



wwPDB EM Validation Summary Report ⓘ

Nov 20, 2022 – 03:35 pm GMT

PDB ID : 2VDC
EMDB ID : EMD-1440
Title : THE 9.5 Å RESOLUTION STRUCTURE OF GLUTAMATE SYNTHASE FROM CRYO-ELECTRON MICROSCOPY AND ITS OLIGOMERIZATION BEHAVIOR IN SOLUTION: FUNCTIONAL IMPLICATIONS.
Authors : Cotteville, M.; Larquet, E.; Jonic, S.; Petoukhov, M.V.; Caprini, G.; Paravisi, S.; Svergun, D.I.; Vanoni, M.A.; Boisset, N.
Deposited on : 2007-10-04
Resolution : 9.50 Å (reported)
Based on initial model : 2VDC

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev43
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

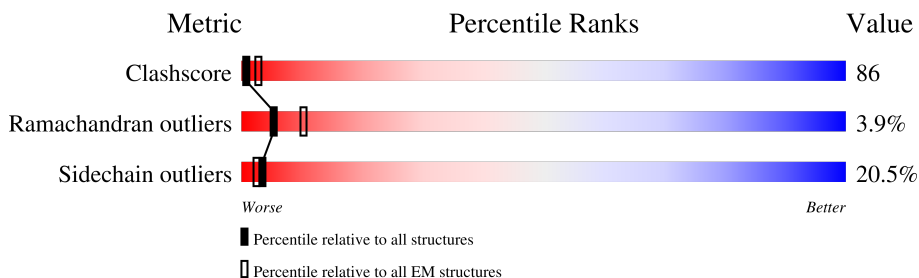
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 9.50 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1472	<div style="display: flex; justify-content: space-between;"> 29% 26% 52% 20% </div>
1	B	1472	<div style="display: flex; justify-content: space-between;"> 29% 30% 49% 17% </div>
1	C	1472	<div style="display: flex; justify-content: space-between;"> 31% 27% 51% 20% </div>
1	D	1472	<div style="display: flex; justify-content: space-between;"> 30% 30% 49% 17% </div>
1	E	1472	<div style="display: flex; justify-content: space-between;"> 30% 26% 51% 20% </div>
1	F	1472	<div style="display: flex; justify-content: space-between;"> 31% 30% 49% 17% </div>
2	G	456	<div style="display: flex; justify-content: space-between;"> 21% 18% 49% 25% 8% </div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	H	456	
2	I	456	
2	J	456	
2	K	456	
2	L	456	

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
3	OMT	A	2473	-	X	-	-
3	OMT	B	2473	-	X	-	-
3	OMT	C	2473	-	X	-	-
3	OMT	D	2473	-	X	-	-
3	OMT	E	2473	-	X	-	-
3	OMT	F	2473	-	X	-	-
6	F3S	A	2476	-	-	X	-
6	F3S	B	2476	-	-	X	-
6	F3S	C	2476	-	-	X	-
6	F3S	D	2476	-	-	X	-
6	F3S	E	2476	-	-	X	-
6	F3S	F	2476	-	-	X	-
7	SF4	G	483	-	-	X	-
7	SF4	H	483	-	-	X	-
7	SF4	I	483	-	-	X	-
7	SF4	J	483	-	-	X	-
7	SF4	K	483	-	-	X	-
7	SF4	L	483	-	-	X	-

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 89598 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.

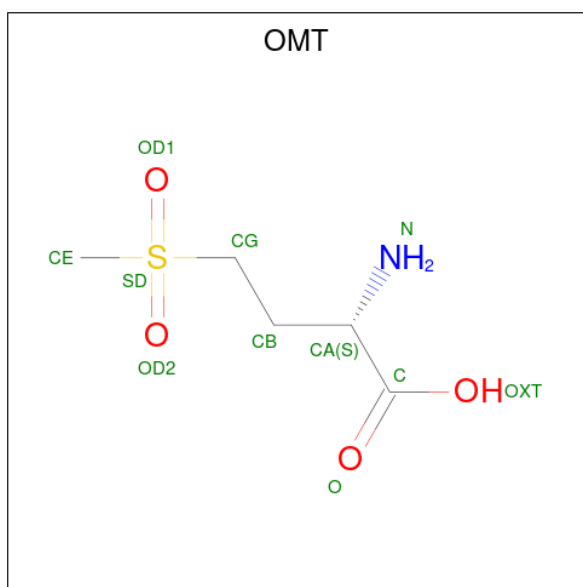
- Molecule 1 is a protein called GLUTAMATE SYNTHASE [NADPH] LARGE CHAIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	1472	11337	7109	2036	2132	60	0	0
1	B	1472	11337	7109	2036	2132	60	0	0
1	C	1472	11337	7109	2036	2132	60	0	0
1	D	1472	11337	7109	2036	2132	60	0	0
1	E	1472	11337	7109	2036	2132	60	0	0
1	F	1472	11337	7109	2036	2132	60	0	0

- Molecule 2 is a protein called GLUTAMATE SYNTHASE [NADPH] SMALL CHAIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	G	456	3468	2163	624	666	15	0	0
2	H	456	3468	2163	624	666	15	0	0
2	I	456	3468	2163	624	666	15	0	0
2	J	456	3468	2163	624	666	15	0	0
2	K	456	3468	2163	624	666	15	0	0
2	L	456	3468	2163	624	666	15	0	0

- Molecule 3 is S-DIOXYMETHIONINE (three-letter code: OMT) (formula: C₅H₁₁NO₄S).



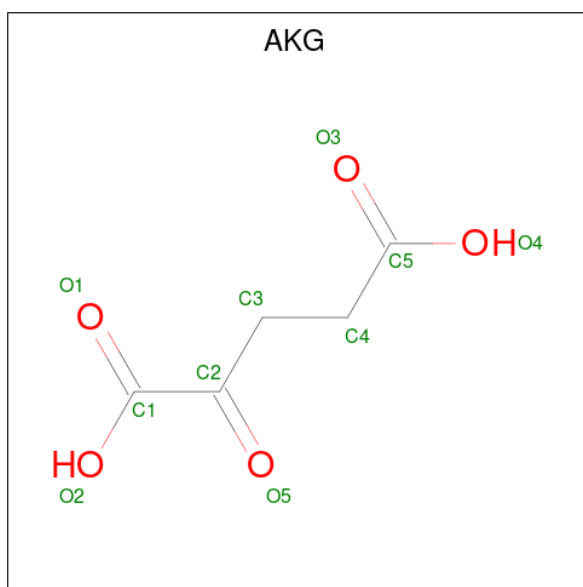
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	S	
3	A	1	Total	C	N	O	S	0
			11	5	1	4	1	
3	B	1	Total	C	N	O	S	0
			11	5	1	4	1	
3	C	1	Total	C	N	O	S	0
			11	5	1	4	1	
3	D	1	Total	C	N	O	S	0
			11	5	1	4	1	
3	E	1	Total	C	N	O	S	0
			11	5	1	4	1	
3	F	1	Total	C	N	O	S	0
			11	5	1	4	1	

- Molecule 4 is FLAVIN MONONUCLEOTIDE (three-letter code: FMN) (formula: C₁₇H₂₁N₄O₉P).



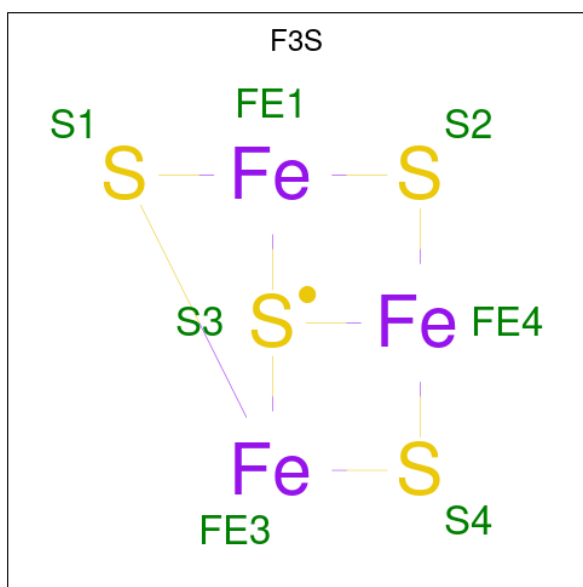
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
4	A	1	Total	C	N	O	P	0
			31	17	4	9	1	
4	B	1	Total	C	N	O	P	0
			31	17	4	9	1	
4	C	1	Total	C	N	O	P	0
			31	17	4	9	1	
4	D	1	Total	C	N	O	P	0
			31	17	4	9	1	
4	E	1	Total	C	N	O	P	0
			31	17	4	9	1	
4	F	1	Total	C	N	O	P	0
			31	17	4	9	1	

- Molecule 5 is 2-OXOGLUTARIC ACID (three-letter code: AKG) (formula: C₅H₆O₅).



Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
5	A	1	10	5	5	0
5	B	1	10	5	5	0
5	C	1	10	5	5	0
5	D	1	10	5	5	0
5	E	1	10	5	5	0
5	F	1	10	5	5	0

- Molecule 6 is FE3-S4 CLUSTER (three-letter code: F3S) (formula: Fe₃S₄).



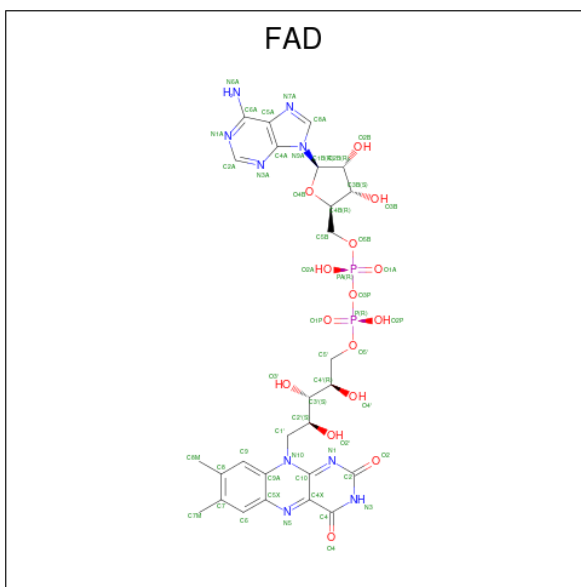
Mol	Chain	Residues	Atoms			AltConf
			Total	Fe	S	
6	A	1	7	3	4	0
6	B	1	7	3	4	0
6	C	1	7	3	4	0
6	D	1	7	3	4	0
6	E	1	7	3	4	0
6	F	1	7	3	4	0

- Molecule 7 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe₄S₄).



Mol	Chain	Residues	Atoms			AltConf
			Total	Fe	S	
7	G	1	16	8	8	0
7	G	1	16	8	8	0
7	H	1	16	8	8	0
7	H	1	16	8	8	0
7	I	1	16	8	8	0
7	I	1	16	8	8	0
7	J	1	16	8	8	0
7	J	1	16	8	8	0
7	K	1	16	8	8	0
7	K	1	16	8	8	0
7	L	1	16	8	8	0
7	L	1	16	8	8	0

- Molecule 8 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).

