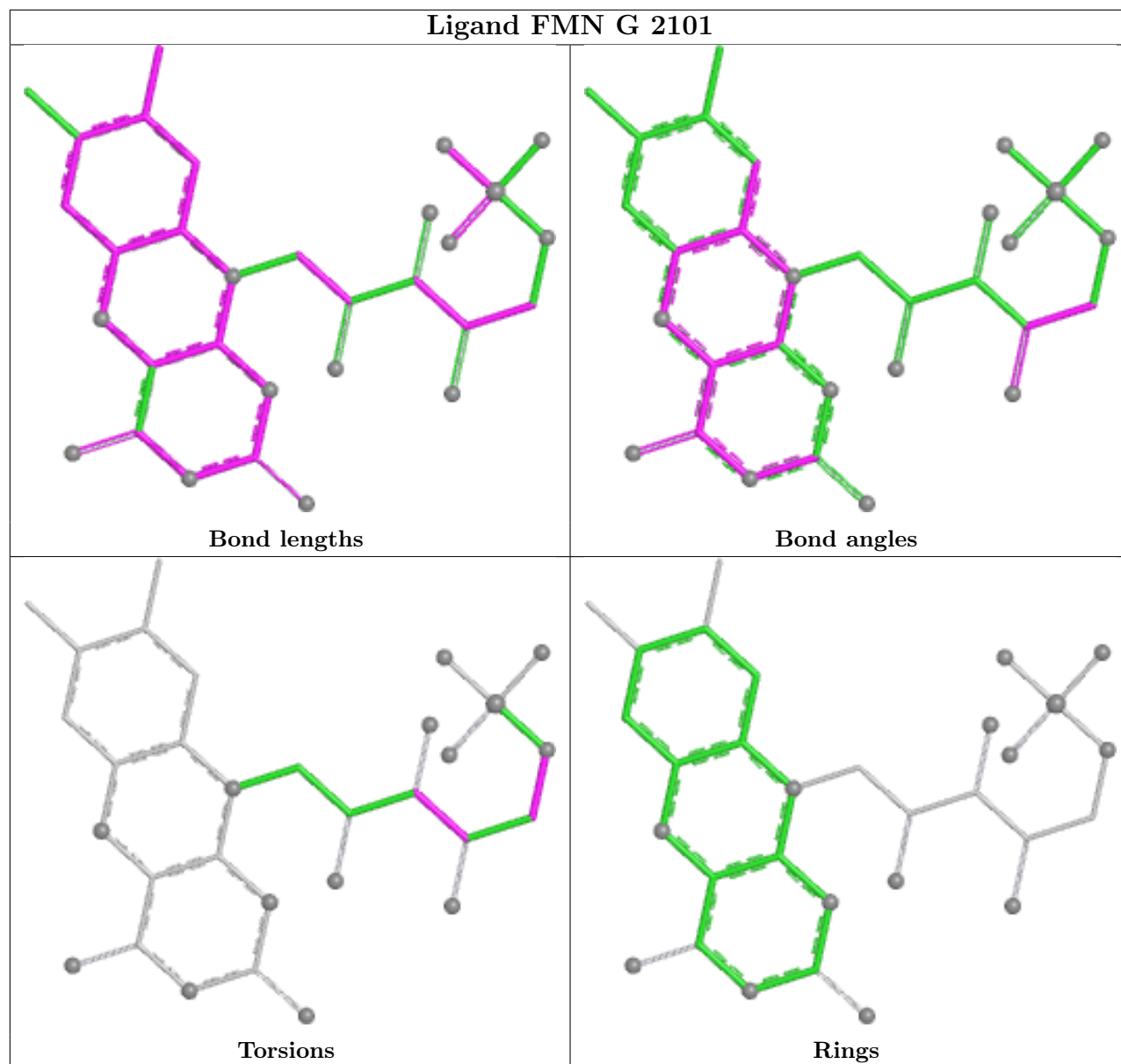


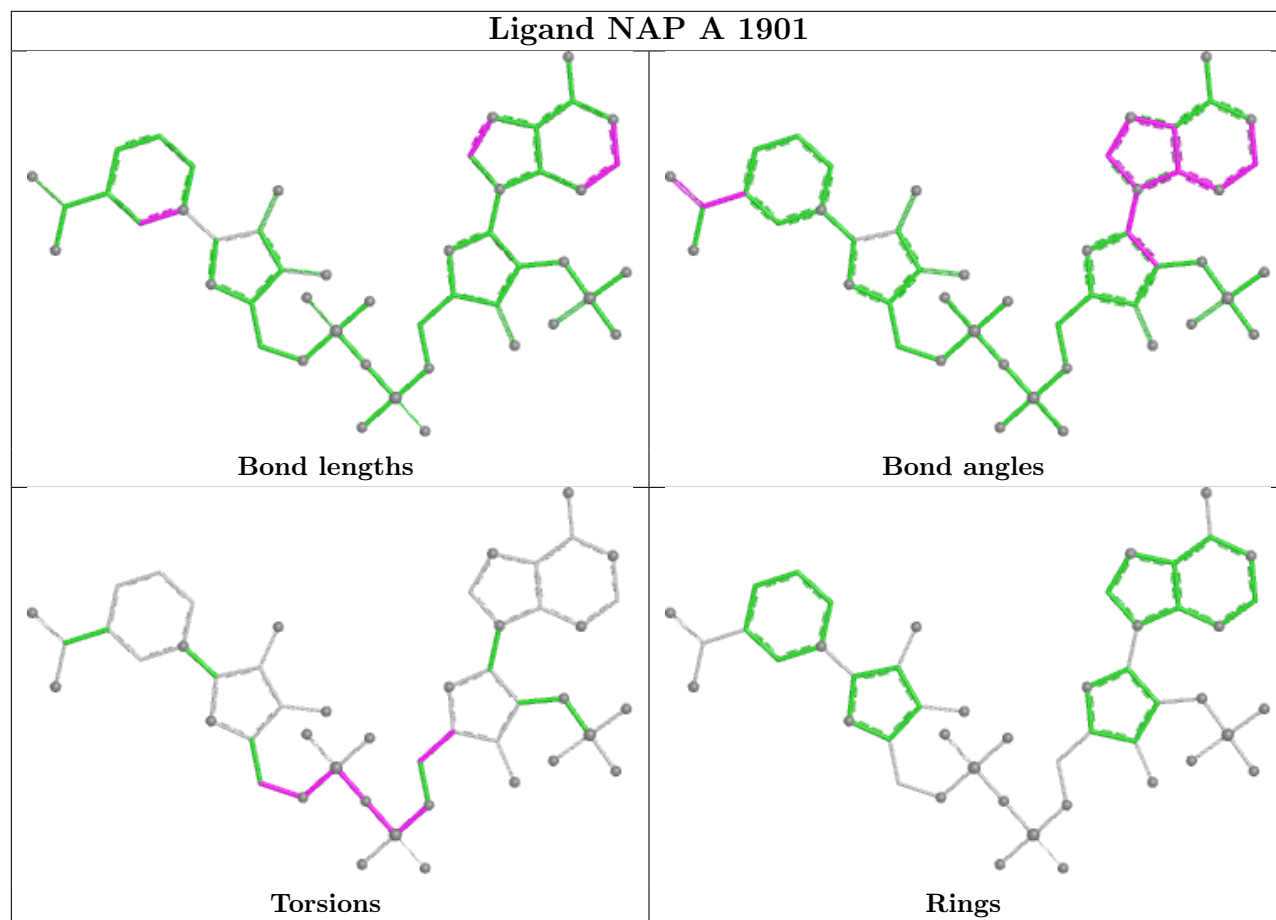


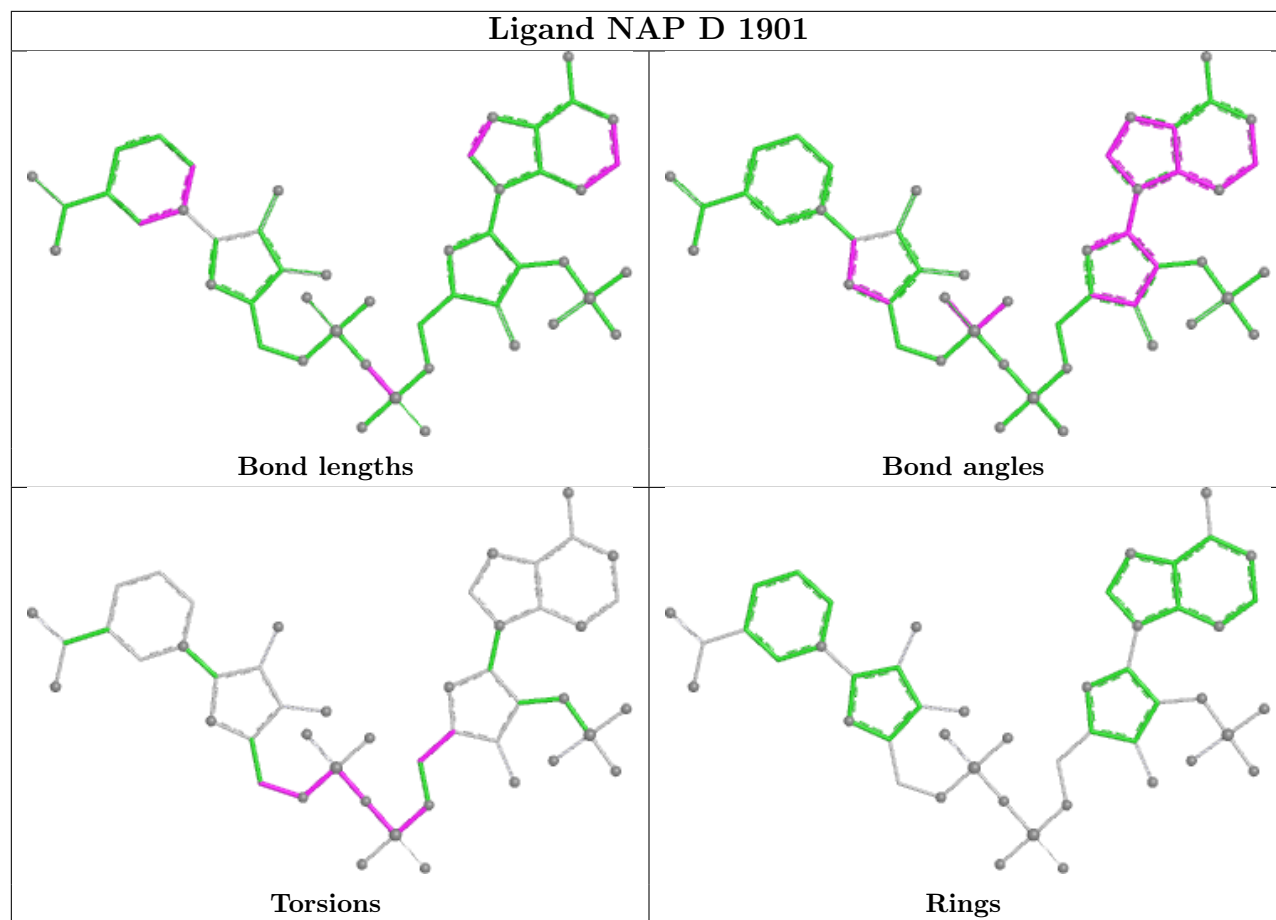


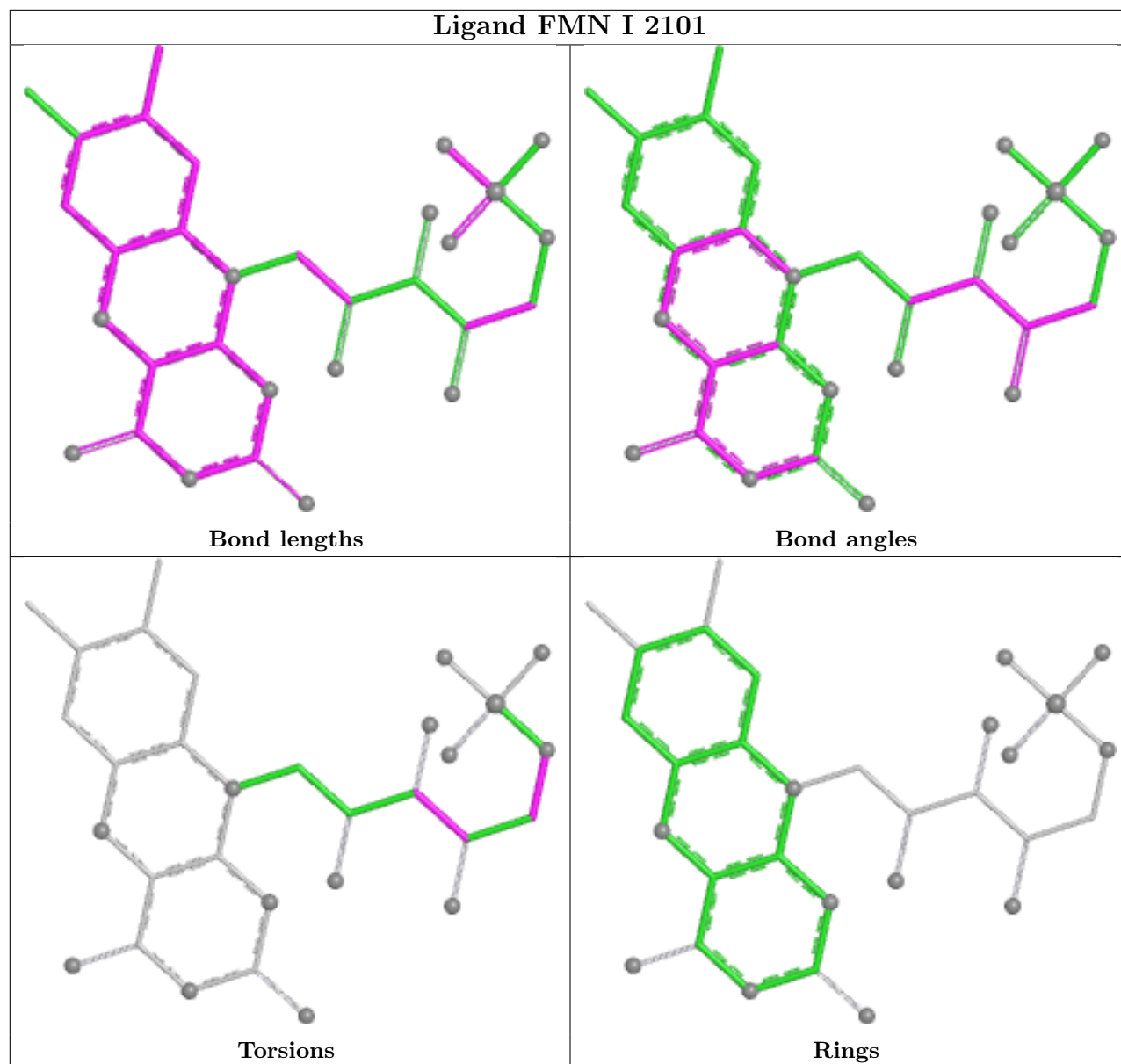


Ligand FMN G 2101

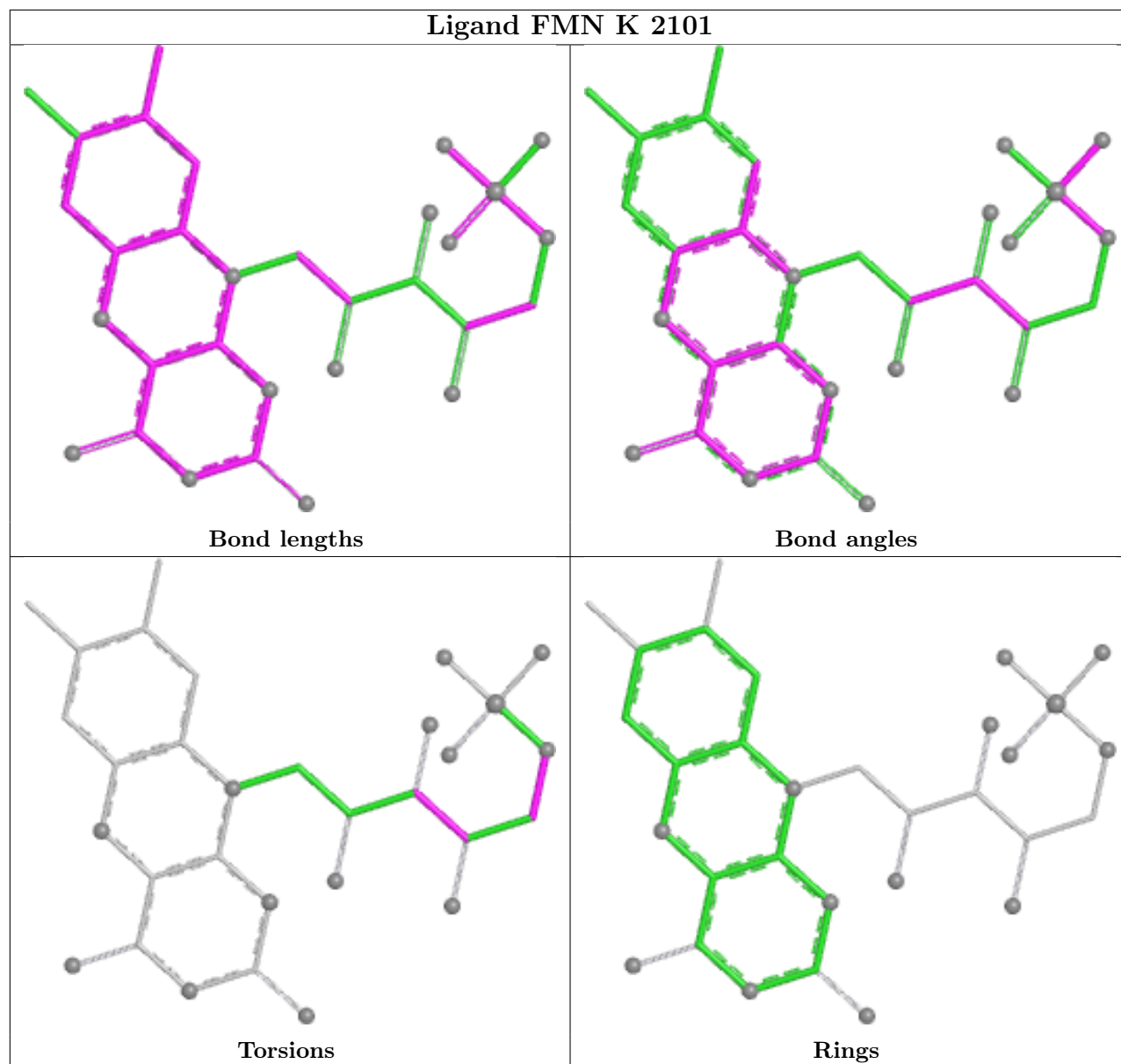




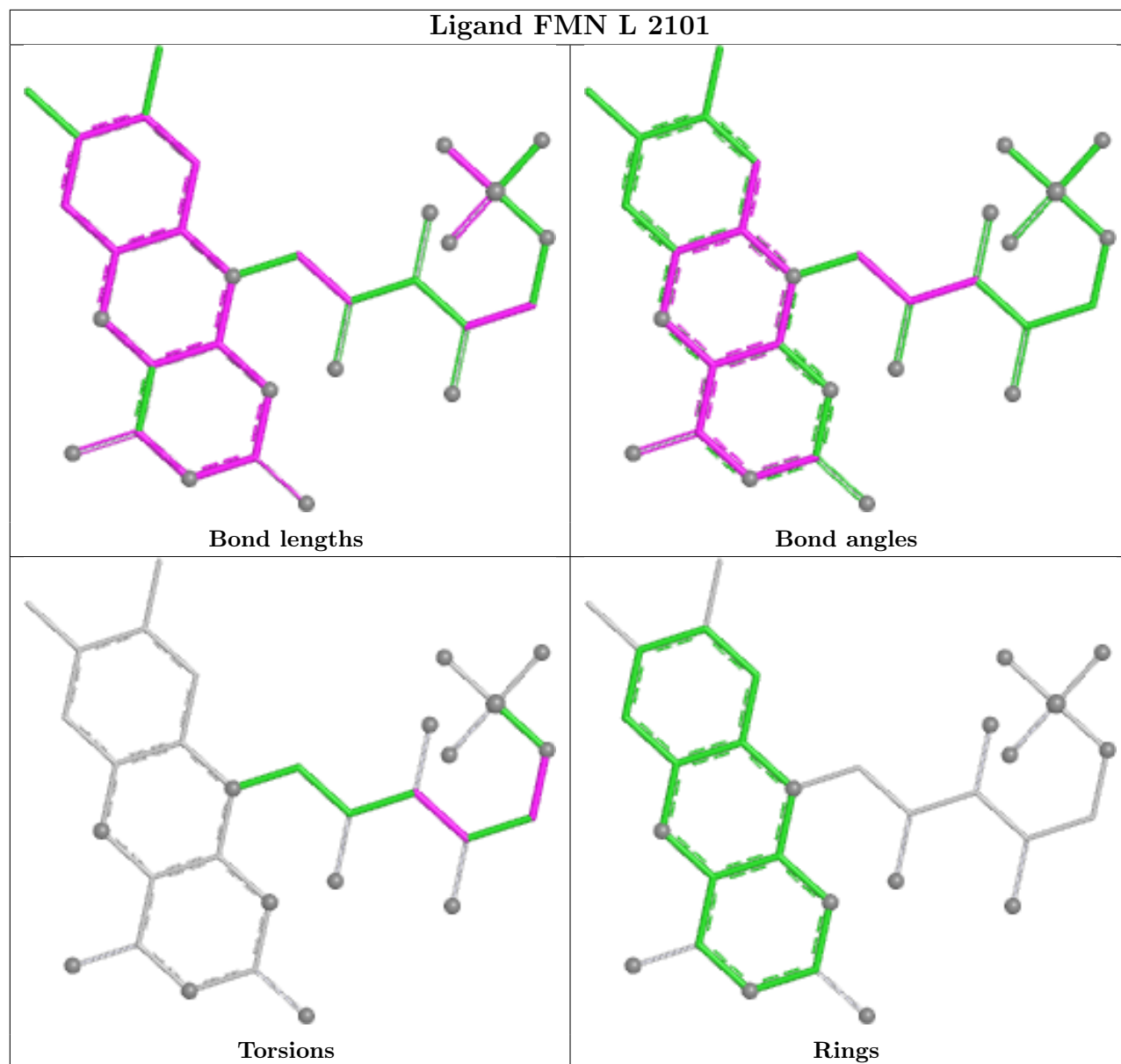


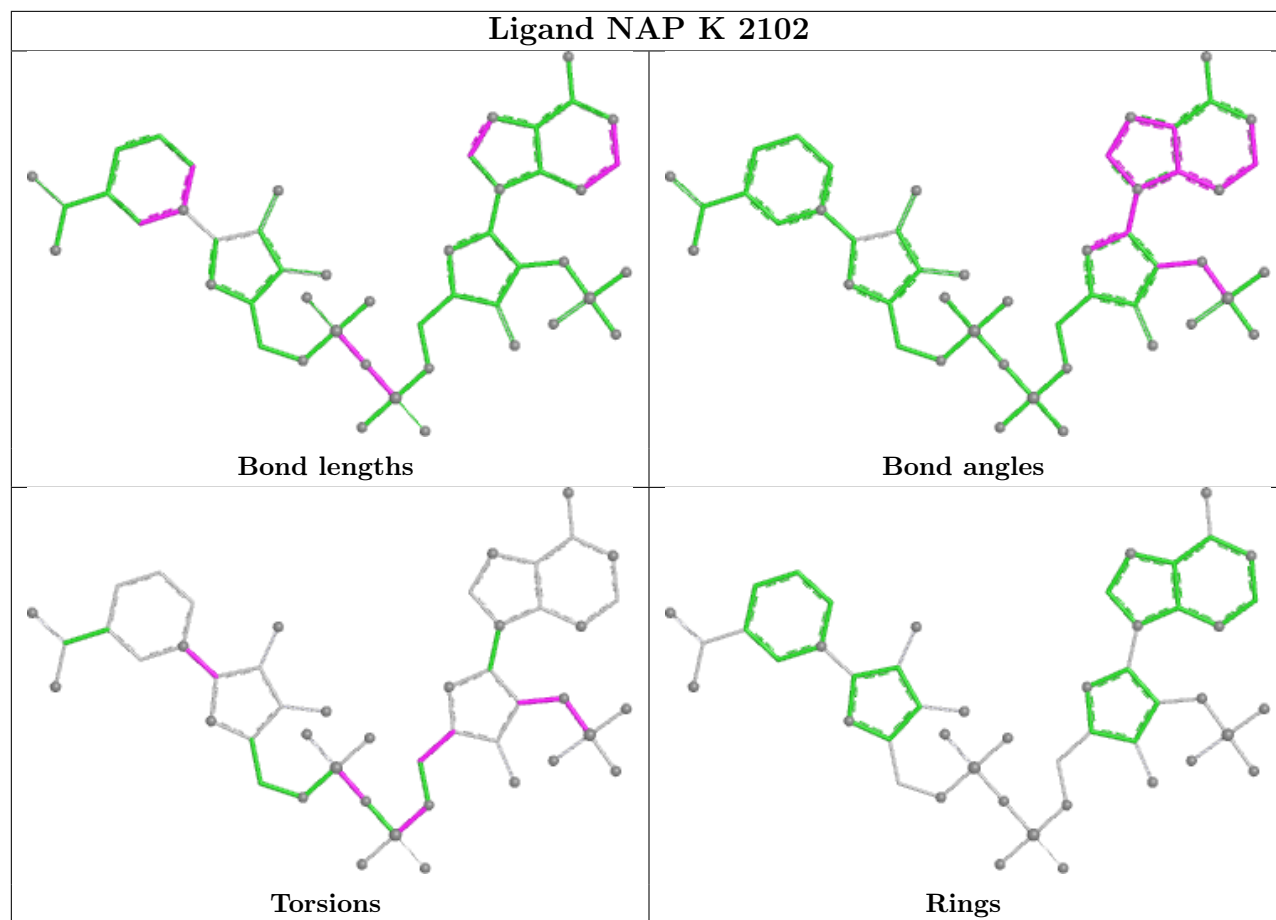