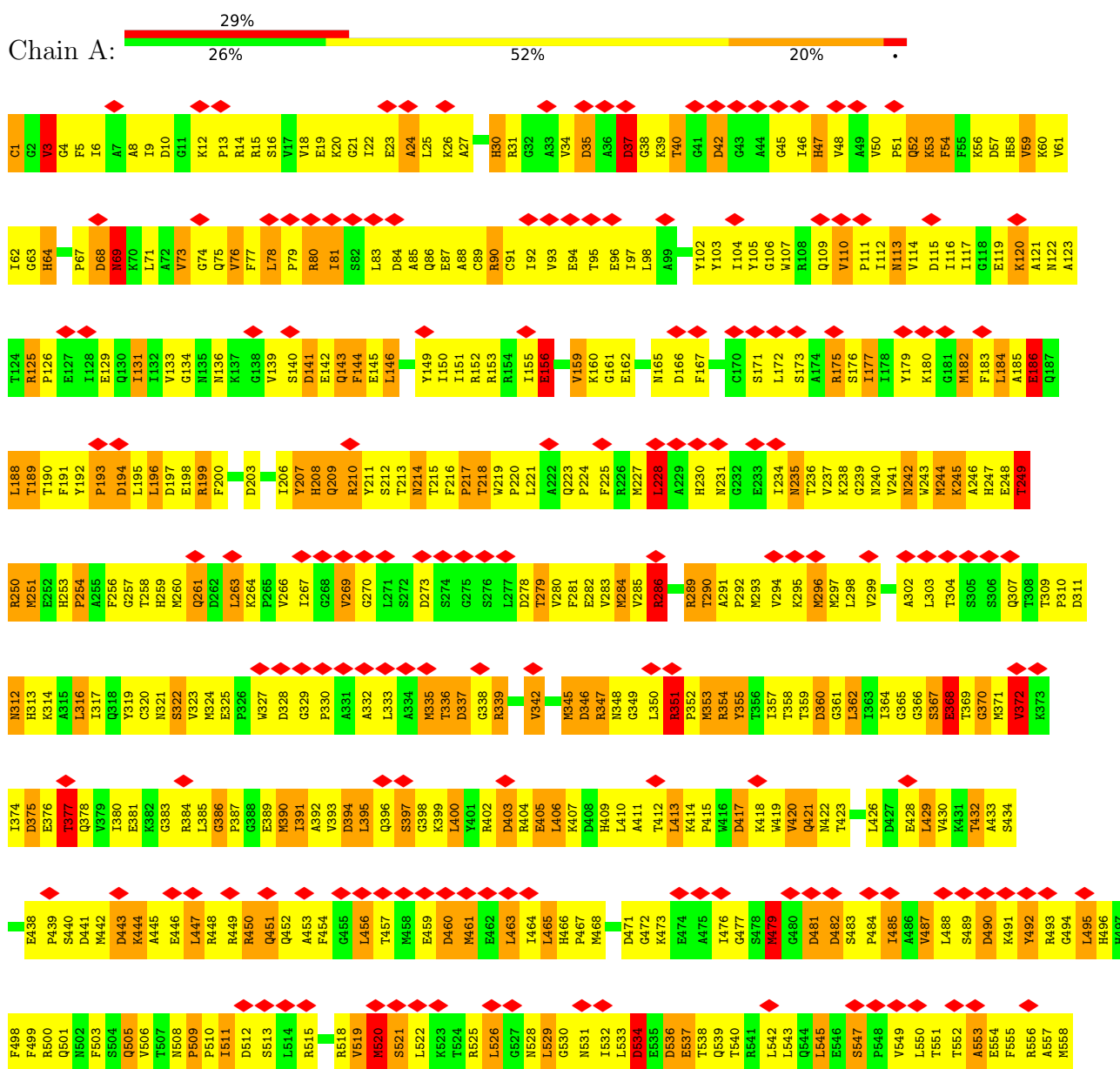


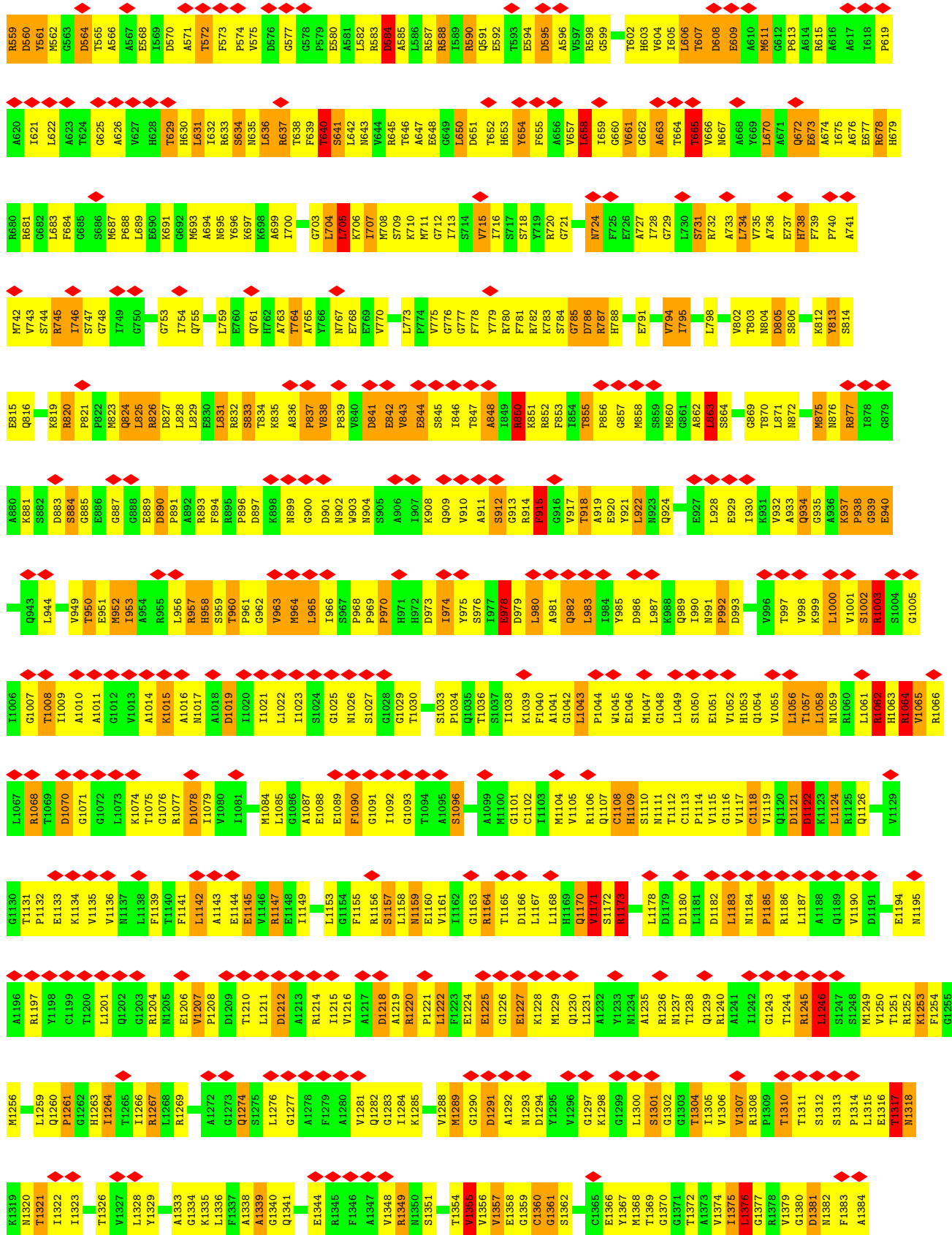
Mol	Chain	Residues	Atoms				AltConf	
			Total	C	N	O		P
8	G	1	53	27	9	15	2	0
8	H	1	53	27	9	15	2	0
8	I	1	53	27	9	15	2	0
8	J	1	53	27	9	15	2	0
8	K	1	53	27	9	15	2	0
8	L	1	53	27	9	15	2	0

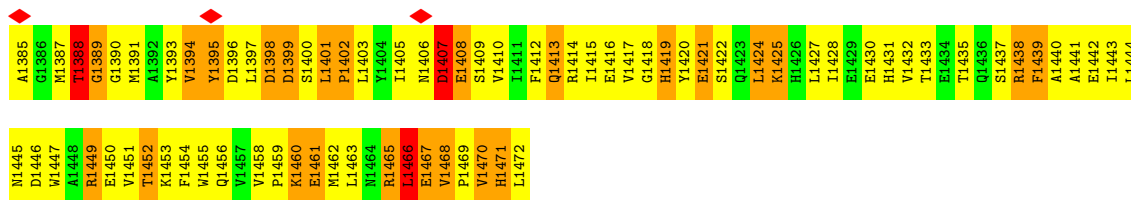
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

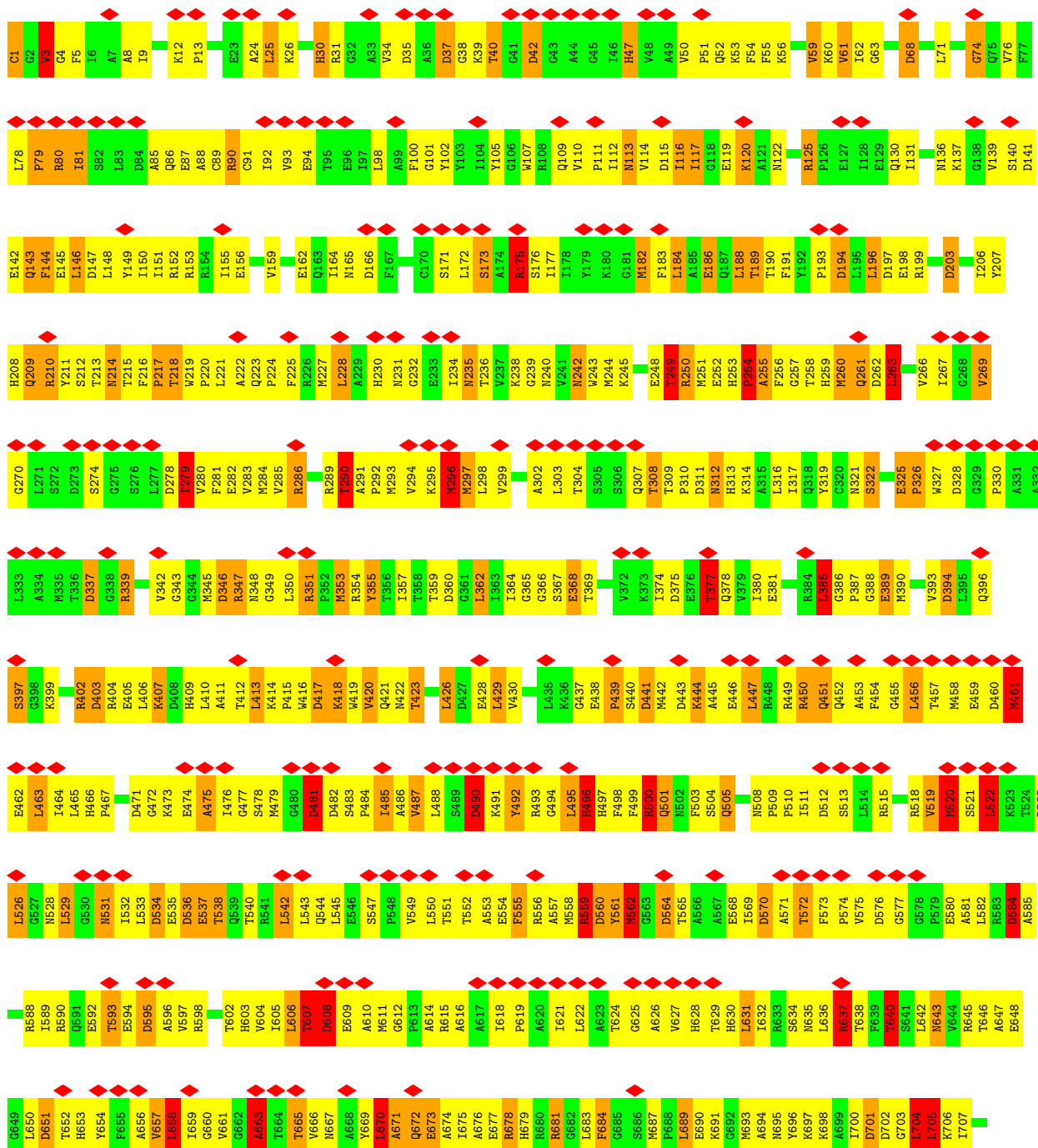
• Molecule 1: GLUTAMATE SYNTHASE [NADPH] LARGE CHAIN

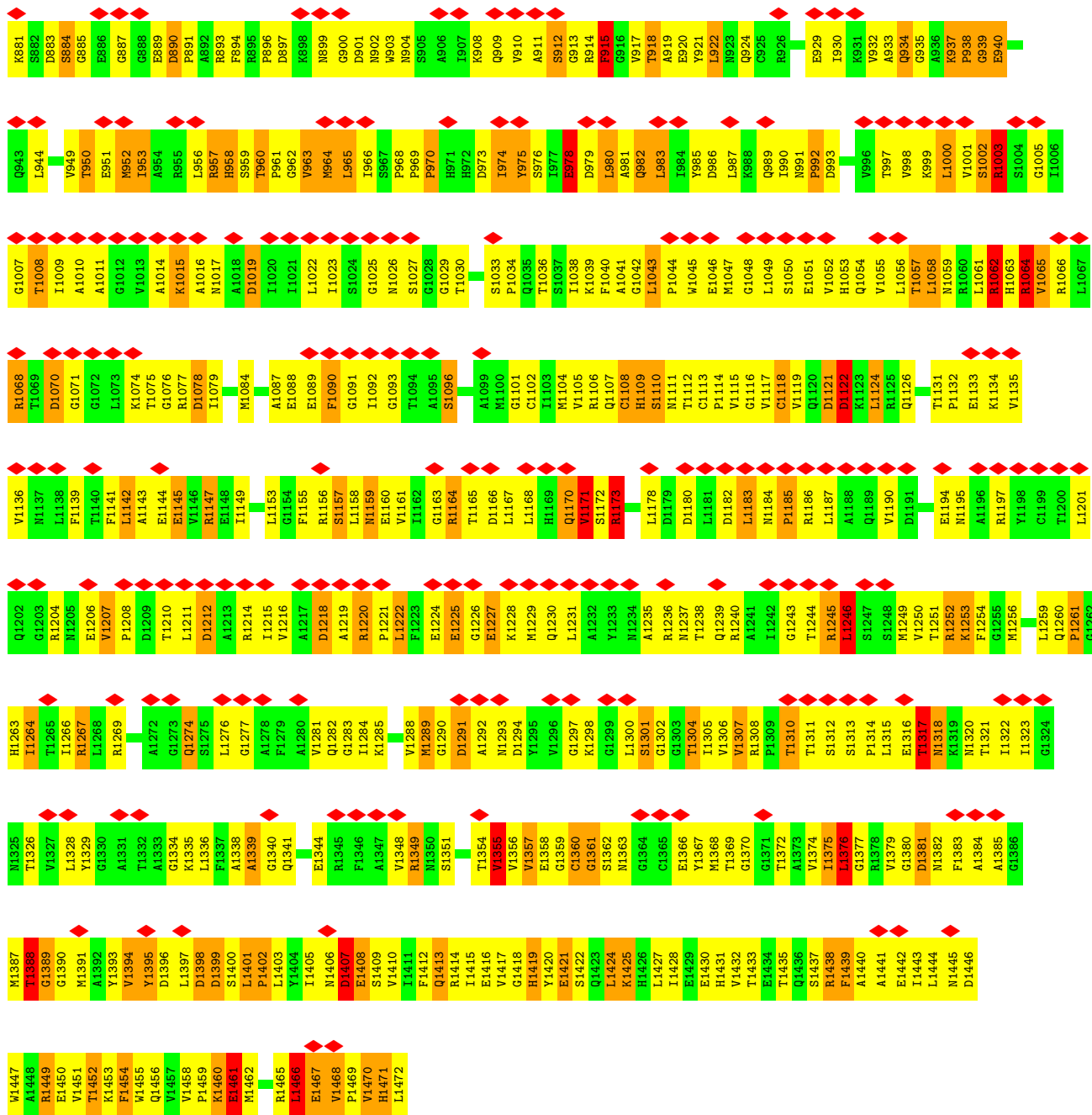




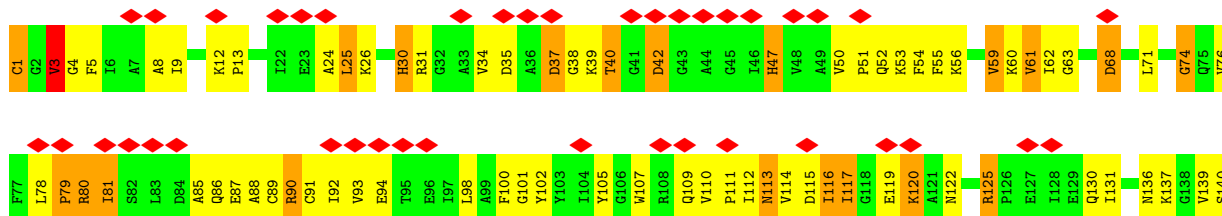


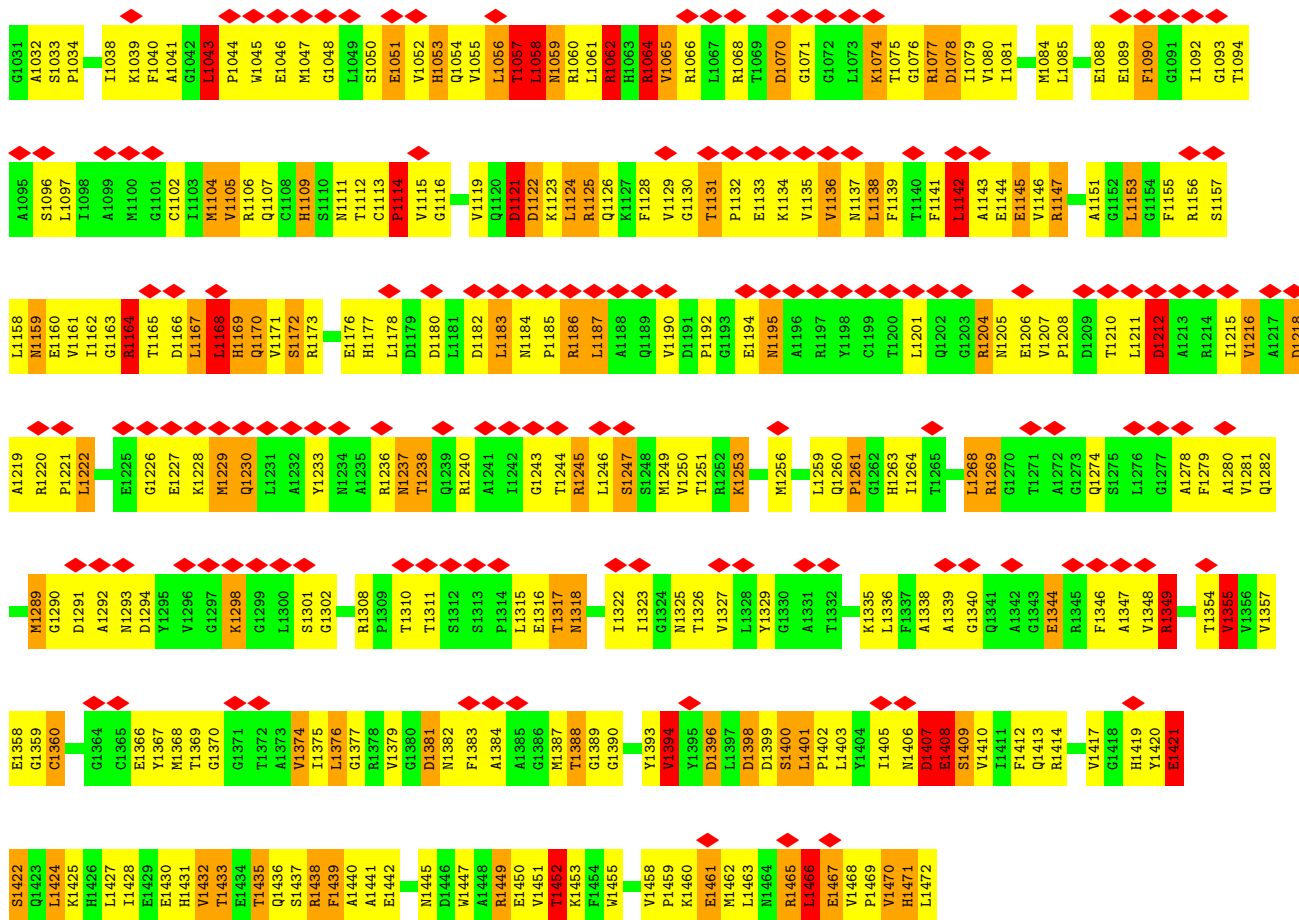
• Molecule 1: GLUTAMATE SYNTHASE [NADPH] LARGE CHAIN



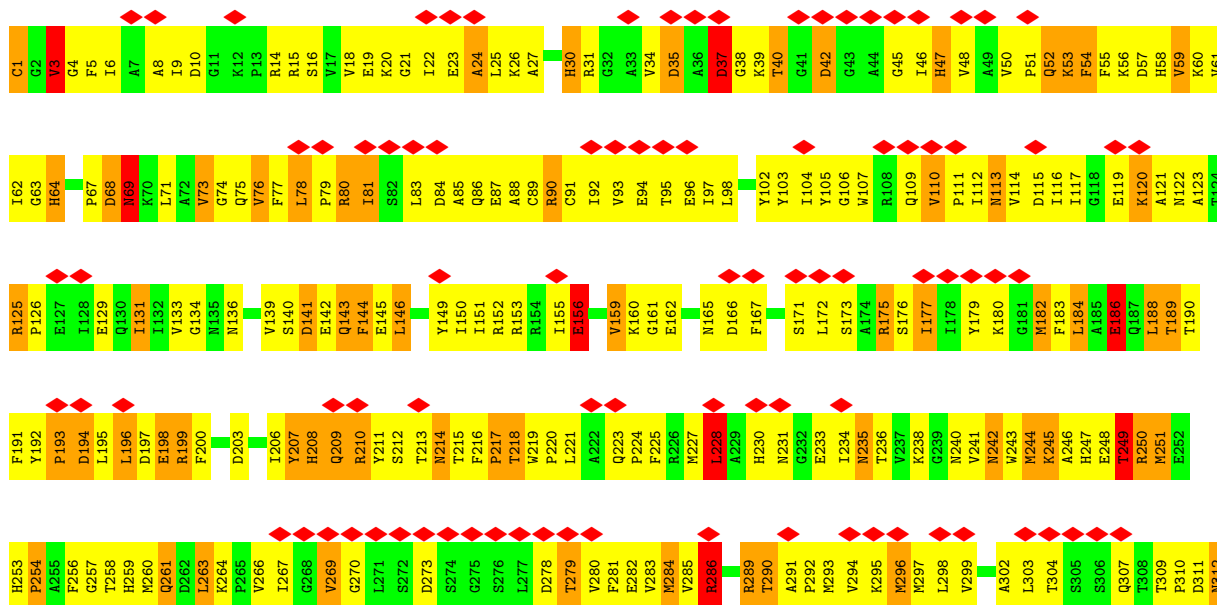


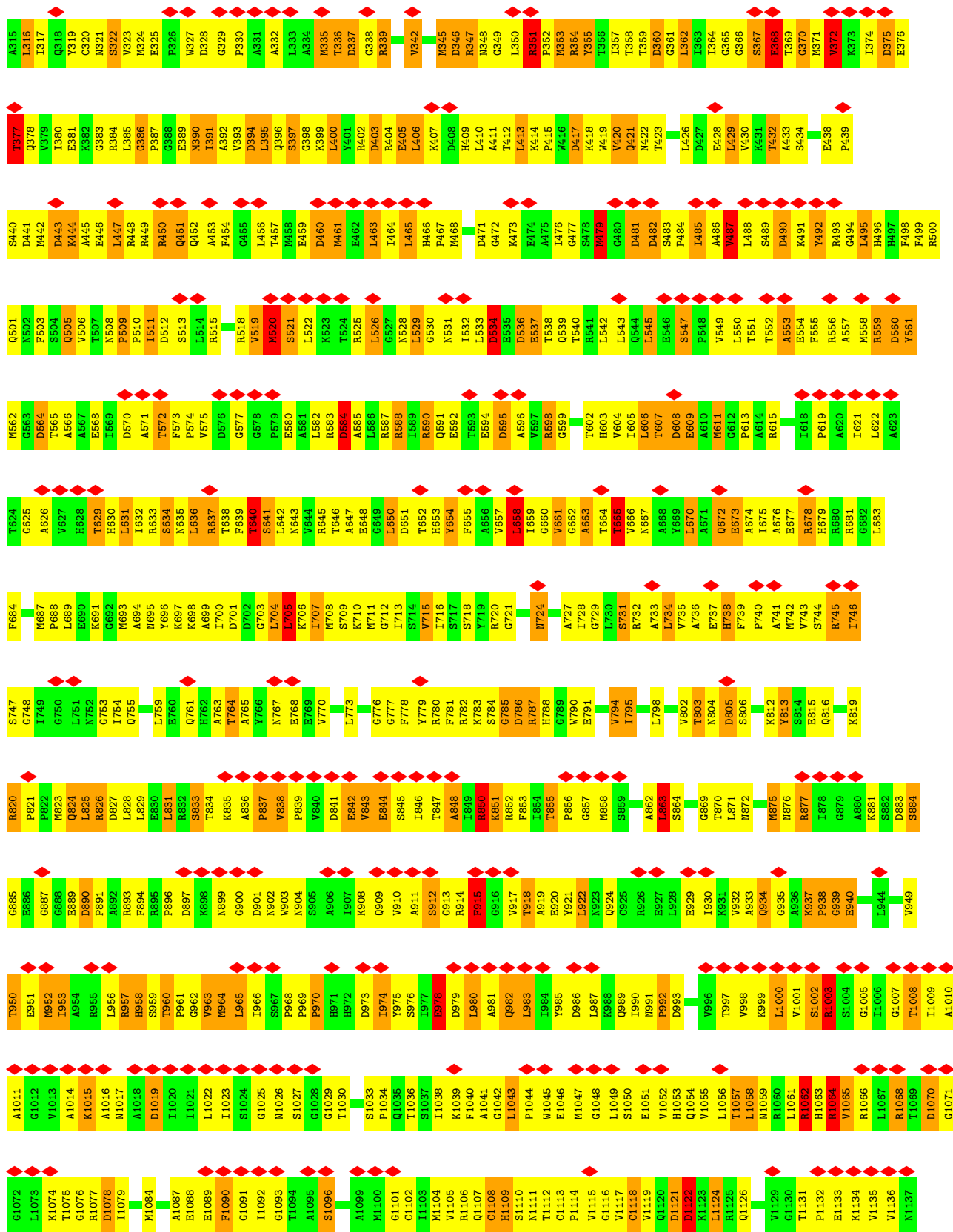
● Molecule 1: GLUTAMATE SYNTHASE [NADPH] LARGE CHAIN

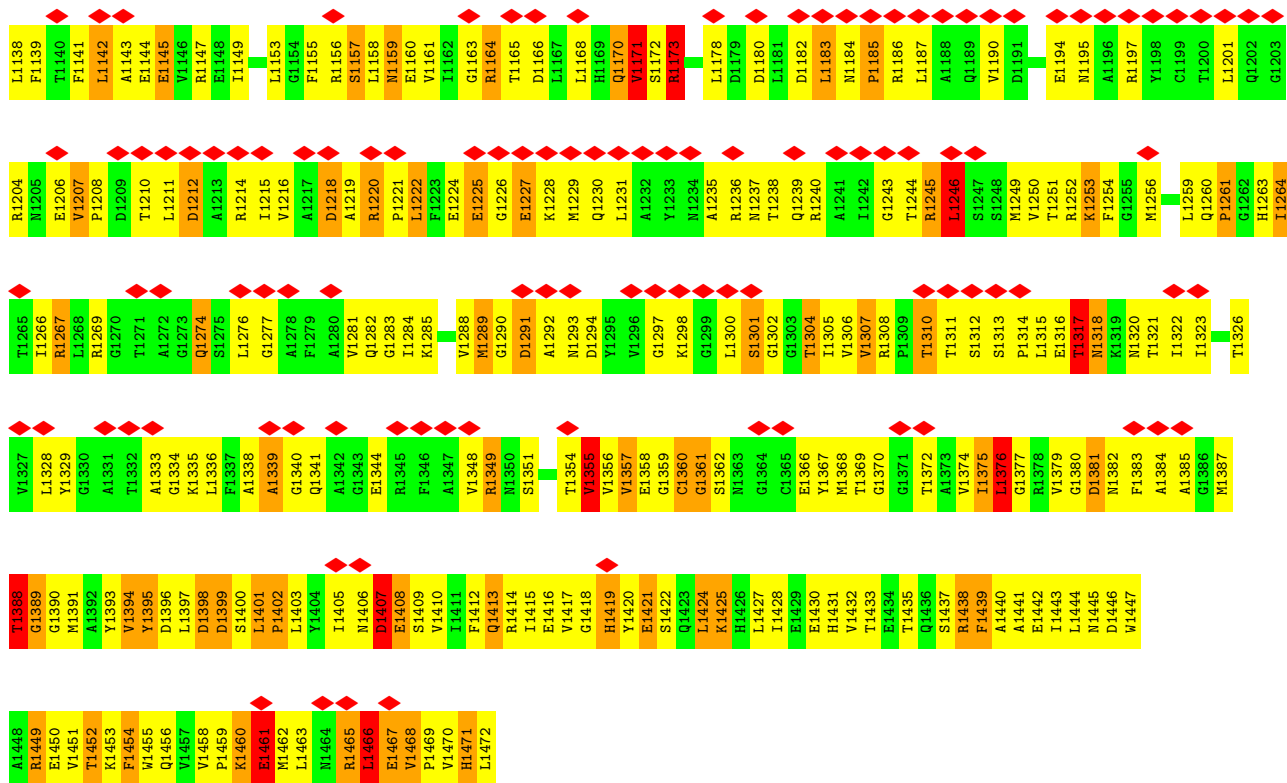




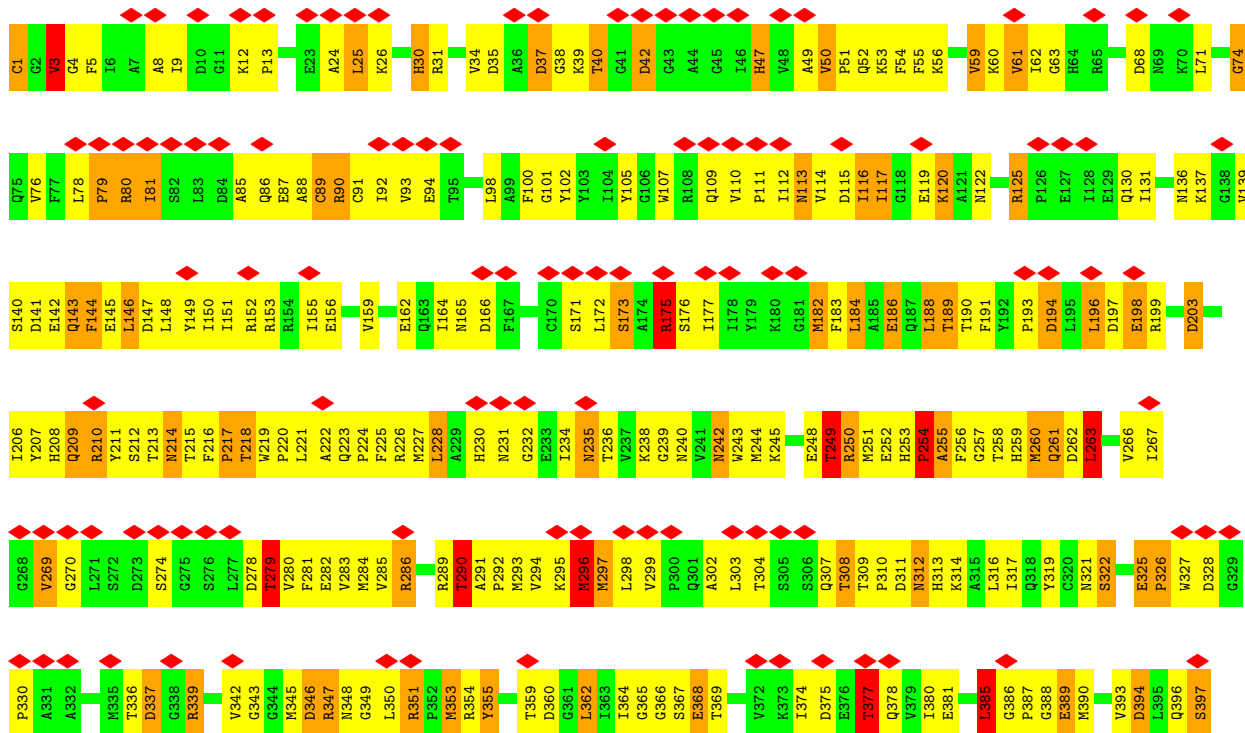
• Molecule 1: GLUTAMATE SYNTHASE [NADPH] LARGE CHAIN