Ligand FMN K 2101

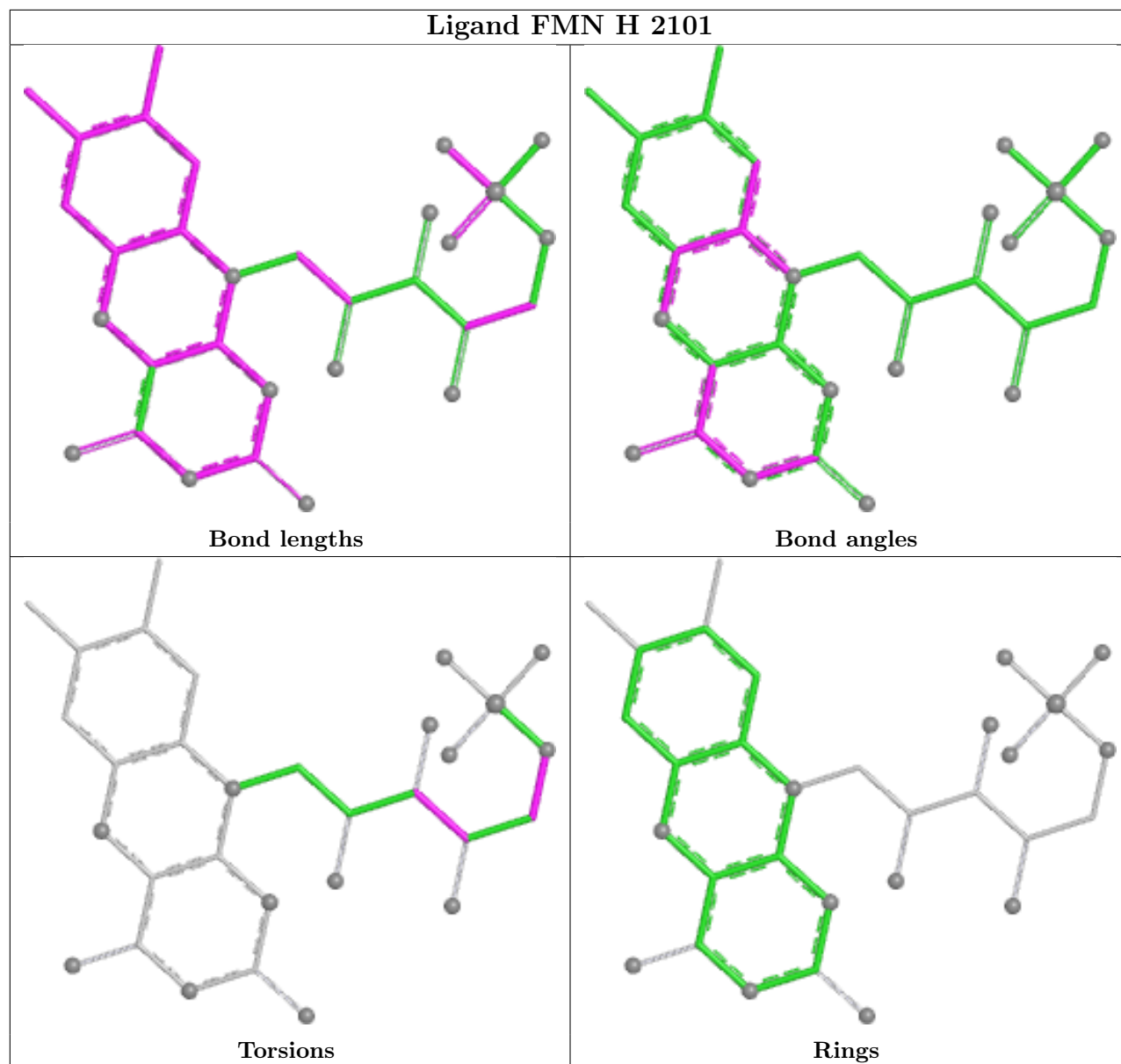


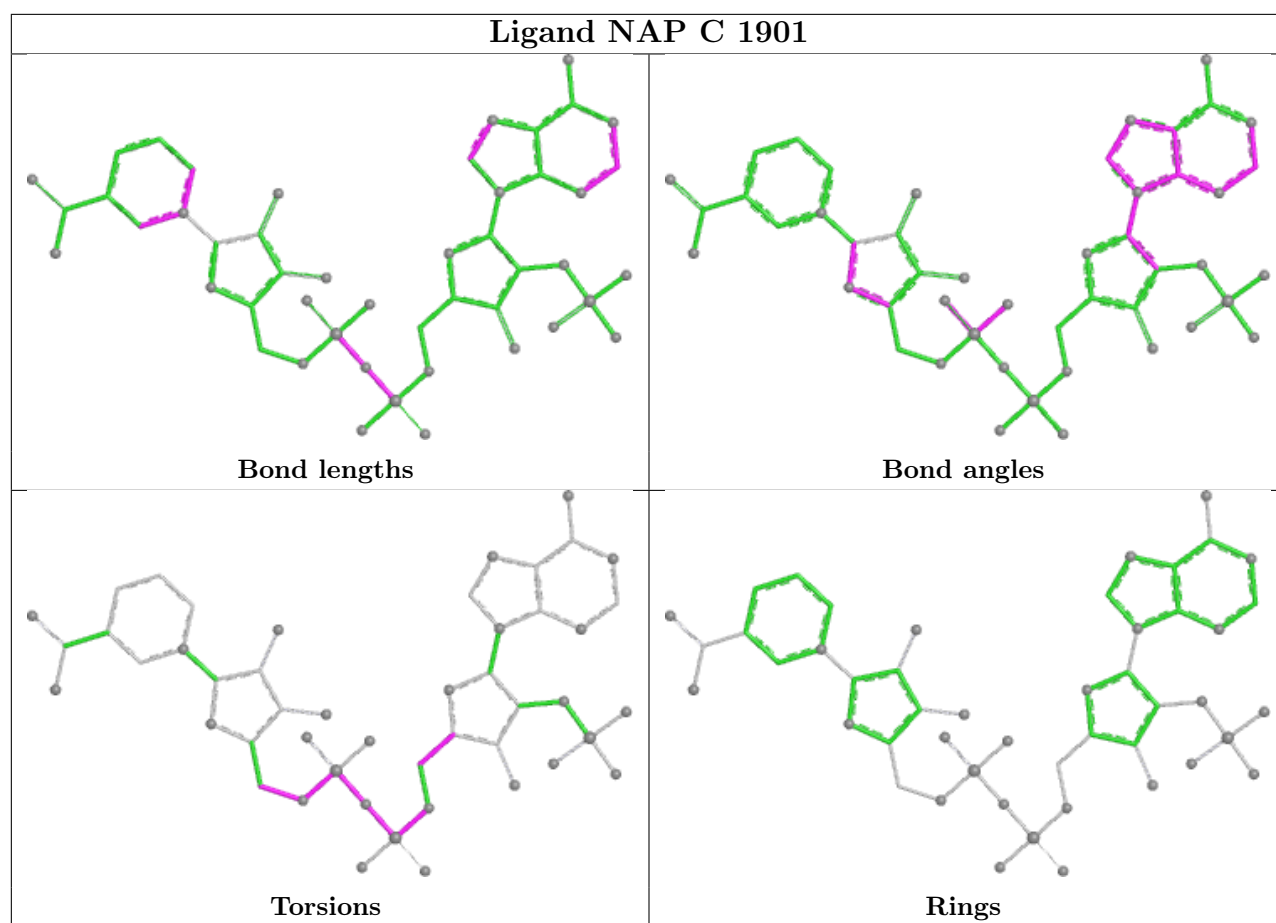
Ligand FMN L 2101

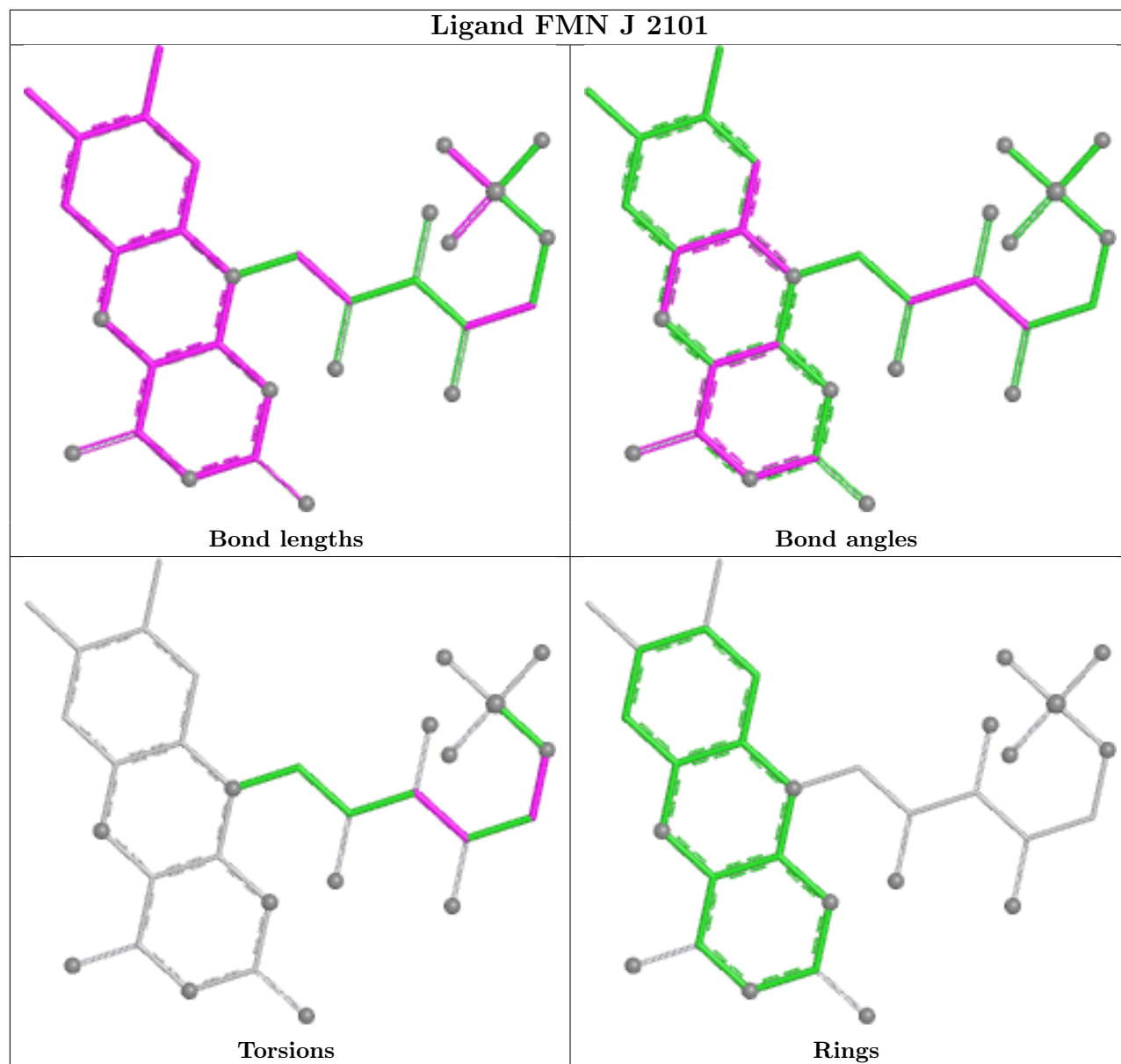


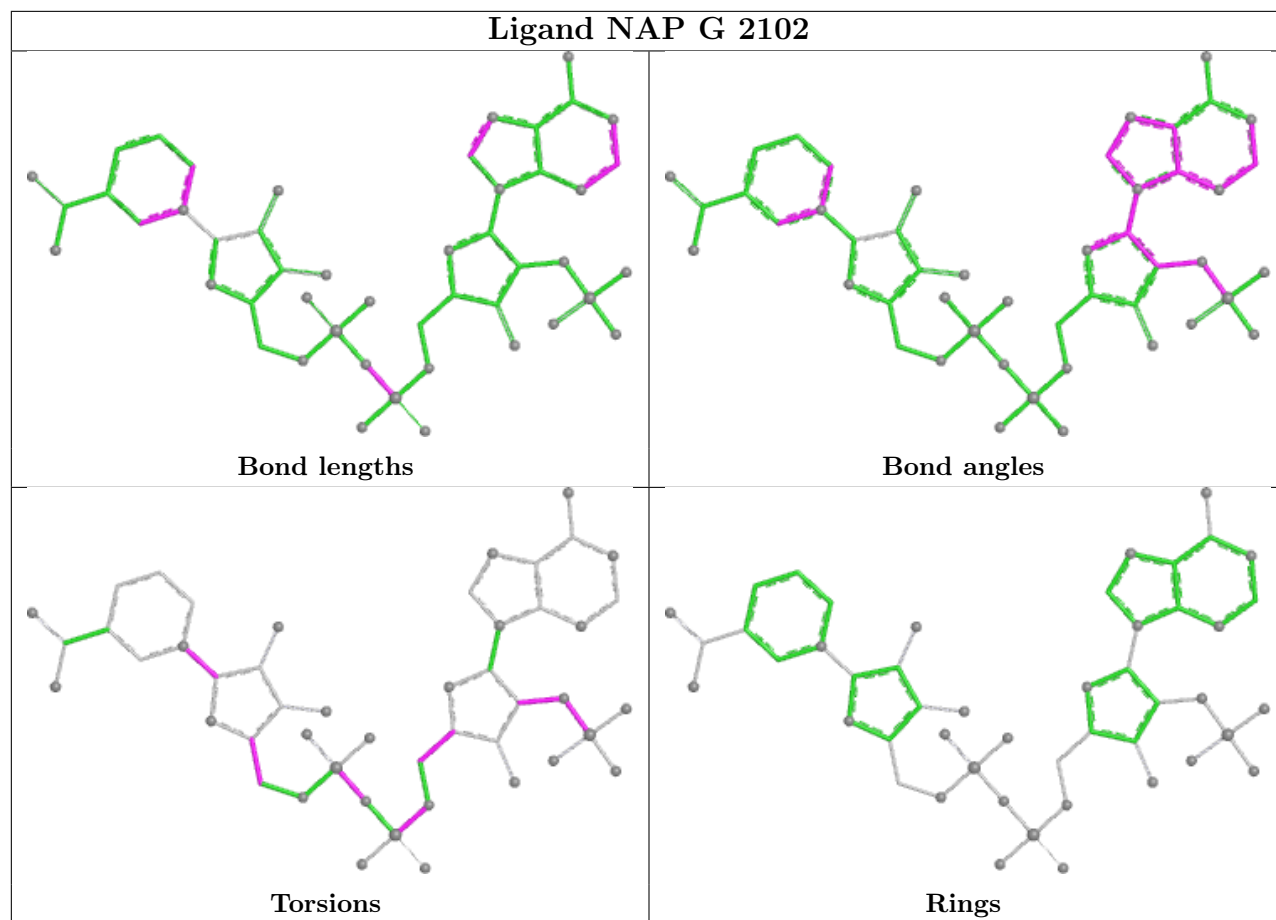


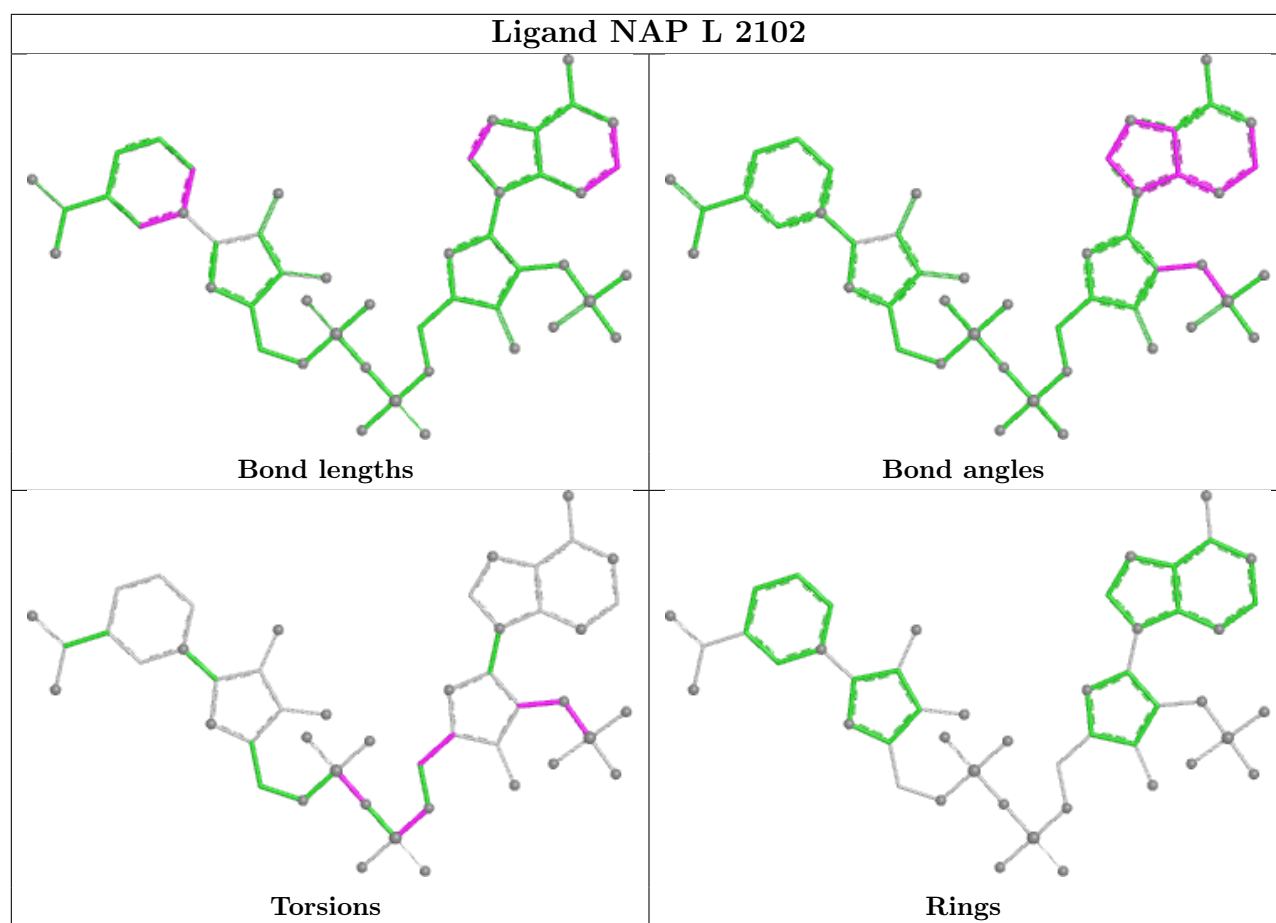
Ligand FMN H 2101

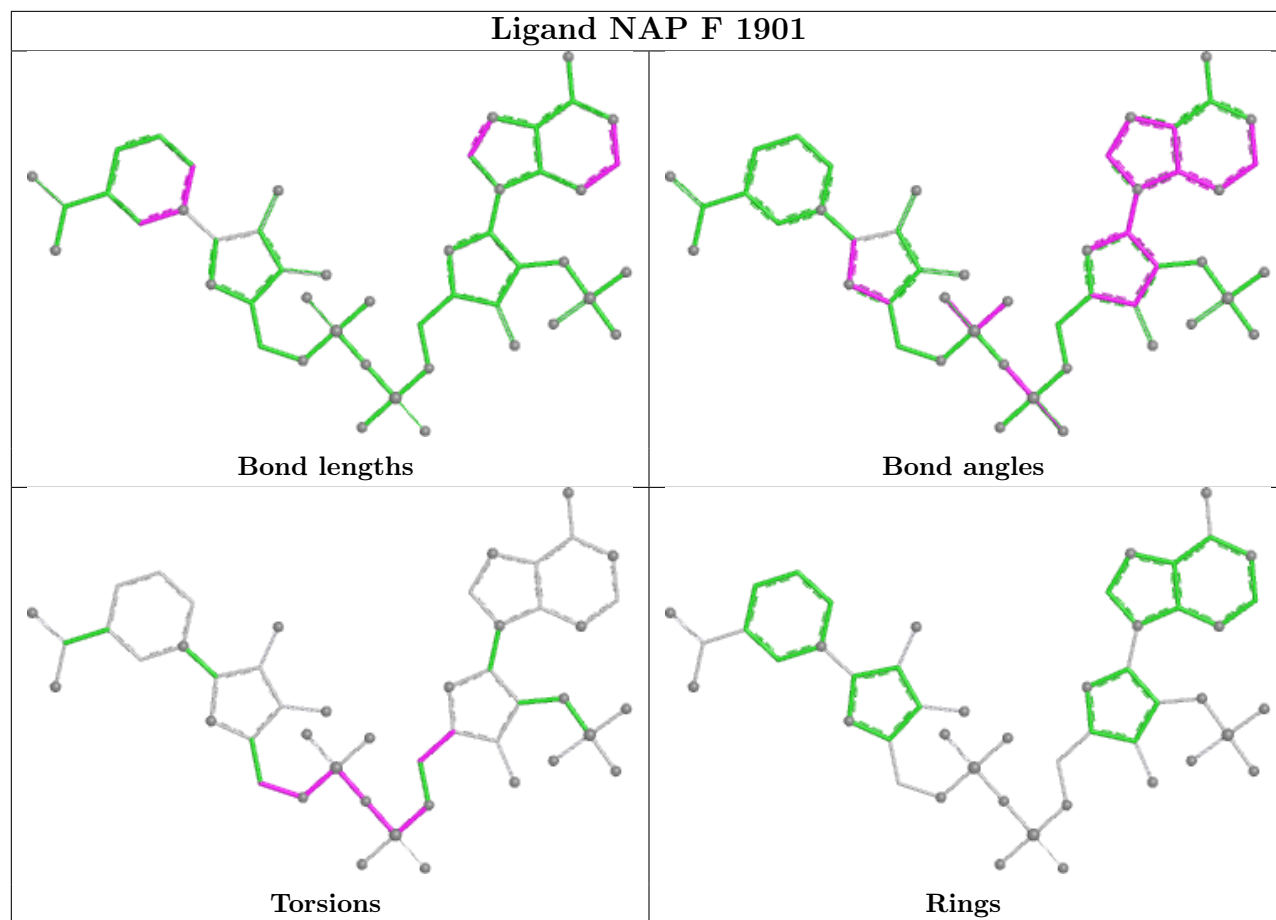












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2	OWAB(Å ²)	Q < 0.9
1	A	1457/1878 (77%)	-0.75	0 100 100	16, 50, 103, 146	0
1	B	1464/1878 (77%)	-0.79	2 (0%) 92 86	17, 50, 106, 157	0
1	C	1462/1878 (77%)	-0.80	0 100 100	15, 48, 107, 155	0
1	D	1467/1878 (78%)	-0.77	0 100 100	17, 52, 106, 151	0
1	E	1456/1878 (77%)	-0.78	2 (0%) 92 86	17, 50, 106, 152	0
1	F	1461/1878 (77%)	-0.82	1 (0%) 92 86	17, 47, 106, 156	0
2	G	2060/2060 (100%)	-0.49	2 (0%) 92 86	24, 83, 128, 156	0
2	H	2060/2060 (100%)	-0.57	0 100 100	24, 85, 129, 155	0
2	I	2060/2060 (100%)	-0.50	3 (0%) 92 86	20, 85, 129, 158	0
2	J	2060/2060 (100%)	-0.48	2 (0%) 92 86	27, 88, 132, 157	0
2	K	2060/2060 (100%)	-0.23	17 (0%) 82 65	25, 90, 133, 157	0
2	L	2060/2060 (100%)	-0.51	0 100 100	22, 86, 131, 158	0
All	All	21127/23628 (89%)	-0.60	29 (0%) 92 86	15, 74, 125, 158	0

The worst 5 of 29 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	K	163	ALA	5.4
1	B	1452	SER	3.5
2	I	1911	THR	2.9
2	K	552	VAL	2.8
2	K	284	GLY	2.7