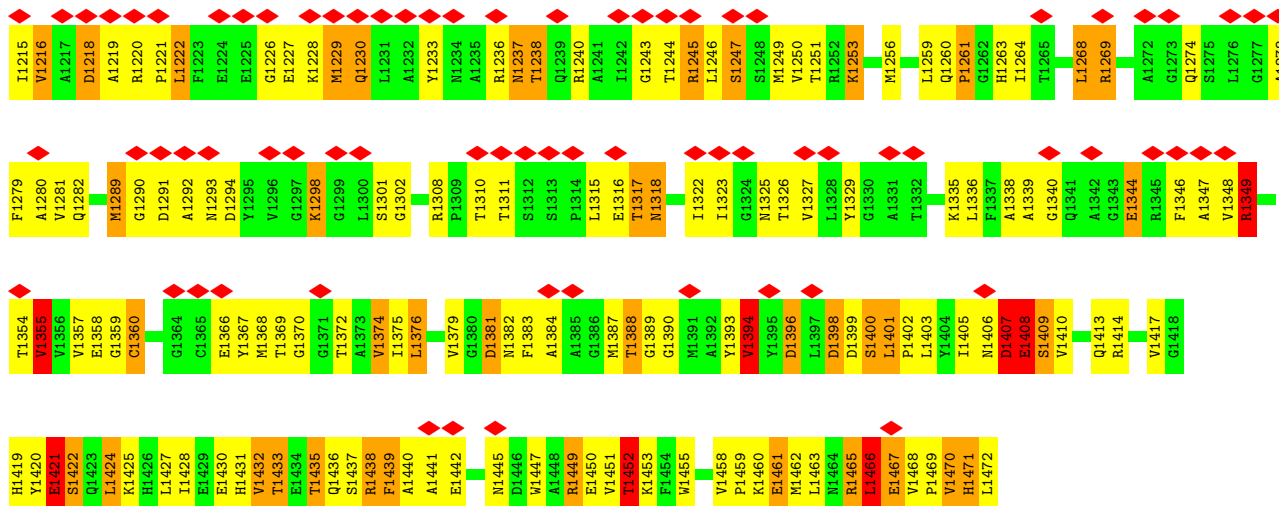




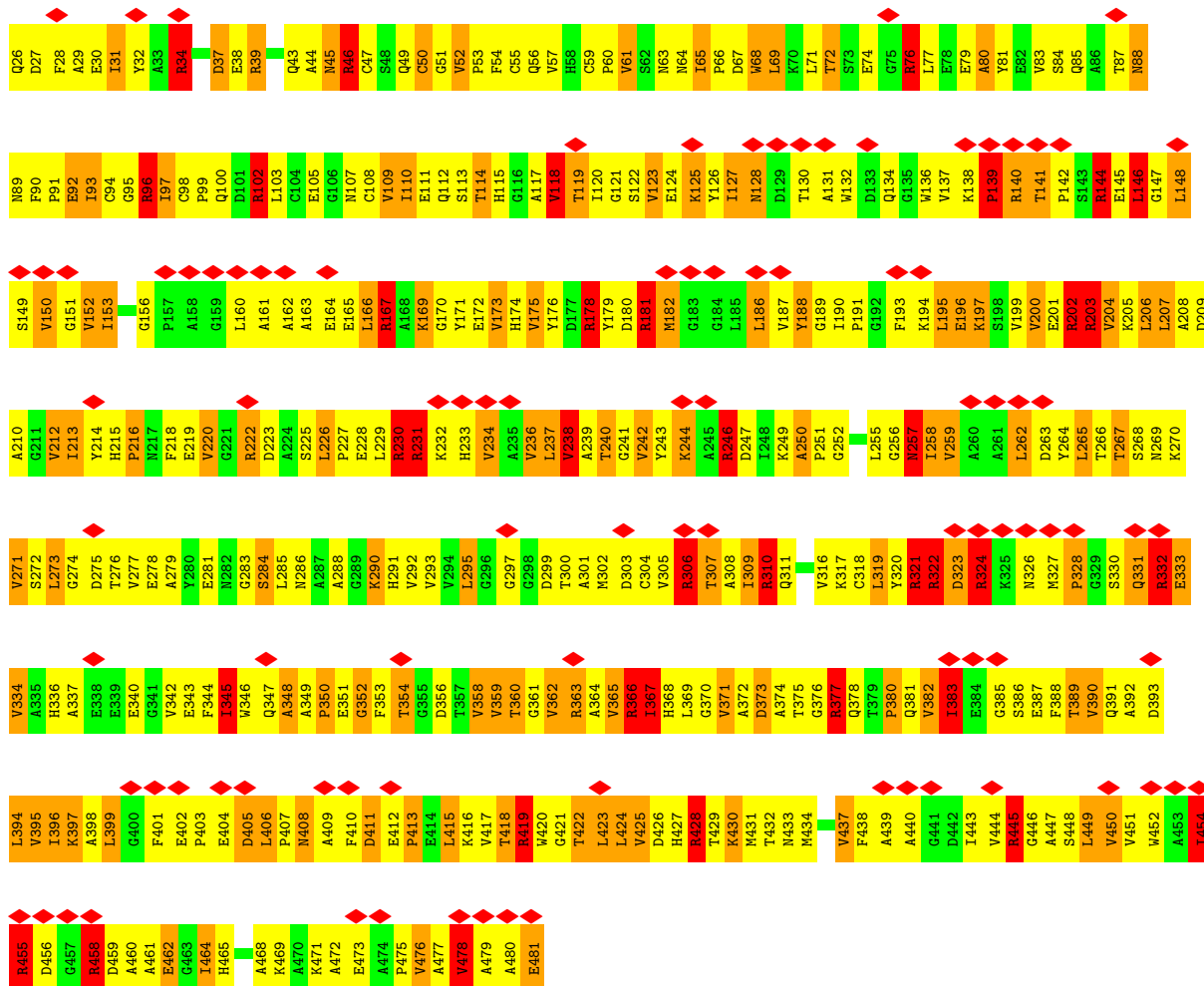
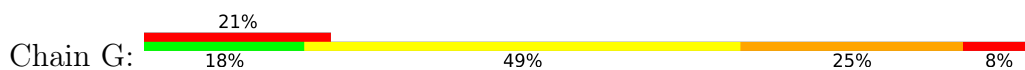


• Molecule 1: GLUTAMATE SYNTHASE [NADPH] LARGE CHAIN

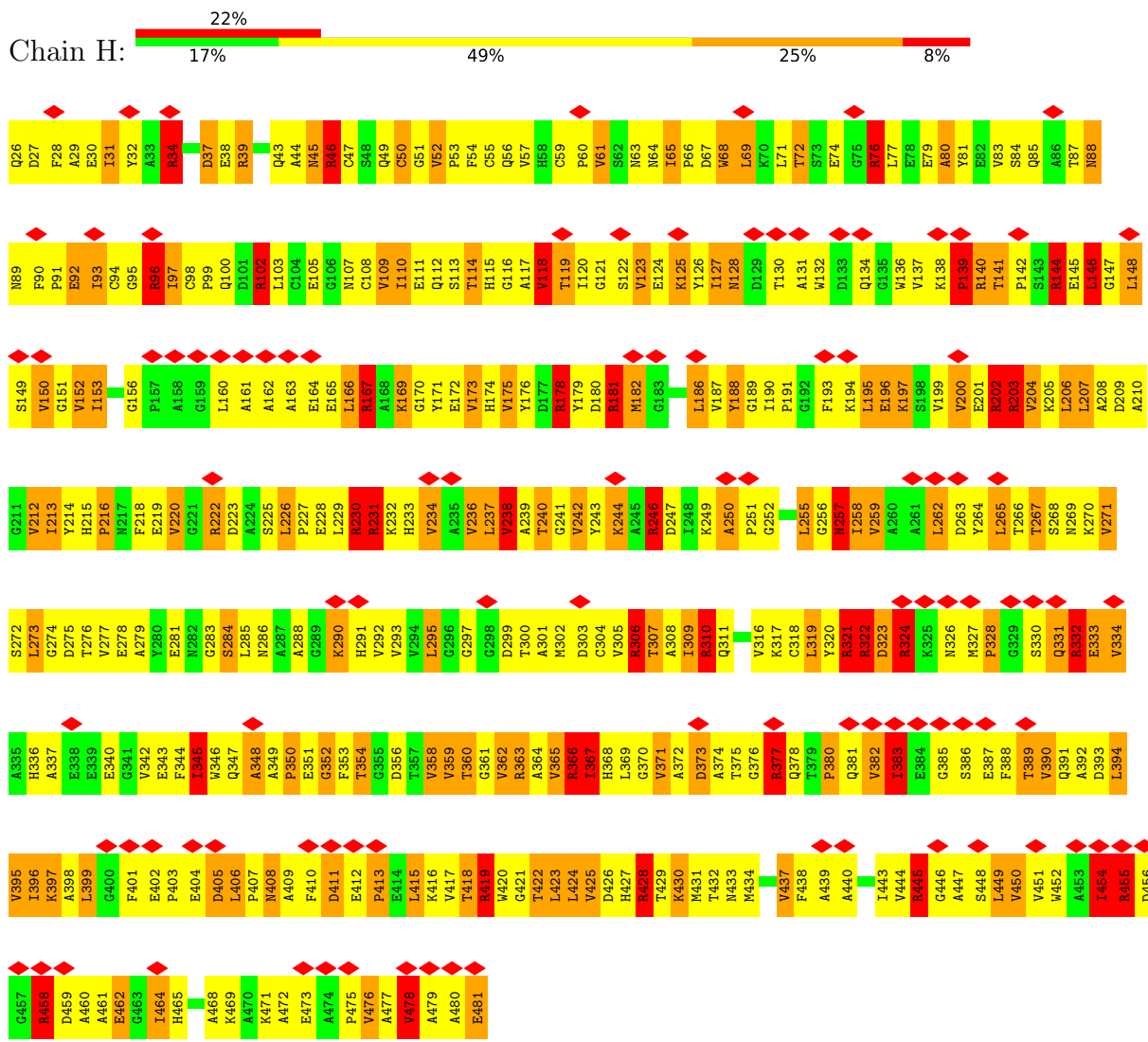


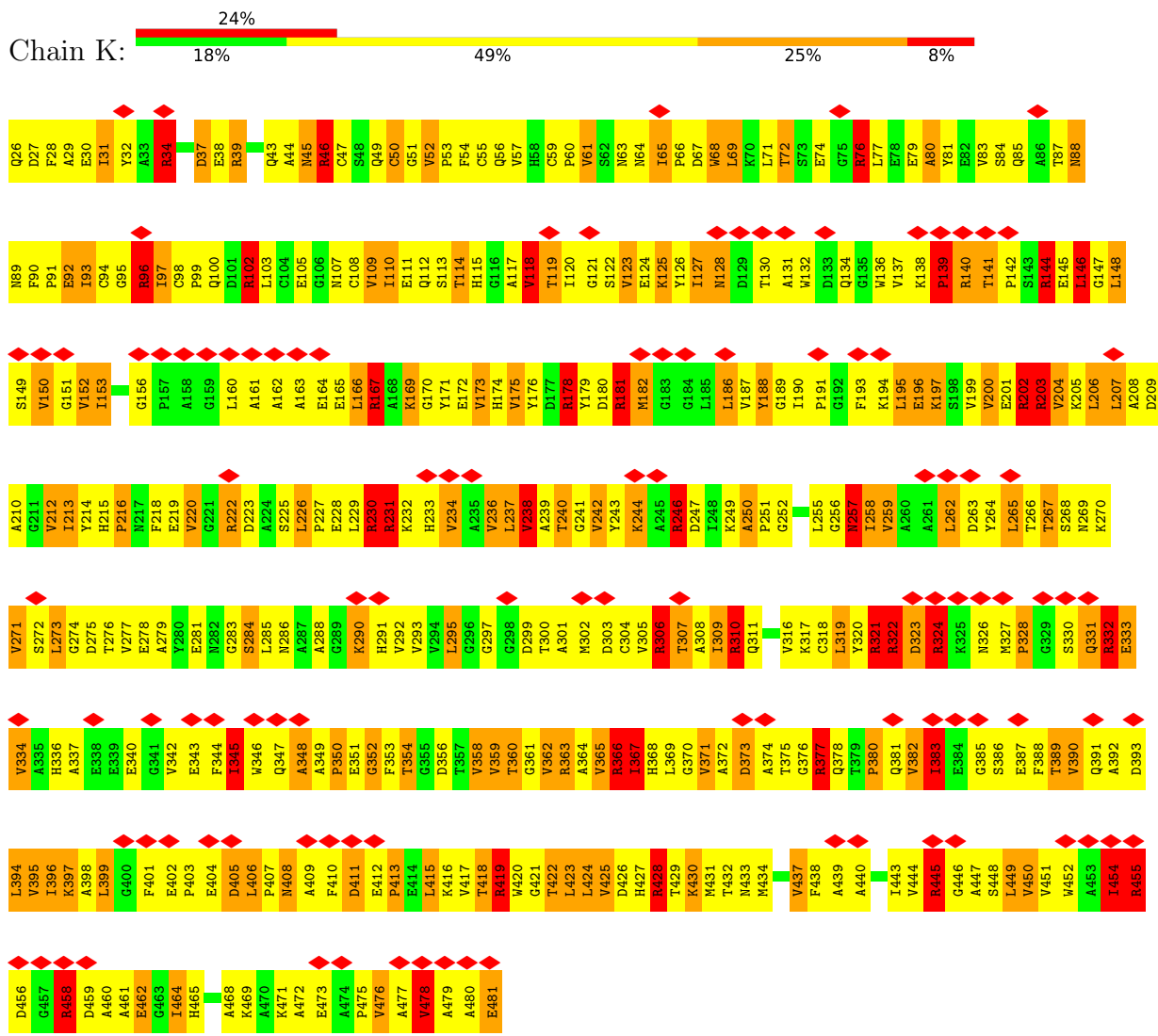


• Molecule 2: GLUTAMATE SYNTHASE [NADPH] SMALL CHAIN

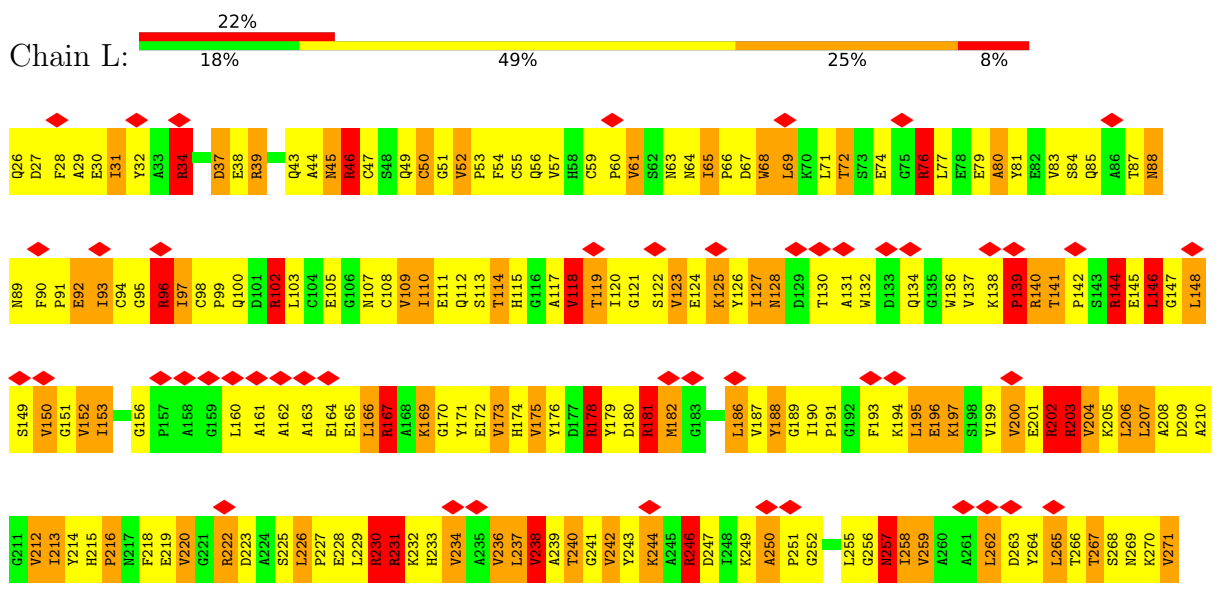


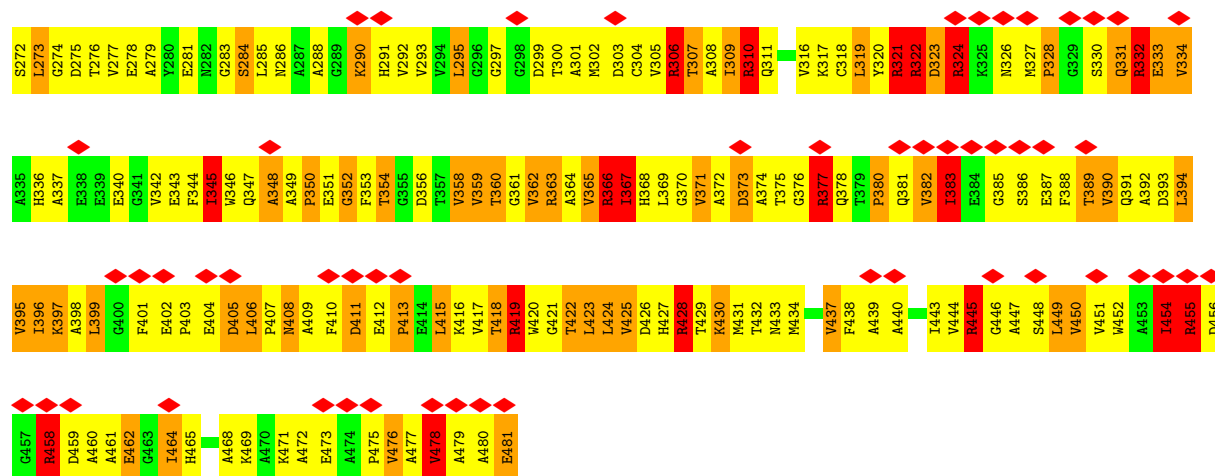
• Molecule 2: GLUTAMATE SYNTHASE [NADPH] SMALL CHAIN





• Molecule 2: GLUTAMATE SYNTHASE [NADPH] SMALL CHAIN





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	12800	Depositor
Resolution determination method	Not provided	
CTF correction method	WIENER FILTERING OF VOLUMES FROM FOCAL SERIES	Depositor
Microscope	JEOL 2010UHR	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	10	Depositor
Minimum defocus (nm)	1700	Depositor
Maximum defocus (nm)	3200	Depositor
Magnification	50000	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	1332.420	Depositor
Minimum map value	-799.538	Depositor
Average map value	5.063	Depositor
Map value standard deviation	98.686	Depositor
Recommended contour level	125.0	Depositor
Map size (\AA)	304.8, 304.8, 304.8	wwPDB
Map dimensions	192, 192, 192	wwPDB
Map angles ($^\circ$)	90, 90, 90	wwPDB
Pixel spacing (\AA)	1.5875, 1.5875, 1.5875	Depositor

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: AKG, F3S, FAD, OMT, SF4, 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	1.06	7/11545 (0.1%)	1.58	200/15613 (1.3%)
1	B	1.10	7/11545 (0.1%)	1.58	192/15613 (1.2%)
1	C	1.06	8/11545 (0.1%)	1.58	201/15613 (1.3%)
1	D	1.10	7/11545 (0.1%)	1.58	191/15613 (1.2%)
1	E	1.06	7/11545 (0.1%)	1.58	200/15613 (1.3%)
1	F	1.10	7/11545 (0.1%)	1.58	194/15613 (1.2%)
2	G	1.00	0/3533	1.78	76/4793 (1.6%)
2	H	1.00	0/3533	1.78	76/4793 (1.6%)
2	I	1.00	0/3533	1.78	76/4793 (1.6%)
2	J	1.00	0/3533	1.78	76/4793 (1.6%)
2	K	1.00	0/3533	1.78	76/4793 (1.6%)
2	L	1.00	0/3533	1.78	76/4793 (1.6%)
All	All	1.07	43/90468 (0.0%)	1.63	1634/122436 (1.3%)

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	1	3
1	B	0	2
1	C	1	3
1	D	0	2
1	E	1	3
1	F	0	2
2	G	0	31
2	H	0	31
2	I	0	31
2	J	0	31
2	K	0	31

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
2	L	0	31
All	All	3	201

The worst 5 of 43 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	838	VAL	CA-CB	-7.81	1.38	1.54
1	A	838	VAL	CA-CB	-7.78	1.38	1.54
1	E	838	VAL	CA-CB	-7.76	1.38	1.54
1	E	746	ILE	CA-CB	-7.49	1.37	1.54
1	A	746	ILE	CA-CB	-7.46	1.37	1.54

The worst 5 of 1634 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	45	ASN	CB-CG-OD1	-39.98	41.63	121.60
2	L	45	ASN	CB-CG-OD1	-39.98	41.63	121.60
2	G	45	ASN	CB-CG-OD1	-39.98	41.65	121.60
2	J	45	ASN	CB-CG-OD1	-39.98	41.65	121.60
2	I	45	ASN	CB-CG-OD1	-39.95	41.70	121.60

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	915	PHE	CA
1	C	915	PHE	CA
1	E	915	PHE	CA

5 of 201 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1002	SER	Mainchain
1	A	1171	VAL	Peptide
1	A	325	GLU	Mainchain
1	B	1168	LEU	Mainchain
1	B	725	PHE	Mainchain

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	11337	0	11347	1766	0
1	B	11337	0	11350	1542	0
1	C	11337	0	11347	1762	0
1	D	11337	0	11350	1536	0
1	E	11337	0	11347	1774	0
1	F	11337	0	11350	1543	0
2	G	3468	0	3397	1086	0
2	H	3468	0	3397	1079	0
2	I	3468	0	3397	1089	0
2	J	3468	0	3399	1075	0
2	K	3468	0	3399	1080	0
2	L	3468	0	3399	1078	0
3	A	11	0	10	3	0
3	B	11	0	10	0	0
3	C	11	0	10	3	0
3	D	11	0	10	0	0
3	E	11	0	10	3	0
3	F	11	0	10	1	0
4	A	31	0	19	4	0
4	B	31	0	19	7	0
4	C	31	0	19	3	0
4	D	31	0	19	7	0
4	E	31	0	19	4	0
4	F	31	0	19	6	0
5	A	10	0	4	0	0
5	B	10	0	4	2	0
5	C	10	0	4	0	0
5	D	10	0	4	2	0
5	E	10	0	4	0	0
5	F	10	0	4	1	0
6	A	7	0	0	3	0
6	B	7	0	0	3	0
6	C	7	0	0	3	0
6	D	7	0	0	3	0
6	E	7	0	0	6	0
6	F	7	0	0	3	0
7	G	16	0	0	2	0
7	H	16	0	0	2	0
7	I	16	0	0	2	0
7	J	16	0	0	2	0
7	K	16	0	0	2	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	L	16	0	0	2	0
8	G	53	0	31	18	0
8	H	53	0	31	18	0
8	I	53	0	31	18	0
8	J	53	0	31	18	0
8	K	53	0	31	18	0
8	L	53	0	31	17	0
All	All	89598	0	88863	15415	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 86.

The worst 5 of 15415 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:B:1263:HIS:CE1	1:D:900:GLY:CA	1.77	1.66
1:A:782:ARG:CG	2:J:53:PRO:HD2	1.19	1.65
1:E:782:ARG:CG	2:L:53:PRO:HD2	1.19	1.64
1:F:182:MET:CE	1:F:217:PRO:HB2	1.30	1.61
1:A:902:ASN:HB2	1:C:1227:GLU:CG	1.13	1.61

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1470/1472 (100%)	1174 (80%)	231 (16%)	65 (4%)	2	22
1	B	1470/1472 (100%)	1191 (81%)	215 (15%)	64 (4%)	2	22
1	C	1470/1472 (100%)	1175 (80%)	230 (16%)	65 (4%)	2	22
1	D	1470/1472 (100%)	1191 (81%)	215 (15%)	64 (4%)	2	22

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	1470/1472 (100%)	1174 (80%)	231 (16%)	65 (4%)	2	22
1	F	1470/1472 (100%)	1192 (81%)	214 (15%)	64 (4%)	2	22
2	G	454/456 (100%)	419 (92%)	25 (6%)	10 (2%)	6	35
2	H	454/456 (100%)	420 (92%)	24 (5%)	10 (2%)	6	35
2	I	454/456 (100%)	420 (92%)	24 (5%)	10 (2%)	6	35
2	J	454/456 (100%)	419 (92%)	25 (6%)	10 (2%)	6	35
2	K	454/456 (100%)	420 (92%)	24 (5%)	10 (2%)	6	35
2	L	454/456 (100%)	420 (92%)	24 (5%)	10 (2%)	6	35
All	All	11544/11568 (100%)	9615 (83%)	1482 (13%)	447 (4%)	5	23

5 of 447 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	25	LEU
1	A	444	LYS
1	A	451	GLN
1	A	705	LEU
1	A	712	GLY

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1201/1201 (100%)	985 (82%)	216 (18%)	1	10
1	B	1201/1201 (100%)	981 (82%)	220 (18%)	1	10
1	C	1201/1201 (100%)	985 (82%)	216 (18%)	1	10
1	D	1201/1201 (100%)	981 (82%)	220 (18%)	1	10
1	E	1201/1201 (100%)	985 (82%)	216 (18%)	1	10
1	F	1201/1201 (100%)	981 (82%)	220 (18%)	1	10
2	G	358/358 (100%)	257 (72%)	101 (28%)	0	2
2	H	358/358 (100%)	257 (72%)	101 (28%)	0	2

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	I	358/358 (100%)	257 (72%)	101 (28%)	0	2
2	J	358/358 (100%)	257 (72%)	101 (28%)	0	2
2	K	358/358 (100%)	257 (72%)	101 (28%)	0	2
2	L	358/358 (100%)	257 (72%)	101 (28%)	0	2
All	All	9354/9354 (100%)	7440 (80%)	1914 (20%)	3	7

5 of 1914 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	336	THR
2	K	347	GLN
1	F	380	ILE
2	K	242	VAL
2	L	399	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 277 such sidechains are listed below:

Mol	Chain	Res	Type
2	G	45	ASN
2	G	433	ASN
2	J	291	HIS
1	C	724	ASN
1	C	635	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry

42 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
6	F3S	D	2476	1	0,9,9	-	-	-		
7	SF4	L	482	2	0,12,12	-	-	-		
8	FAD	L	484	-	53,58,58	1.89	19 (35%)	68,89,89	1.26	9 (13%)
8	FAD	J	484	-	53,58,58	1.89	19 (35%)	68,89,89	1.26	8 (11%)
3	OMT	F	2473	-	9,10,10	4.15	5 (55%)	11,14,14	5.79	5 (45%)
7	SF4	I	482	2	0,12,12	-	-	-		
4	FMN	C	2474	-	33,33,33	1.48	5 (15%)	48,50,50	2.73	20 (41%)
7	SF4	J	483	2	0,12,12	-	-	-		
7	SF4	I	483	2	0,12,12	-	-	-		
4	FMN	D	2474	-	33,33,33	1.37	4 (12%)	48,50,50	2.59	20 (41%)
4	FMN	A	2474	-	33,33,33	1.48	5 (15%)	48,50,50	2.72	20 (41%)
4	FMN	B	2474	-	33,33,33	1.37	4 (12%)	48,50,50	2.59	20 (41%)
6	F3S	C	2476	1	0,9,9	-	-	-		
7	SF4	G	482	2	0,12,12	-	-	-		
7	SF4	G	483	2	0,12,12	-	-	-		
4	FMN	E	2474	-	33,33,33	1.48	5 (15%)	48,50,50	2.73	20 (41%)
7	SF4	H	483	2	0,12,12	-	-	-		
8	FAD	G	484	-	53,58,58	1.89	19 (35%)	68,89,89	1.26	8 (11%)
3	OMT	E	2473	-	9,10,10	4.27	5 (55%)	11,14,14	4.46	6 (54%)
6	F3S	F	2476	1	0,9,9	-	-	-		
7	SF4	H	482	2	0,12,12	-	-	-		
4	FMN	F	2474	-	33,33,33	1.37	4 (12%)	48,50,50	2.59	20 (41%)
5	AKG	B	2475	-	9,9,9	3.48	4 (44%)	11,11,11	2.80	4 (36%)
3	OMT	B	2473	-	9,10,10	4.15	5 (55%)	11,14,14	5.78	5 (45%)
6	F3S	A	2476	1	0,9,9	-	-	-		
7	SF4	J	482	2	0,12,12	-	-	-		
6	F3S	B	2476	1	0,9,9	-	-	-		
5	AKG	E	2475	-	9,9,9	3.08	4 (44%)	11,11,11	2.91	4 (36%)
5	AKG	F	2475	-	9,9,9	3.48	4 (44%)	11,11,11	2.80	4 (36%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	SF4	K	483	2	0,12,12	-	-	-		
3	OMT	A	2473	-	9,10,10	4.28	5 (55%)	11,14,14	4.47	6 (54%)
8	FAD	I	484	-	53,58,58	1.89	19 (35%)	68,89,89	1.26	8 (11%)
7	SF4	K	482	2	0,12,12	-	-	-		
8	FAD	K	484	-	53,58,58	1.89	19 (35%)	68,89,89	1.26	8 (11%)
5	AKG	A	2475	-	9,9,9	3.09	4 (44%)	11,11,11	2.92	4 (36%)
3	OMT	C	2473	-	9,10,10	4.28	5 (55%)	11,14,14	4.47	6 (54%)
3	OMT	D	2473	-	9,10,10	4.14	5 (55%)	11,14,14	5.79	5 (45%)
5	AKG	D	2475	-	9,9,9	3.49	4 (44%)	11,11,11	2.80	4 (36%)
8	FAD	H	484	-	53,58,58	1.89	19 (35%)	68,89,89	1.26	9 (13%)
5	AKG	C	2475	-	9,9,9	3.08	4 (44%)	11,11,11	2.92	4 (36%)
7	SF4	L	483	2	0,12,12	-	-	-		
6	F3S	E	2476	1	0,9,9	-	-	-		

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
8	FAD	L	484	-	-	3/30/50/50	0/6/6/6
6	F3S	D	2476	1	-	-	0/3/3/3
7	SF4	L	482	2	-	-	0/6/5/5
8	FAD	J	484	-	-	3/30/50/50	0/6/6/6
3	OMT	F	2473	-	-	5/10/10/10	-
7	SF4	I	482	2	-	-	0/6/5/5
4	FMN	C	2474	-	-	7/18/18/18	0/3/3/3
7	SF4	J	483	2	-	-	0/6/5/5
7	SF4	I	483	2	-	-	0/6/5/5
4	FMN	D	2474	-	-	4/18/18/18	0/3/3/3
4	FMN	A	2474	-	-	7/18/18/18	0/3/3/3
4	FMN	B	2474	-	-	4/18/18/18	0/3/3/3
6	F3S	C	2476	1	-	-	0/3/3/3
7	SF4	G	482	2	-	-	0/6/5/5
7	SF4	G	483	2	-	-	0/6/5/5
4	FMN	E	2474	-	-	7/18/18/18	0/3/3/3
7	SF4	H	483	2	-	-	0/6/5/5
8	FAD	G	484	-	-	3/30/50/50	0/6/6/6

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	OMT	E	2473	-	-	5/10/10/10	-
6	F3S	F	2476	1	-	-	0/3/3/3
7	SF4	H	482	2	-	-	0/6/5/5
4	FMN	F	2474	-	-	4/18/18/18	0/3/3/3
5	AKG	B	2475	-	-	1/9/9/9	-
3	OMT	B	2473	-	-	5/10/10/10	-
6	F3S	A	2476	1	-	-	0/3/3/3
7	SF4	J	482	2	-	-	0/6/5/5
6	F3S	B	2476	1	-	-	0/3/3/3
5	AKG	E	2475	-	-	2/9/9/9	-
5	AKG	F	2475	-	-	1/9/9/9	-
7	SF4	K	483	2	-	-	0/6/5/5
3	OMT	A	2473	-	-	5/10/10/10	-
8	FAD	I	484	-	-	3/30/50/50	0/6/6/6
7	SF4	K	482	2	-	-	0/6/5/5
8	FAD	K	484	-	-	3/30/50/50	0/6/6/6
5	AKG	A	2475	-	-	2/9/9/9	-
3	OMT	C	2473	-	-	5/10/10/10	-
3	OMT	D	2473	-	-	5/10/10/10	-
5	AKG	D	2475	-	-	1/9/9/9	-
8	FAD	H	484	-	-	3/30/50/50	0/6/6/6
5	AKG	C	2475	-	-	2/9/9/9	-
7	SF4	L	483	2	-	-	0/6/5/5
6	F3S	E	2476	1	-	-	0/3/3/3

The worst 5 of 195 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	2473	OMT	CB-CG	-7.01	1.45	1.52
3	A	2473	OMT	CB-CG	-6.97	1.45	1.52
3	E	2473	OMT	CB-CG	-6.93	1.45	1.52
3	B	2473	OMT	CG-SD	-6.88	1.69	1.78
3	F	2473	OMT	CG-SD	-6.86	1.69	1.78

The worst 5 of 227 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	2473	OMT	OD2-SD-CG	-16.66	96.68	108.34
3	F	2473	OMT	OD2-SD-CG	-16.64	96.69	108.34

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	2473	OMT	OD2-SD-CG	-16.63	96.70	108.34
3	C	2473	OMT	OD2-SD-CE	-11.63	97.22	108.91
3	A	2473	OMT	OD2-SD-CE	-11.61	97.24	108.91

There are no chirality outliers.

5 of 90 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	2473	OMT	C-CA-CB-CG
3	A	2473	OMT	CB-CG-SD-OD1
3	A	2473	OMT	CB-CG-SD-OD2
3	B	2473	OMT	N-CA-CB-CG
3	B	2473	OMT	C-CA-CB-CG

There are no ring outliers.