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

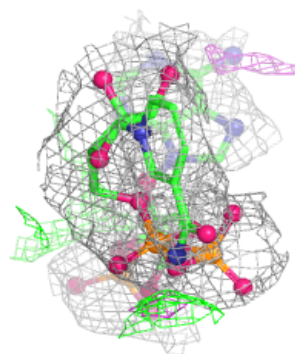
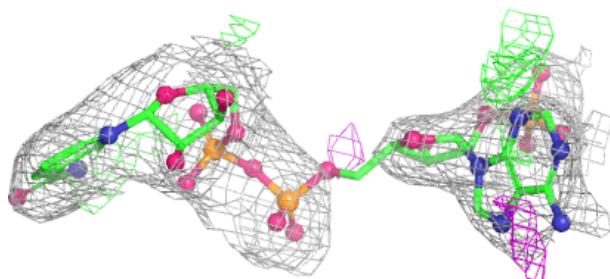
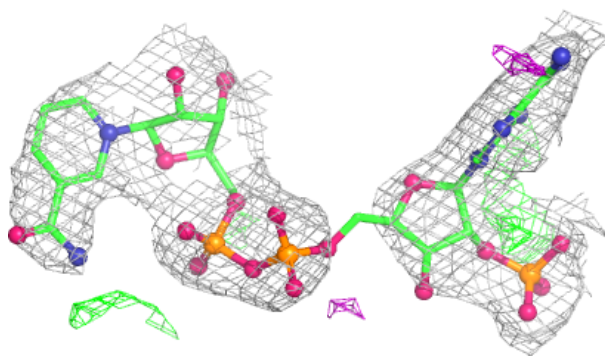
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	NAP	D	1901	48/48	0.90	0.08	21,83,127,174	0
3	NAP	C	1901	48/48	0.91	0.08	23,81,130,171	0
3	NAP	K	2102	48/48	0.91	0.07	43,94,127,131	0
4	FMN	K	2101	31/31	0.92	0.09	27,66,110,123	0
3	NAP	F	1901	48/48	0.93	0.08	19,78,125,159	0
3	NAP	B	1901	48/48	0.93	0.08	23,78,115,145	0
3	NAP	E	1901	48/48	0.93	0.07	24,77,123,157	0
3	NAP	A	1901	48/48	0.94	0.07	19,76,121,169	0
3	NAP	G	2102	48/48	0.94	0.07	42,87,119,128	0
3	NAP	H	2102	48/48	0.95	0.06	37,85,113,122	0
3	NAP	L	2102	48/48	0.95	0.06	37,84,116,120	0
4	FMN	J	2101	31/31	0.95	0.09	23,61,101,113	0
3	NAP	J	2102	48/48	0.95	0.06	35,88,118,120	0
4	FMN	L	2101	31/31	0.95	0.09	19,59,102,114	0
3	NAP	I	2102	48/48	0.96	0.06	29,80,104,116	0
4	FMN	G	2101	31/31	0.96	0.09	26,63,101,111	0
4	FMN	H	2101	31/31	0.96	0.08	25,49,105,113	0
4	FMN	I	2101	31/31	0.97	0.07	22,56,87,103	0

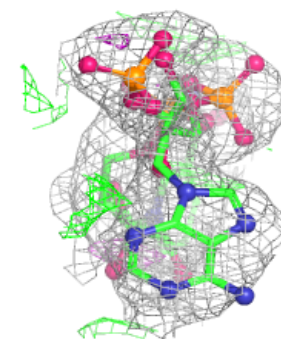
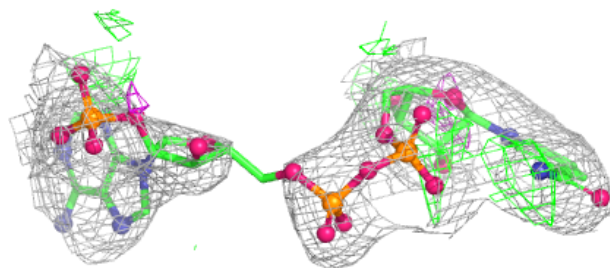
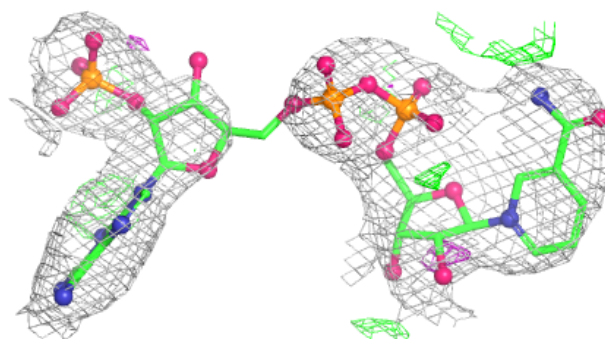
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around NAP D 1901:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

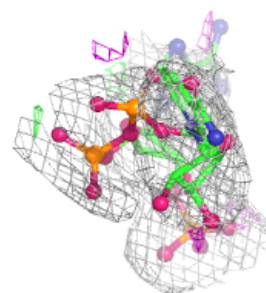
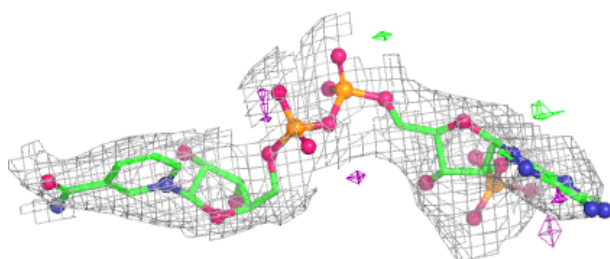
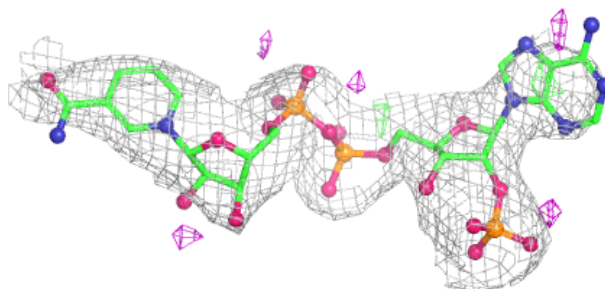
**Electron density around NAP C 1901:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

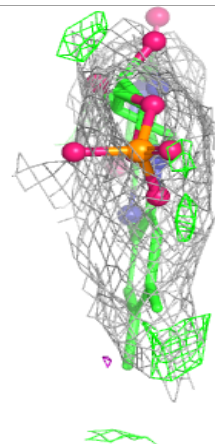
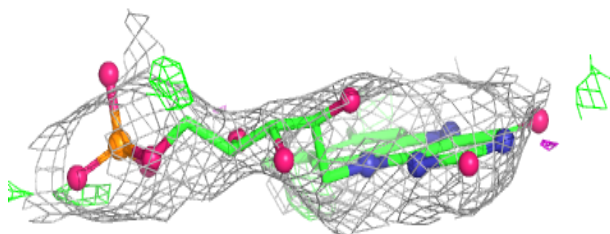
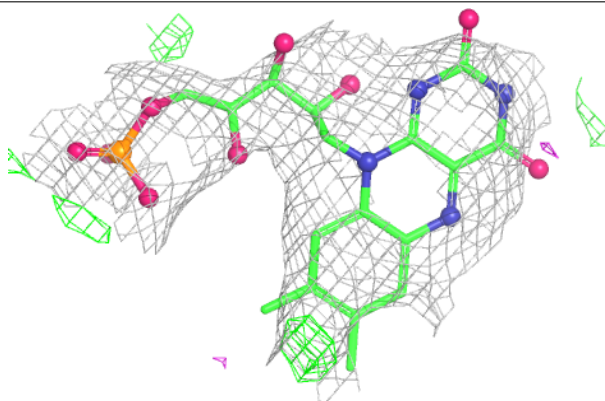


Electron density around NAP K 2102:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

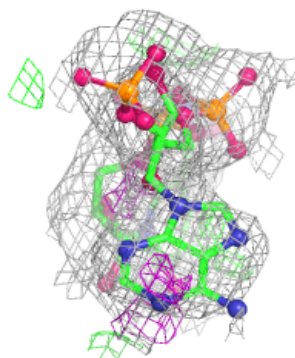
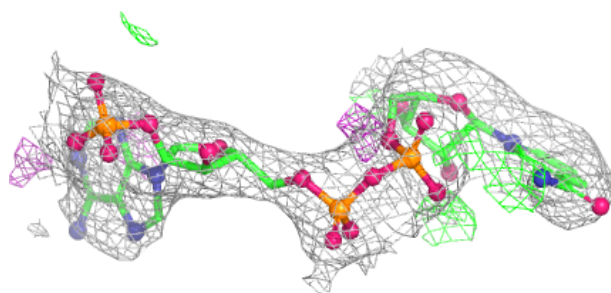
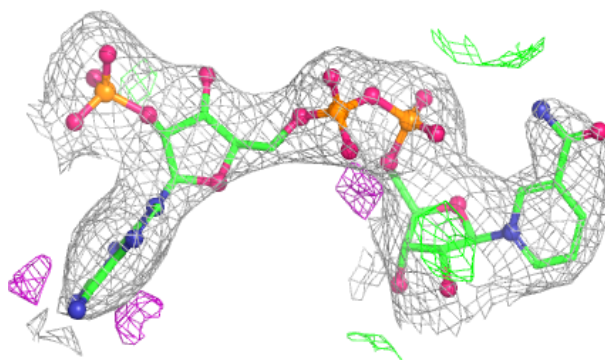
**Electron density around FMN K 2101:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

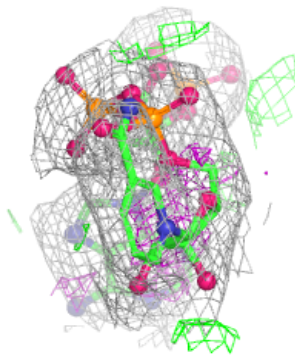
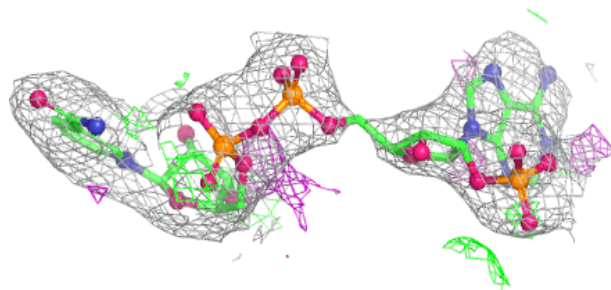
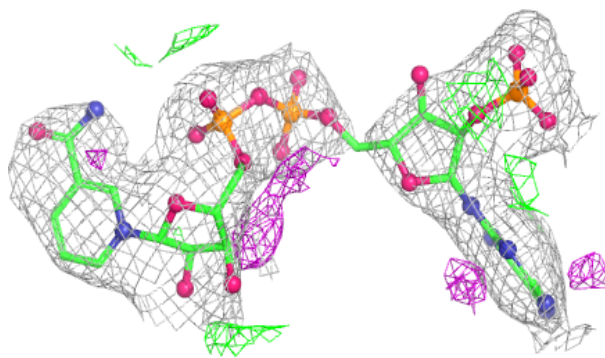


Electron density around NAP F 1901:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