31 monomers are involved in 186 short contacts:

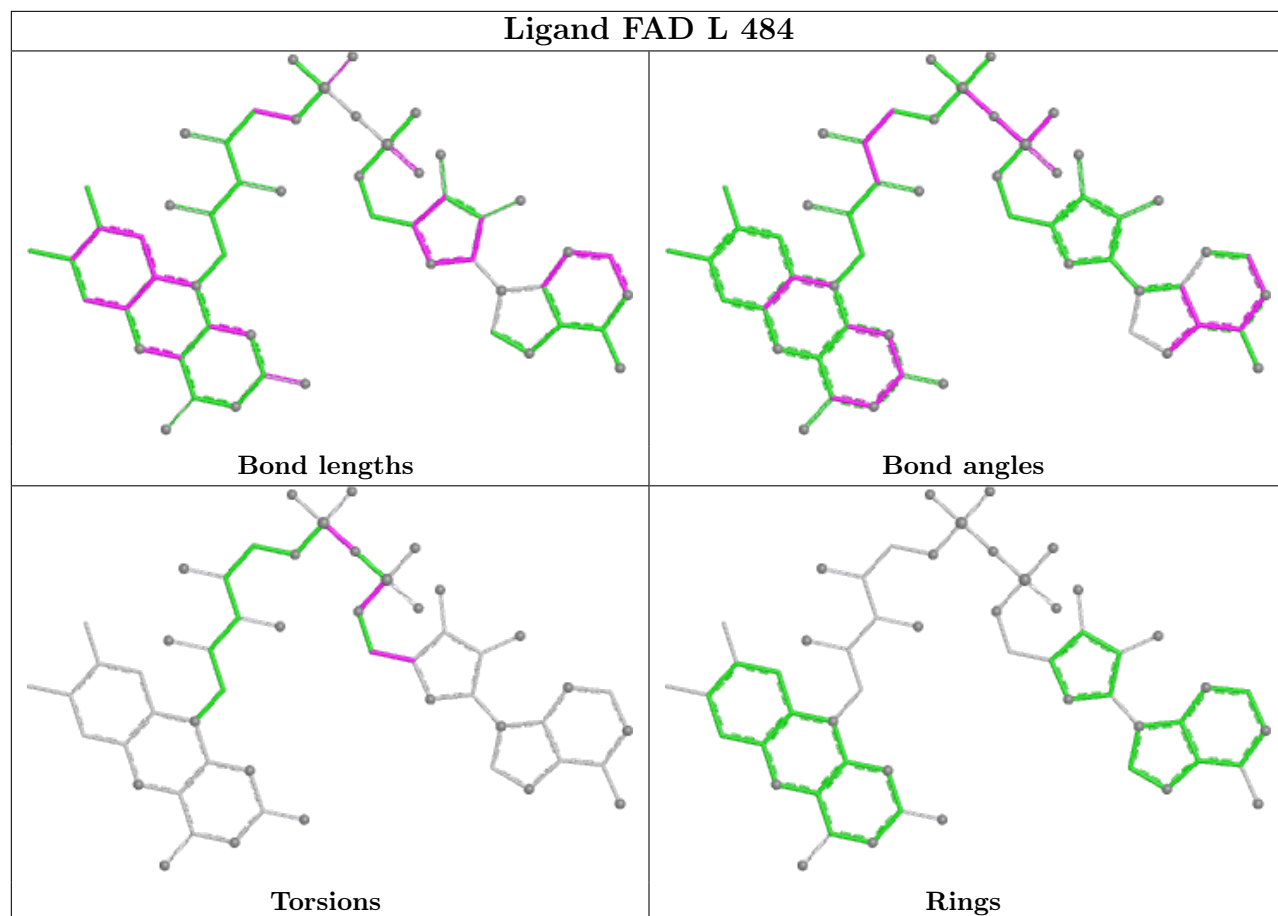
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	D	2476	F3S	3	0
8	L	484	FAD	17	0
8	J	484	FAD	18	0
3	F	2473	OMT	1	0
4	C	2474	FMN	3	0
7	J	483	SF4	2	0
7	I	483	SF4	2	0
4	D	2474	FMN	7	0
4	A	2474	FMN	4	0
4	B	2474	FMN	7	0
6	C	2476	F3S	3	0
7	G	483	SF4	2	0
4	E	2474	FMN	4	0
7	H	483	SF4	2	0
8	G	484	FAD	18	0
3	E	2473	OMT	3	0
6	F	2476	F3S	3	0
4	F	2474	FMN	6	0
5	B	2475	AKG	2	0
6	A	2476	F3S	3	0
6	B	2476	F3S	3	0
5	F	2475	AKG	1	0
7	K	483	SF4	2	0

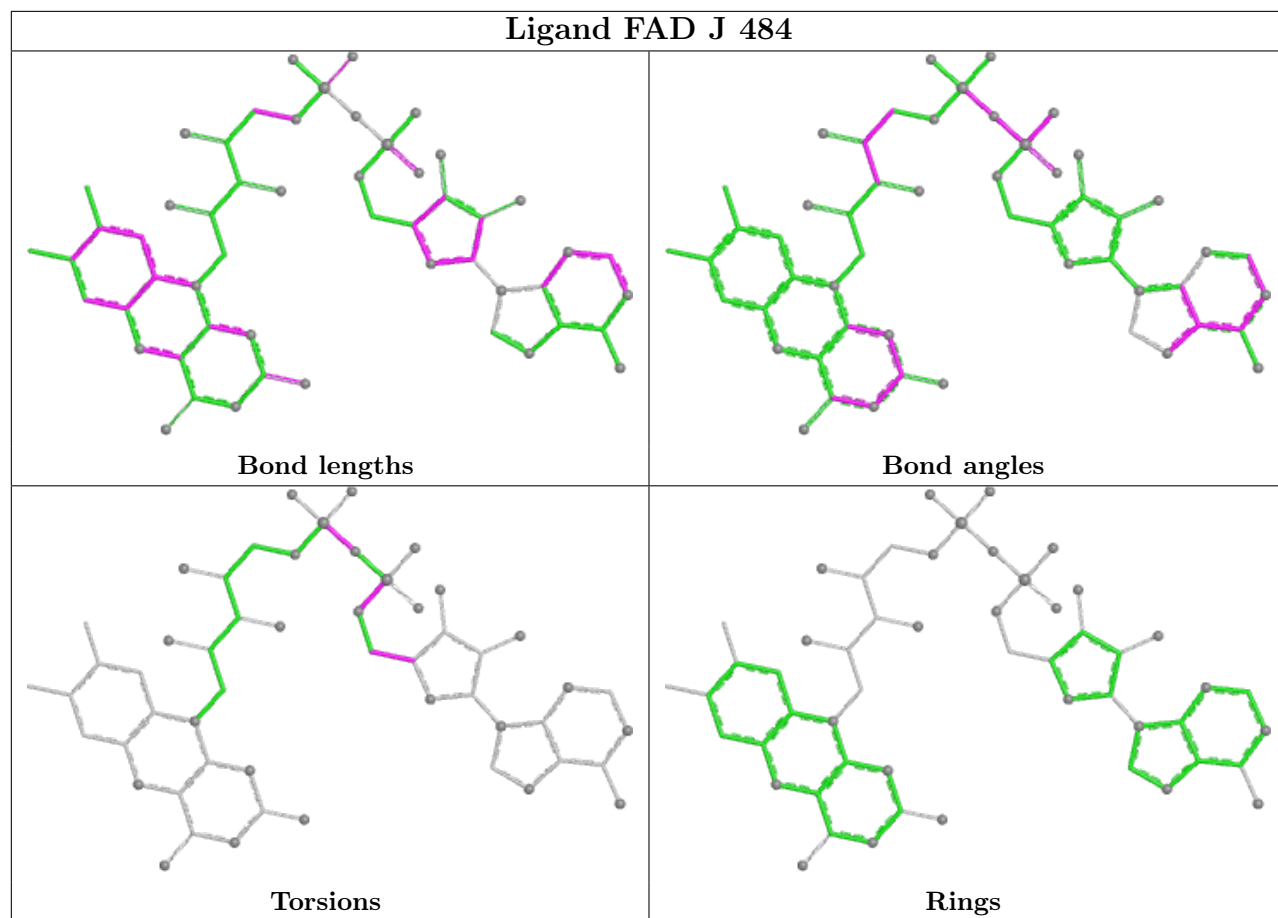
Continued on next page...

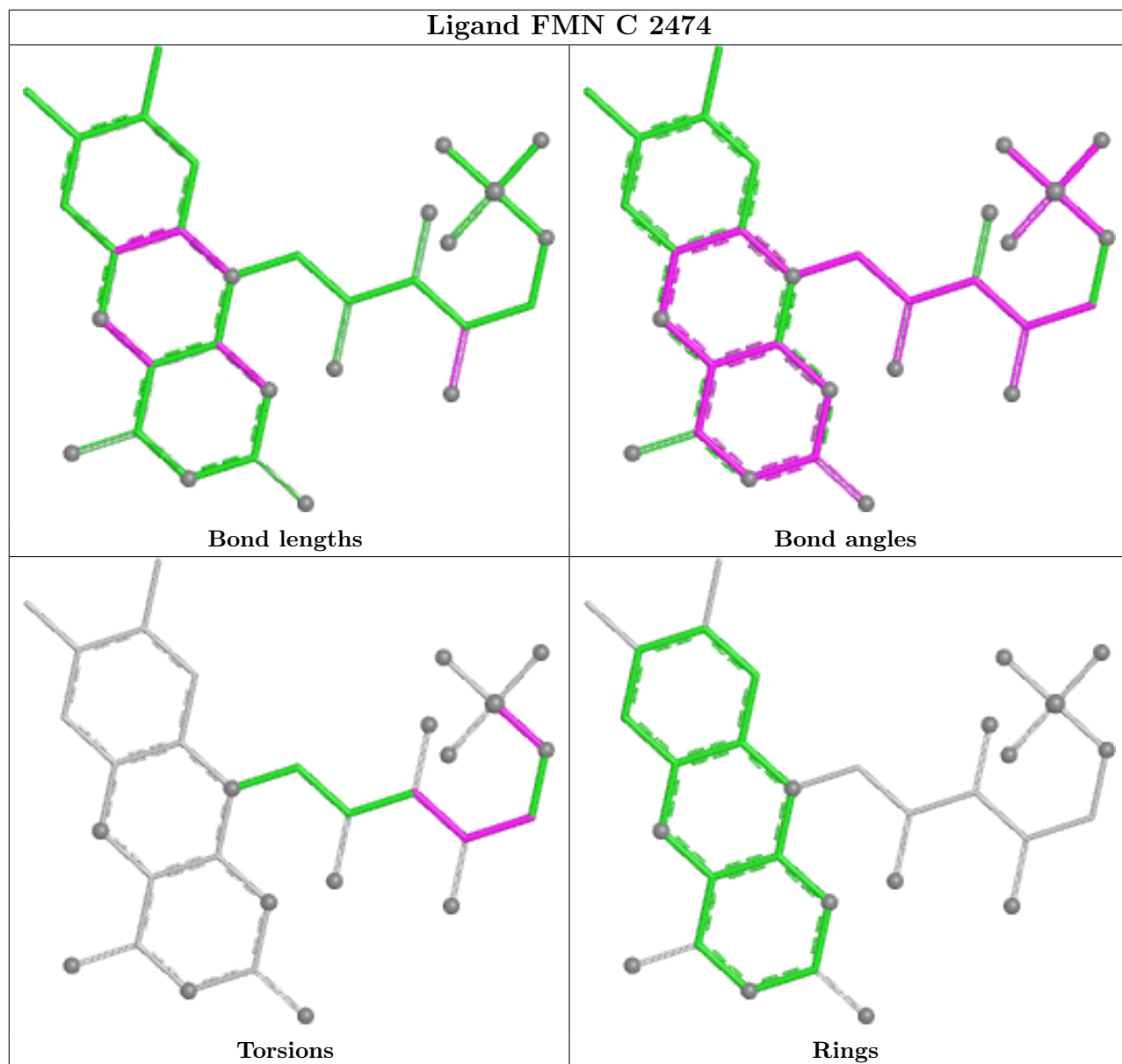
Continued from previous page...

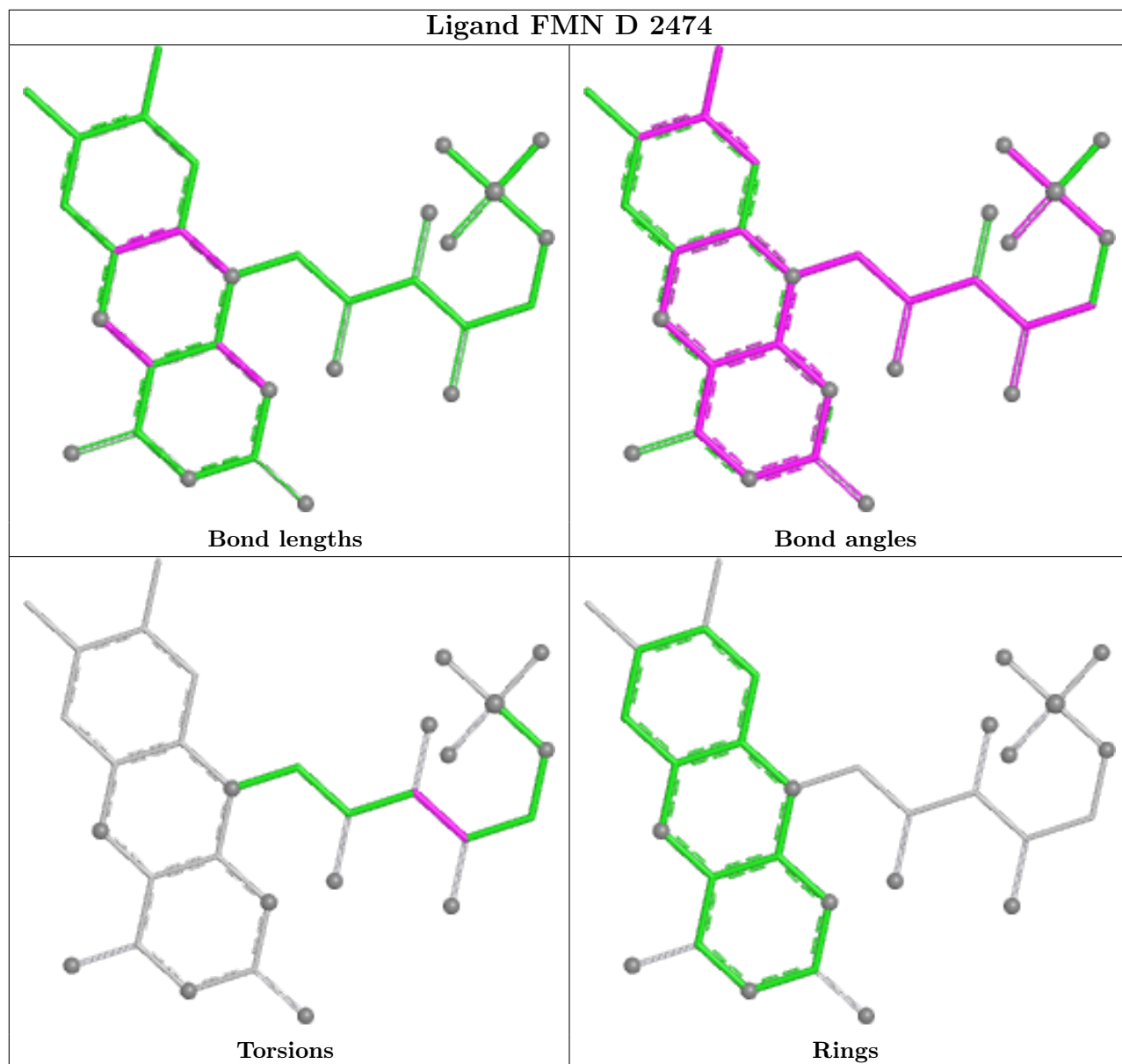
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	2473	OMT	3	0
8	I	484	FAD	18	0
8	K	484	FAD	18	0
3	C	2473	OMT	3	0
5	D	2475	AKG	2	0
8	H	484	FAD	18	0
7	L	483	SF4	2	0
6	E	2476	F3S	6	0

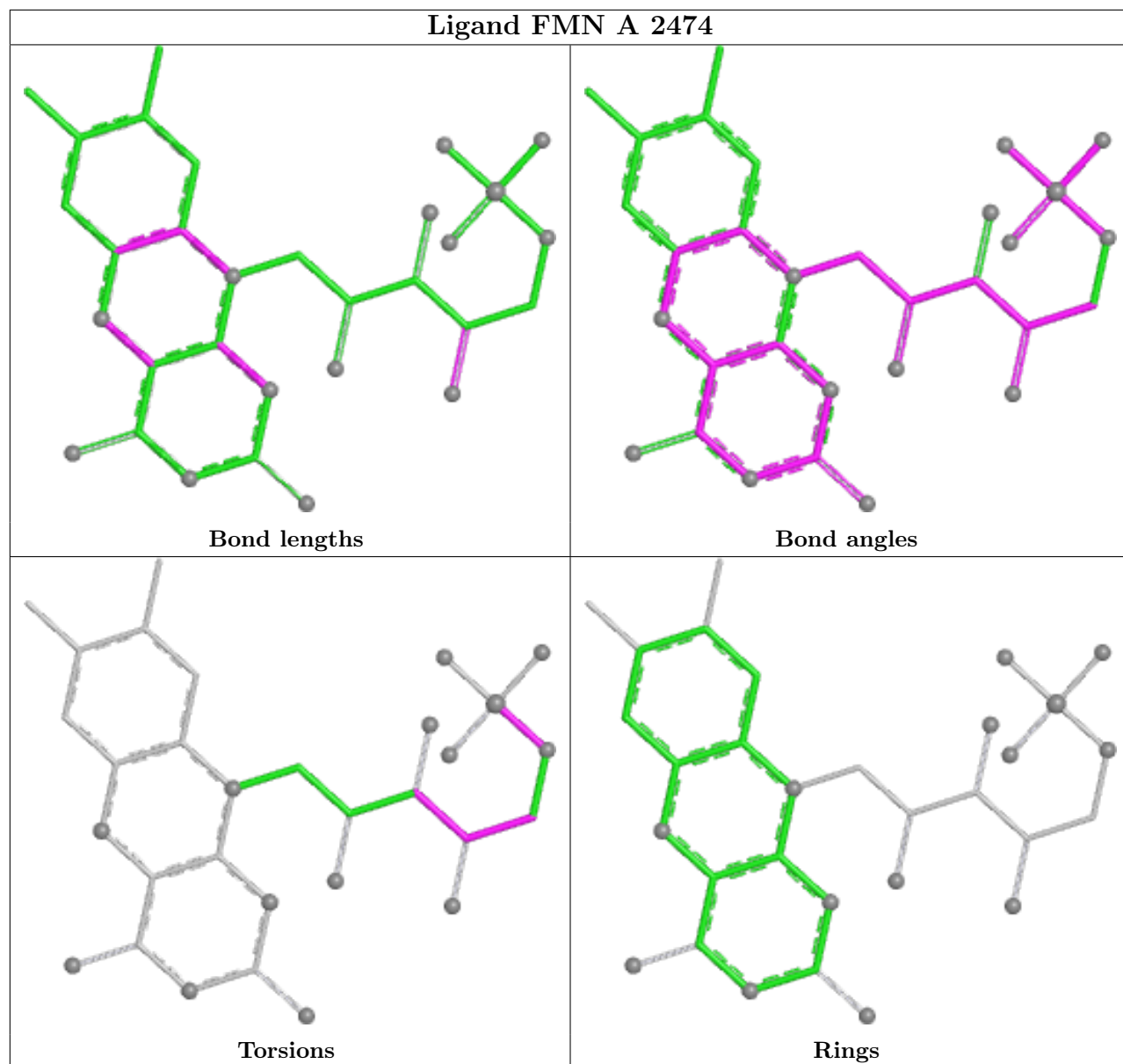
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