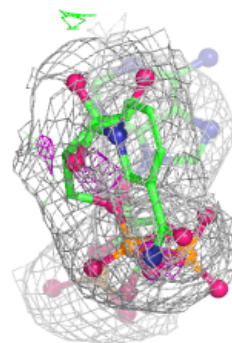
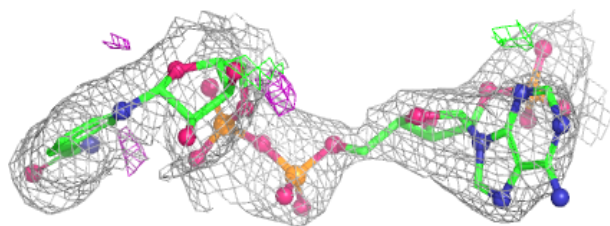
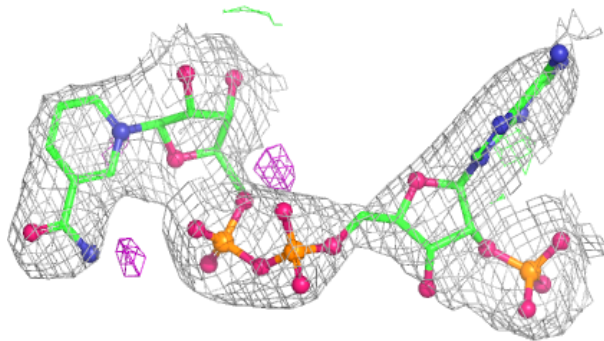
**Electron density around NAP B 1901:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

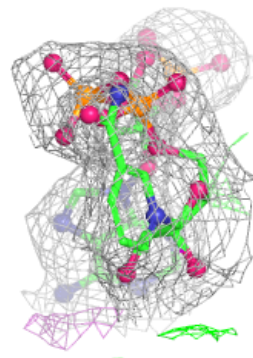
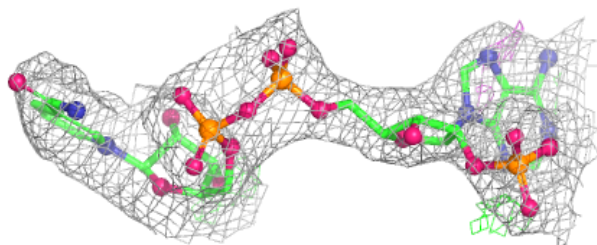
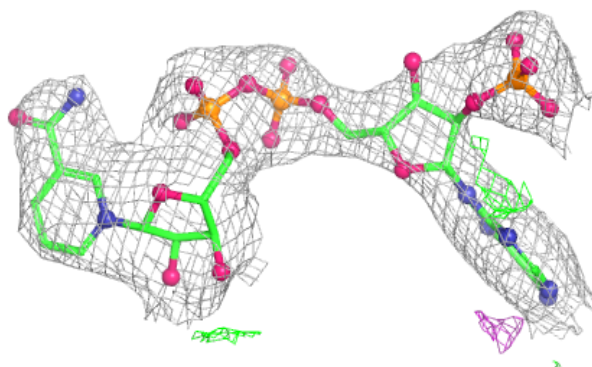


Electron density around NAP E 1901:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

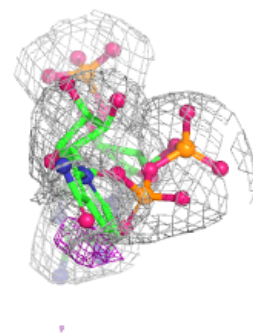
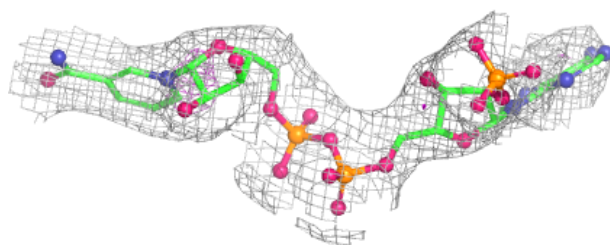
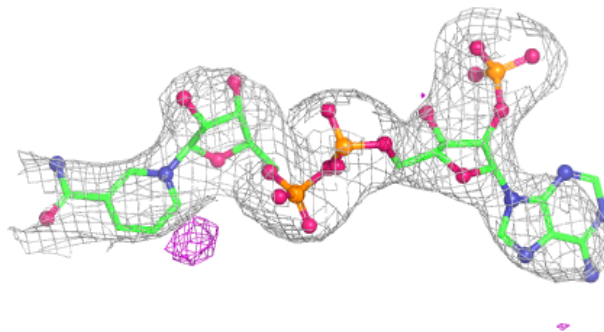
**Electron density around NAP A 1901:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

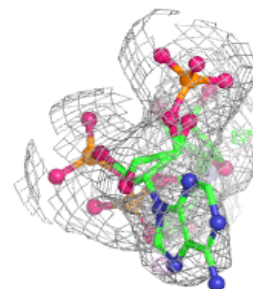
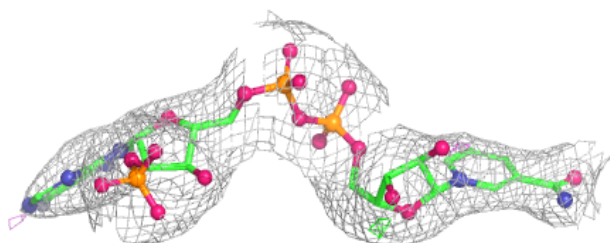
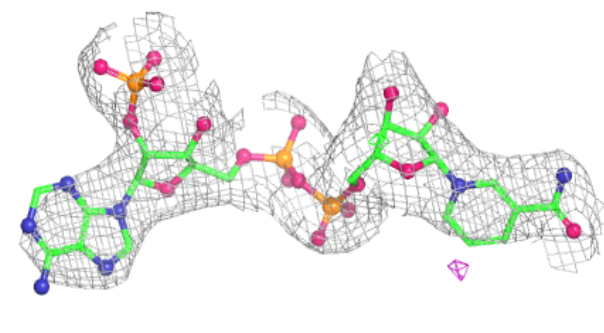


Electron density around NAP G 2102:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

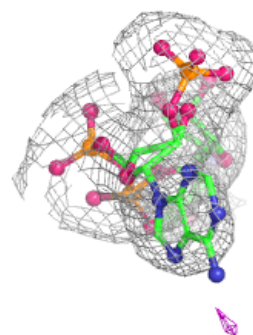
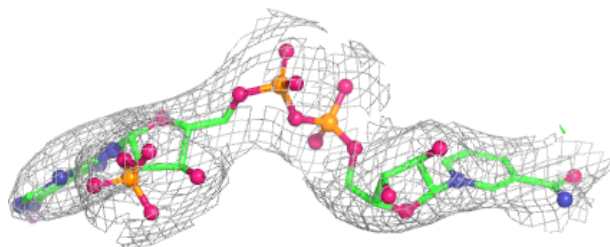
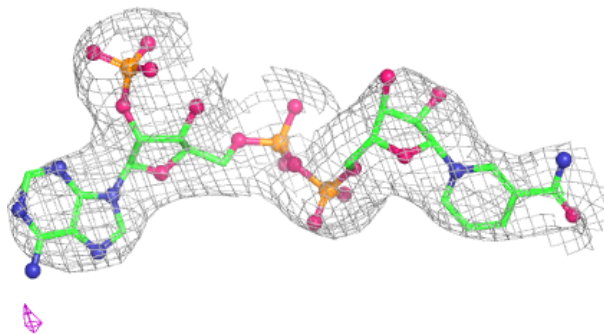
**Electron density around NAP H 2102:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

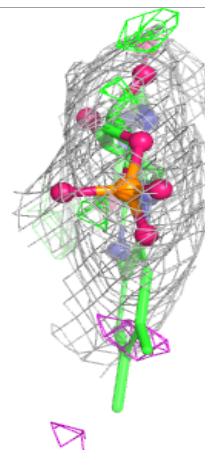
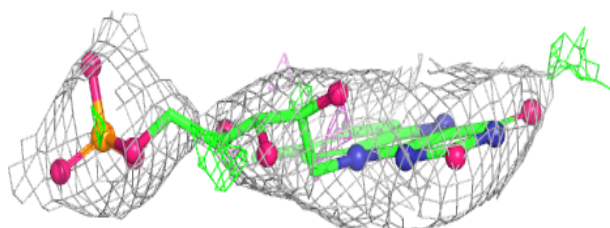
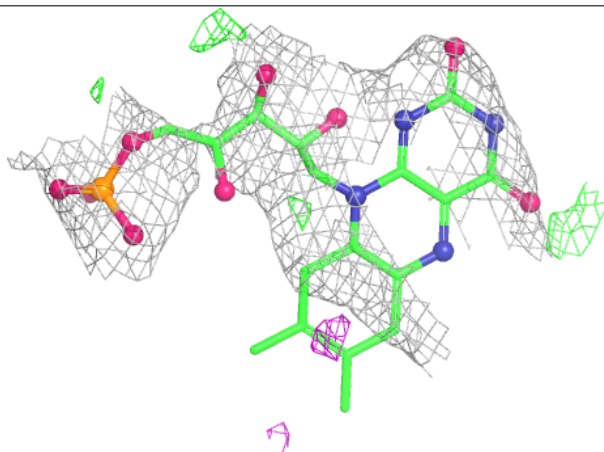


Electron density around NAP L 2102:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

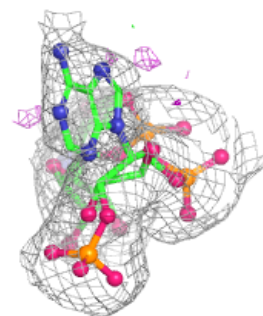
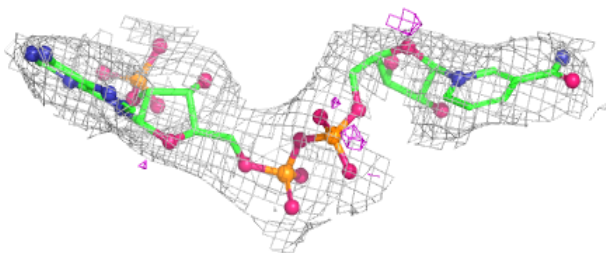
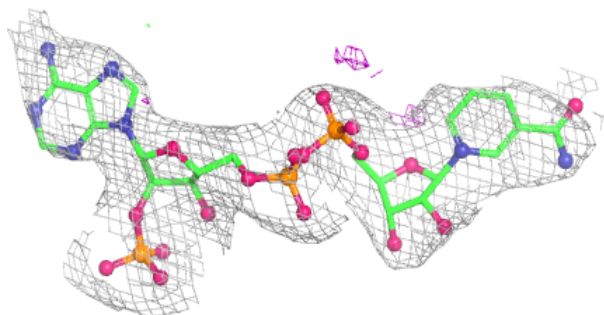
**Electron density around FMN J 2101:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



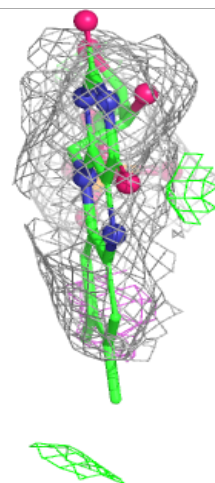
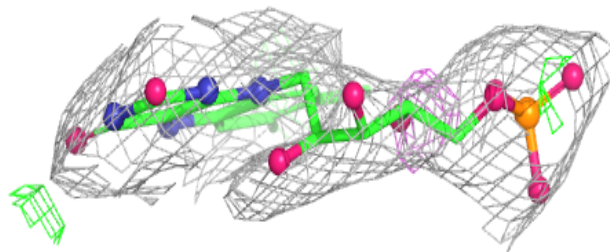
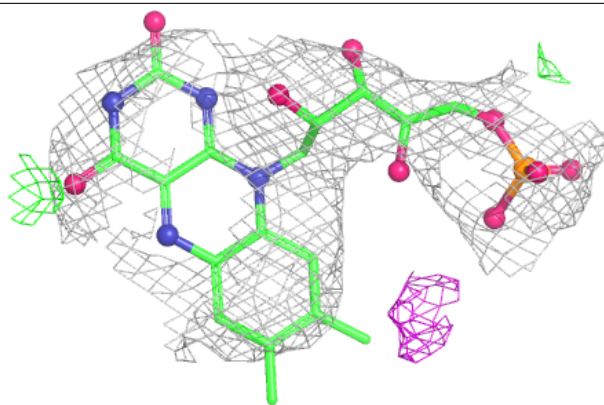
Electron density around NAP J 2102:

$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



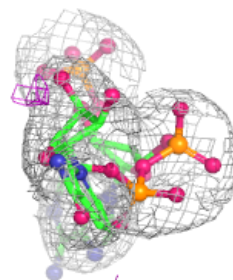
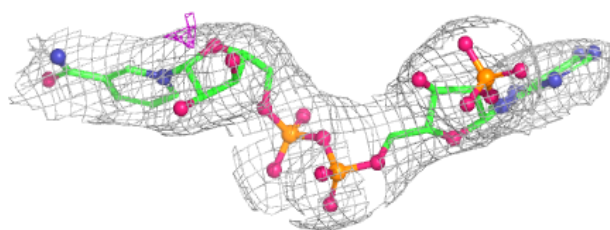
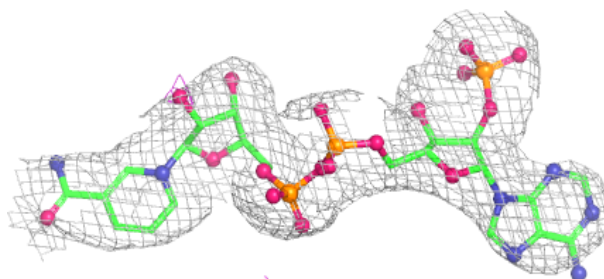
Electron density around FMN L 2101:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

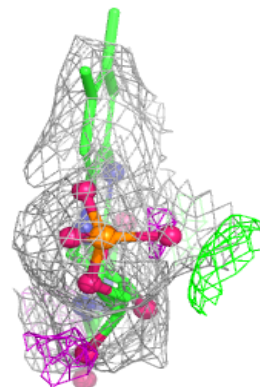
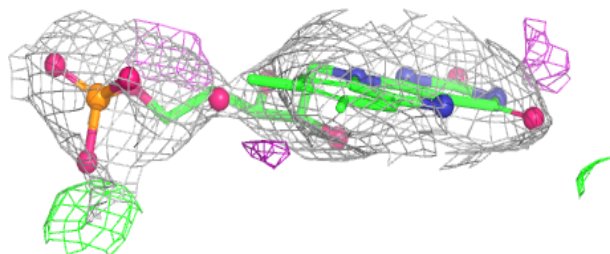
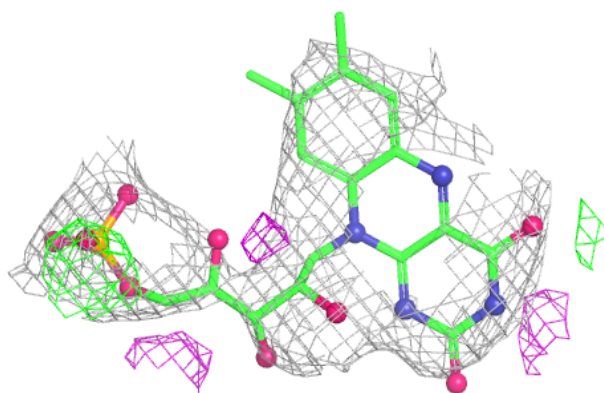


Electron density around NAP I 2102:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

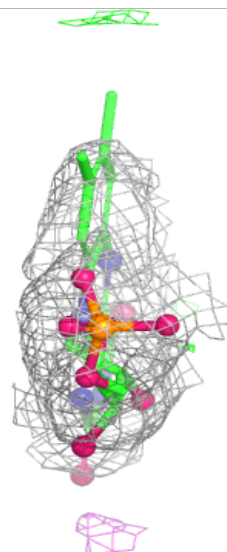
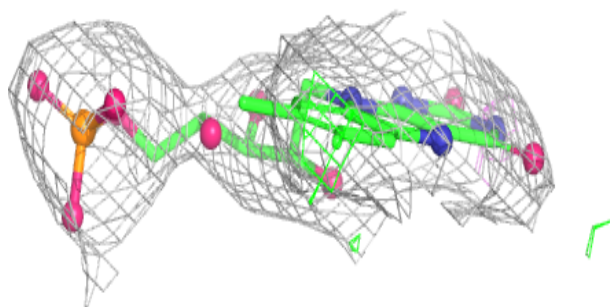
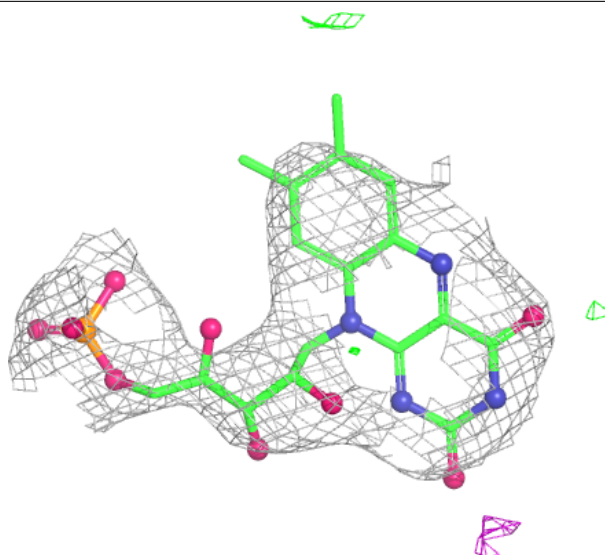
**Electron density around FMN G 2101:**

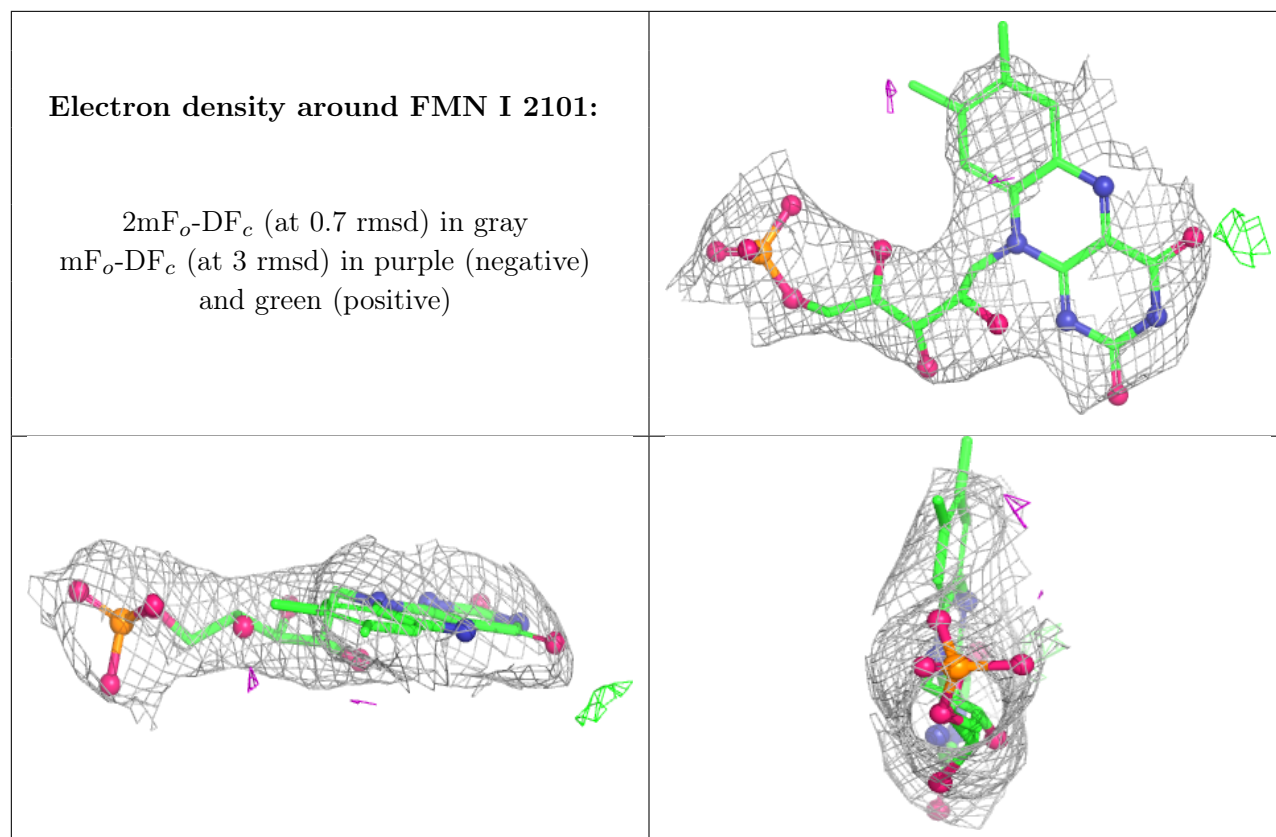
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around FMN H 2101:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





6.5 Other polymers [i](#)

There are no such residues in this entry.