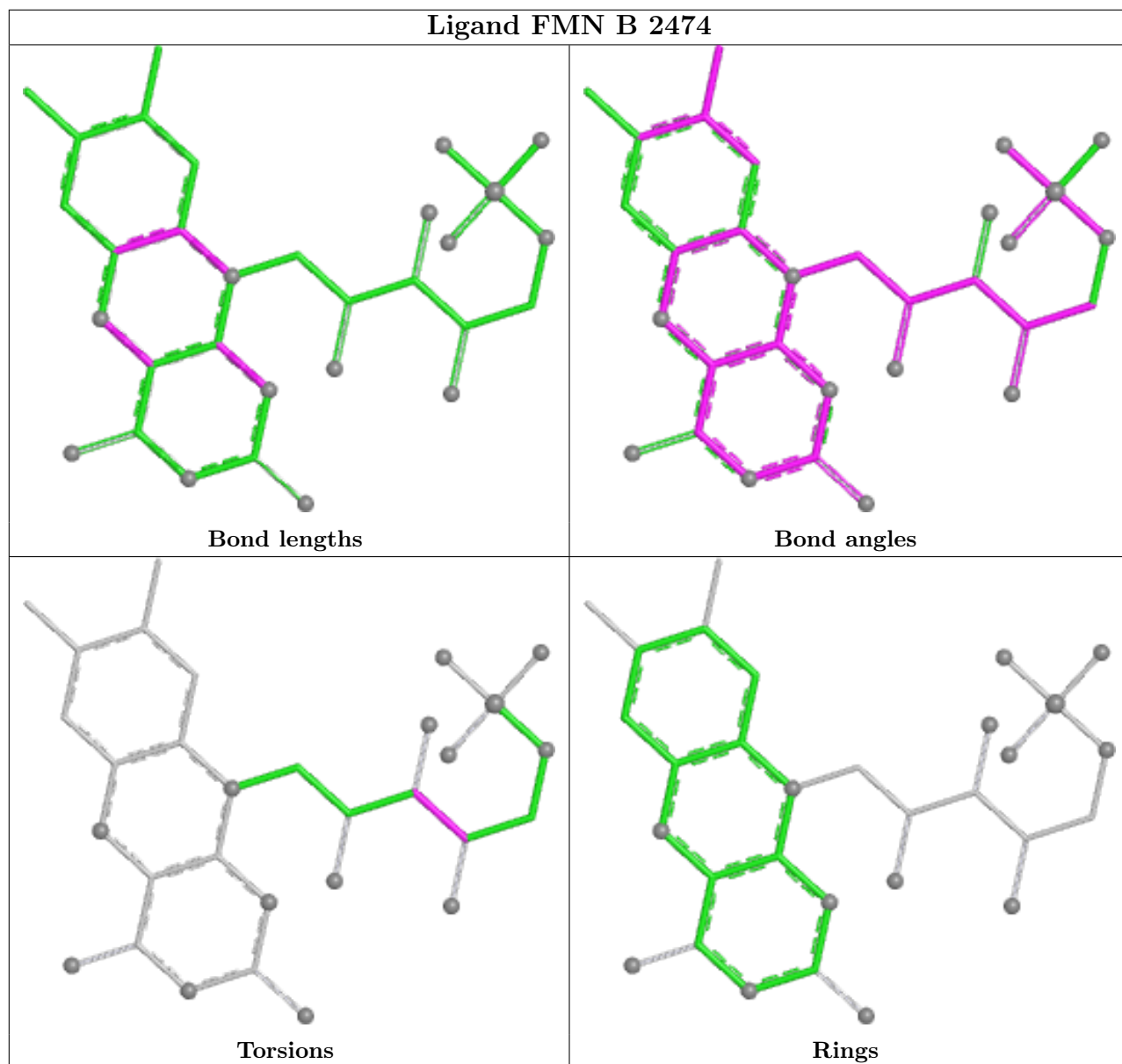


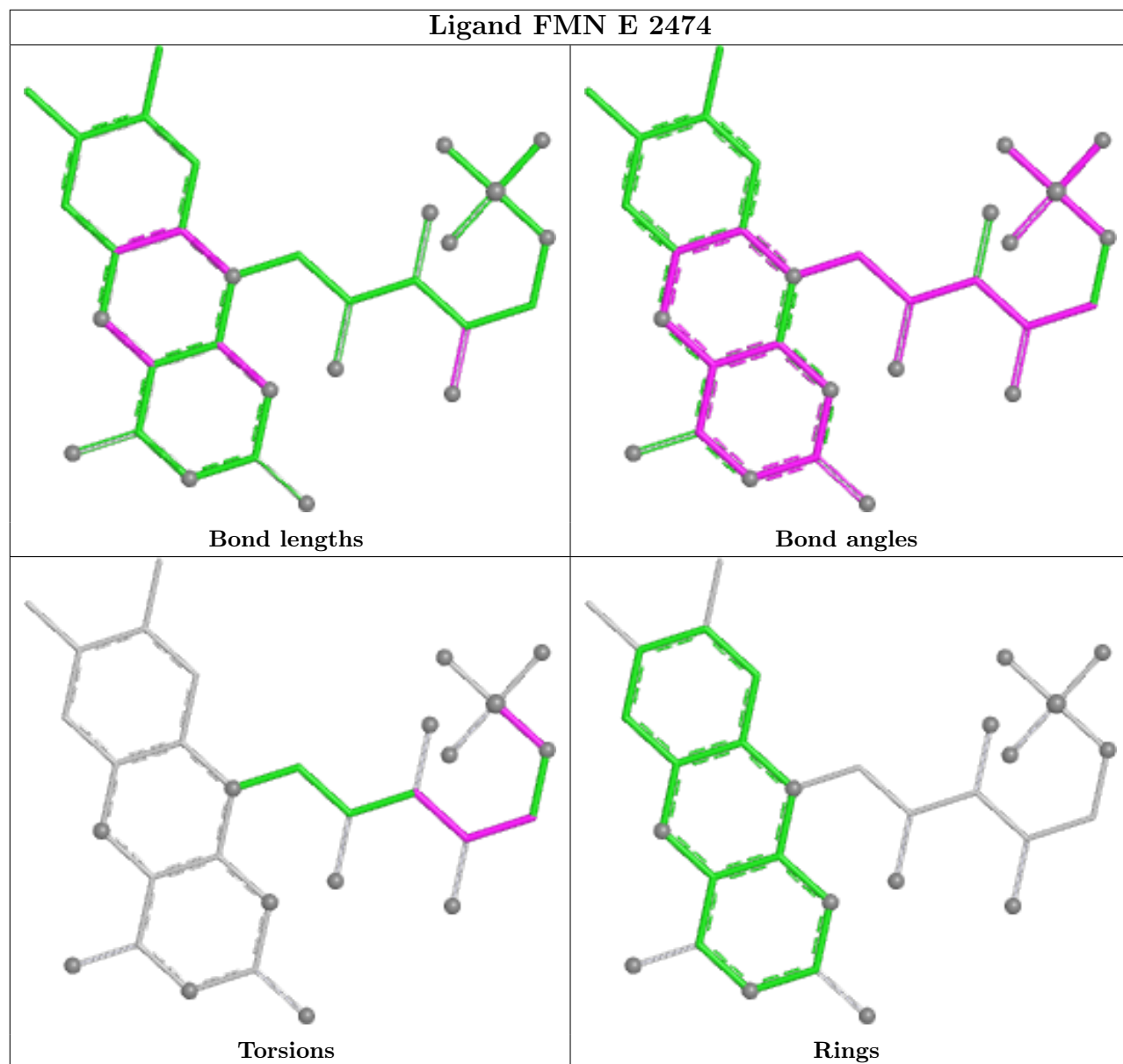


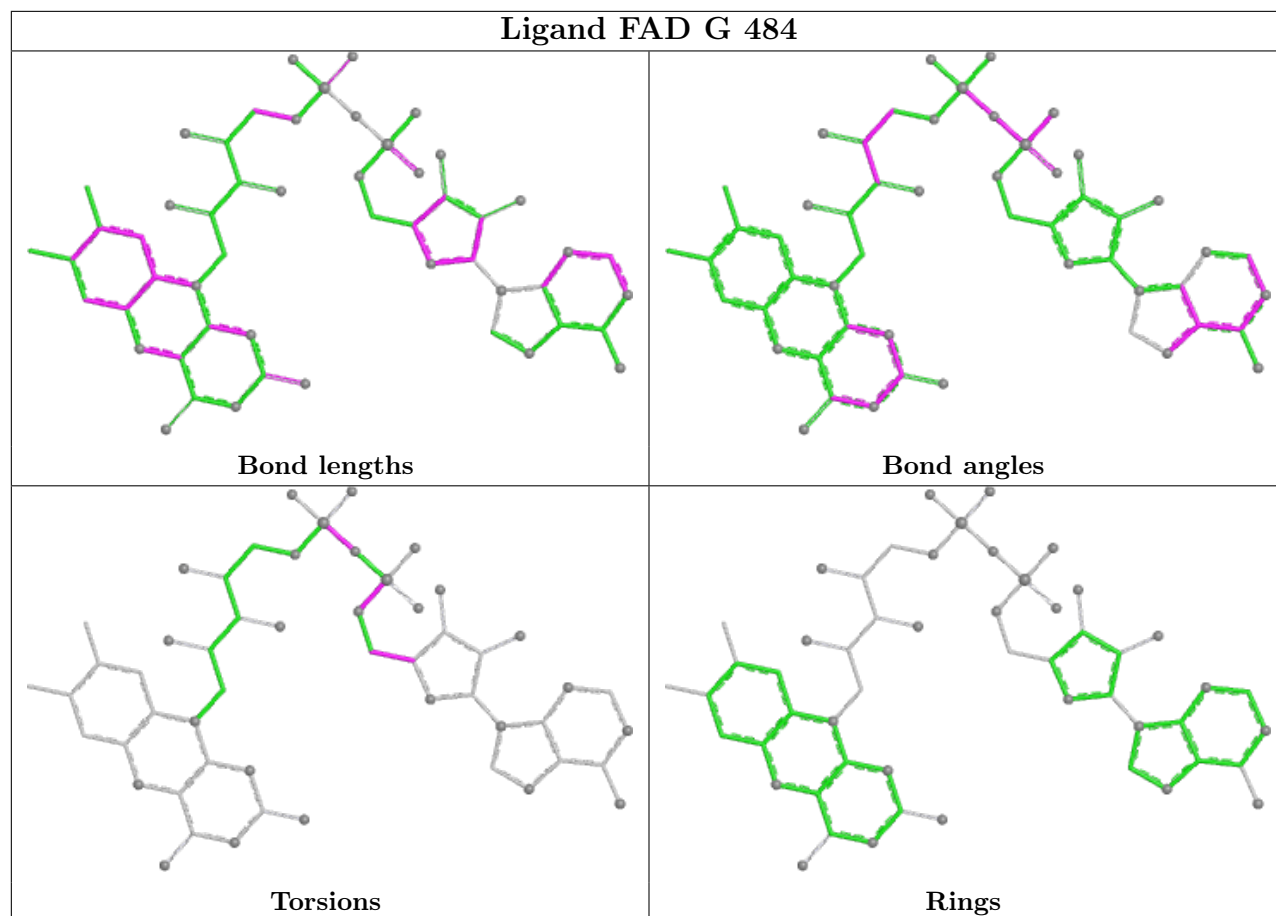


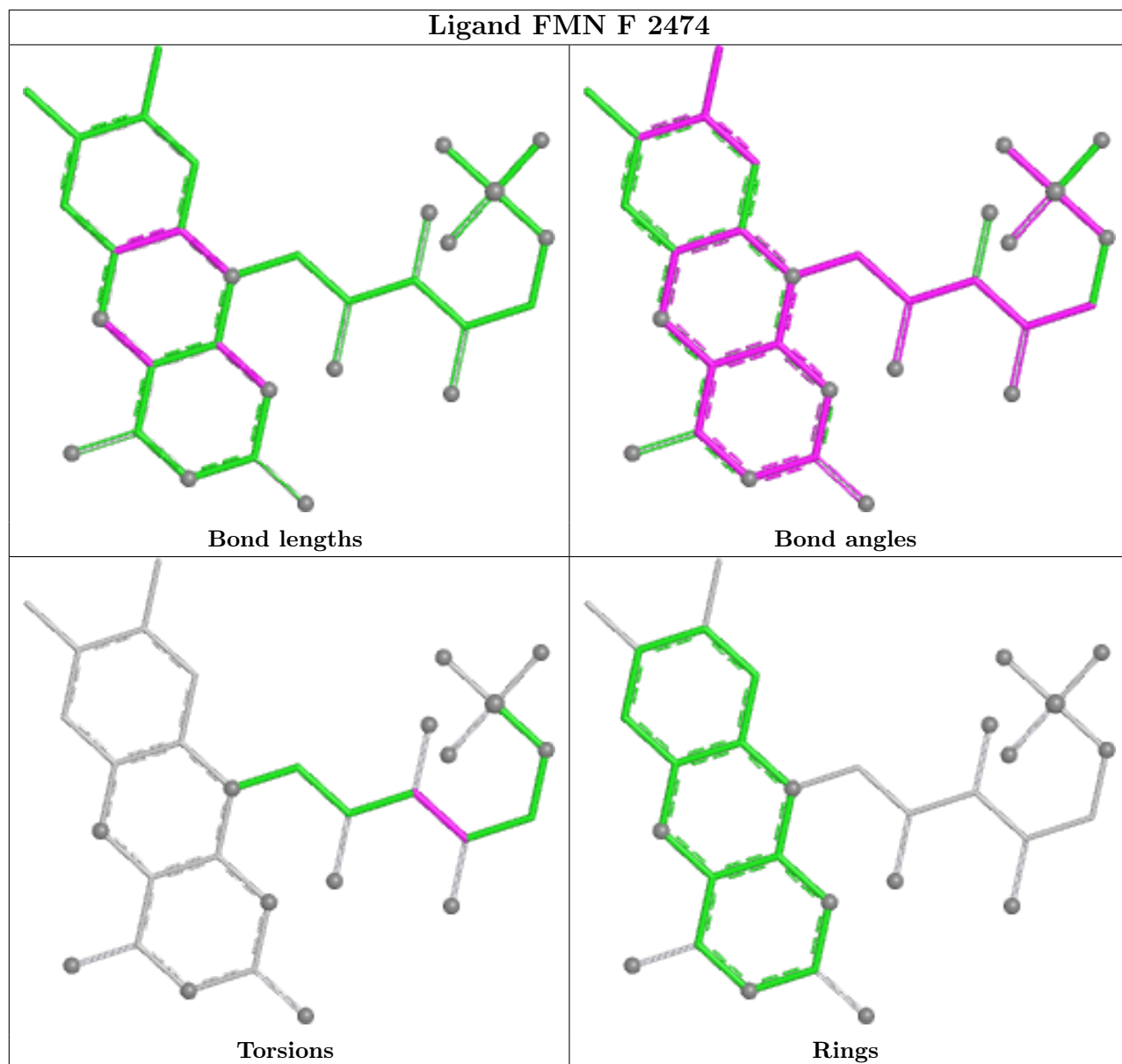


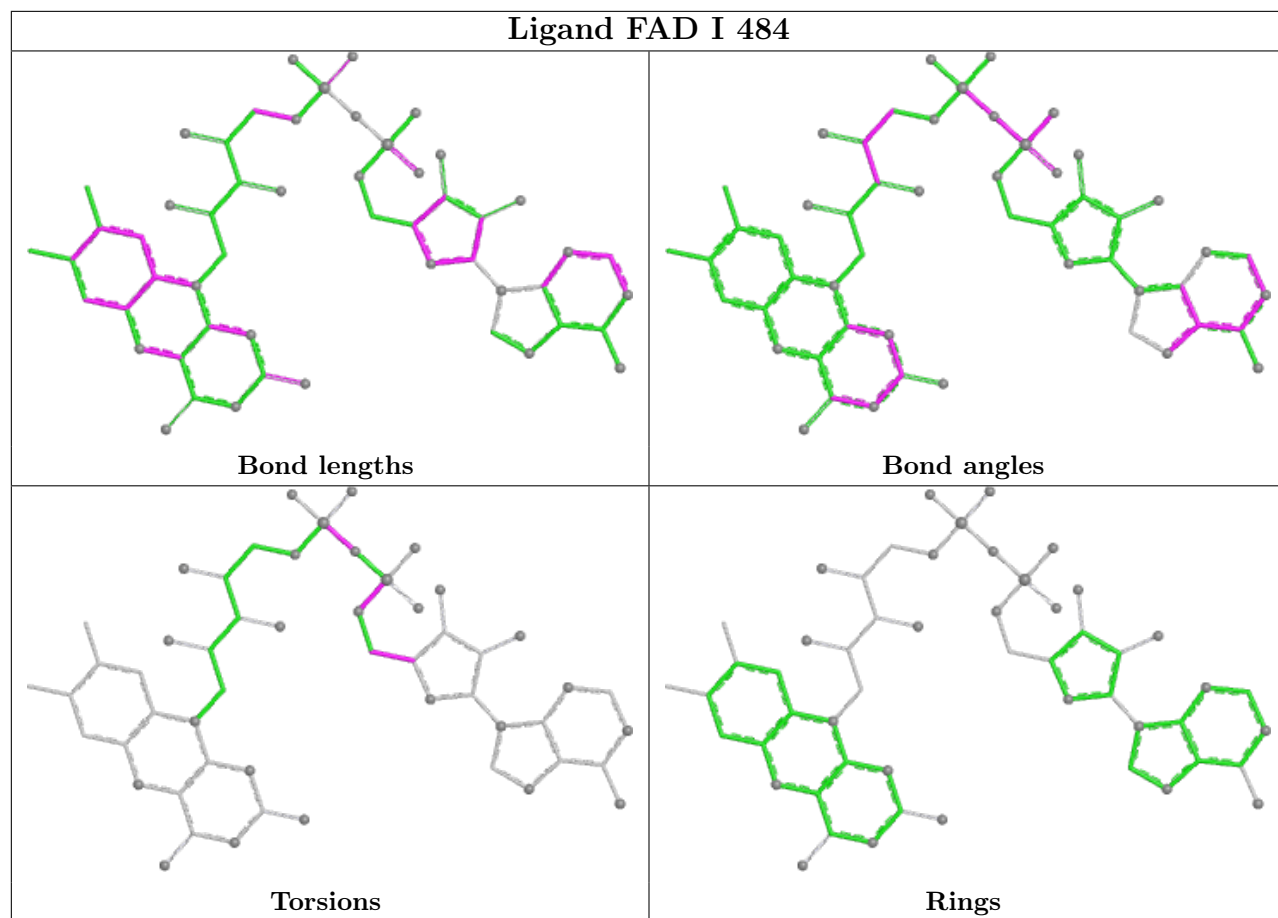


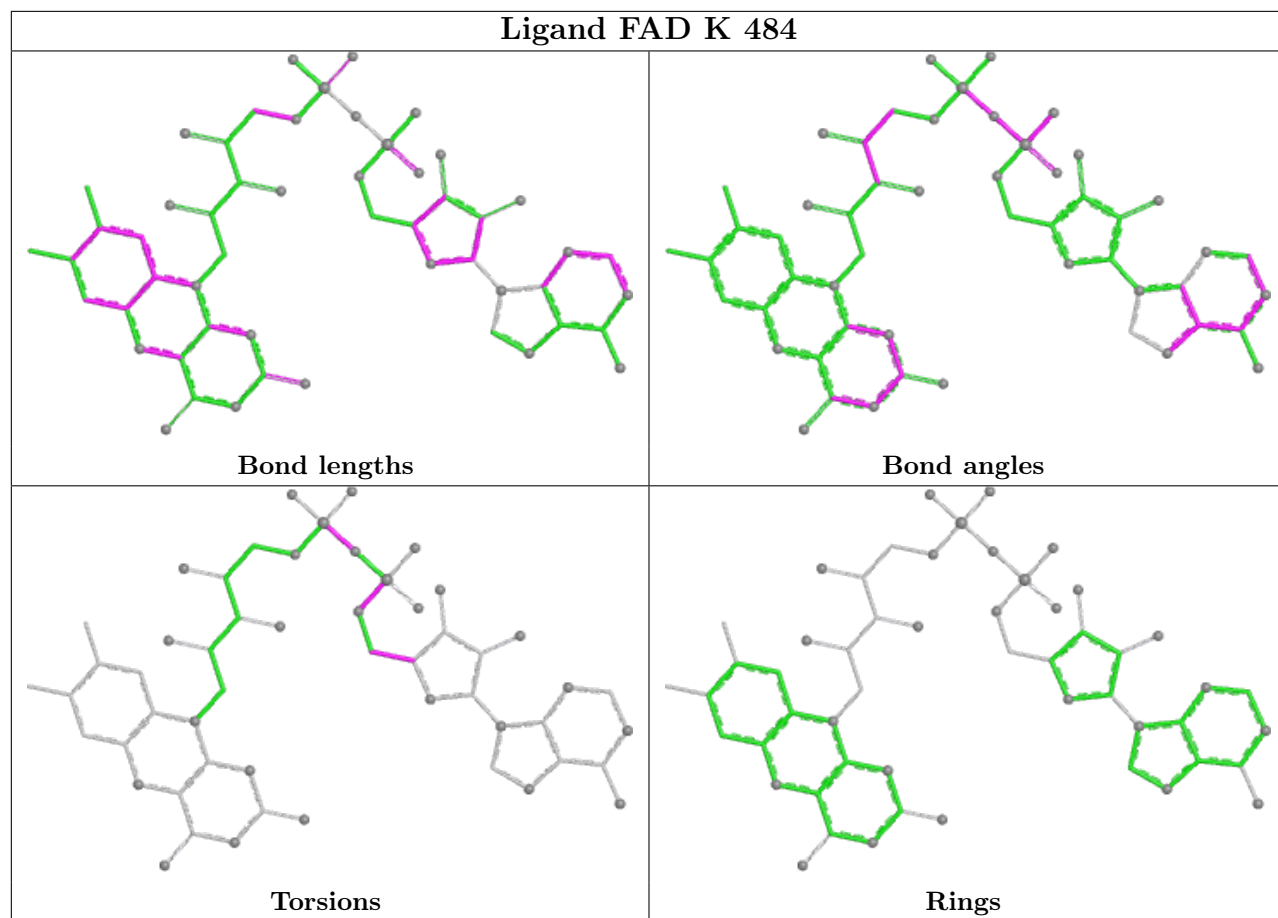


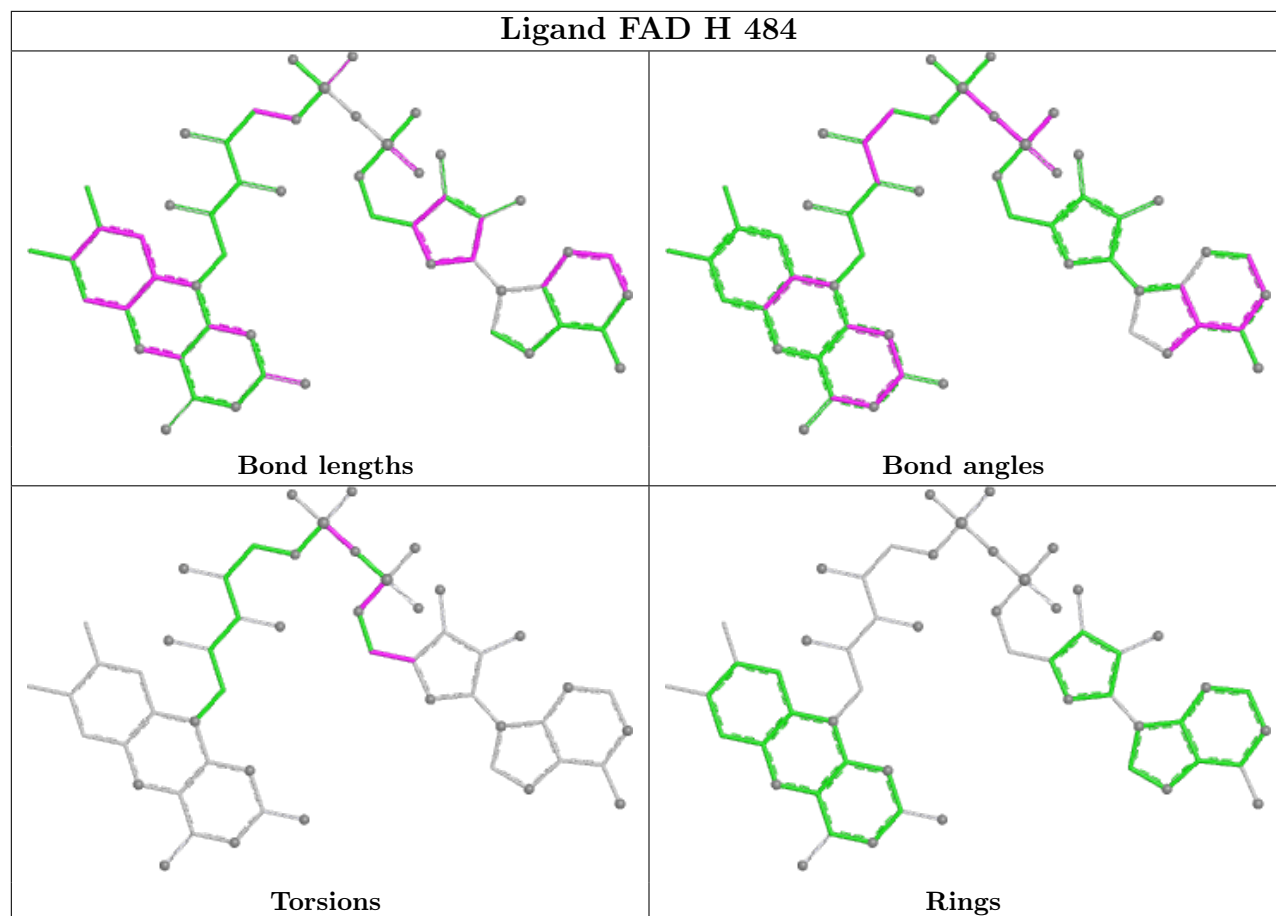












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1440. These allow visual inspection of the internal detail of the map and identification of artifacts.

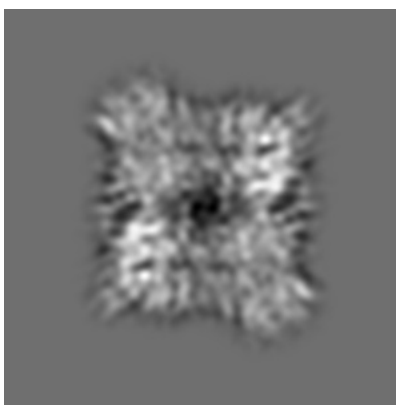
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X



Y



Z

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

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 96



Y Index: 96



Z Index: 96

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: 96



Y Index: 98

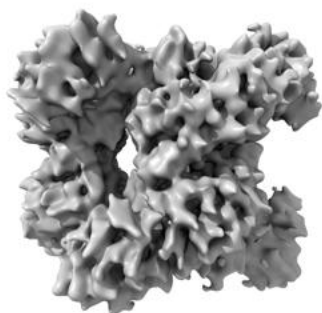


Z Index: 59

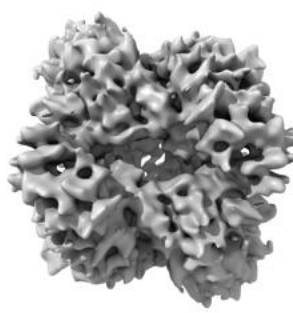
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

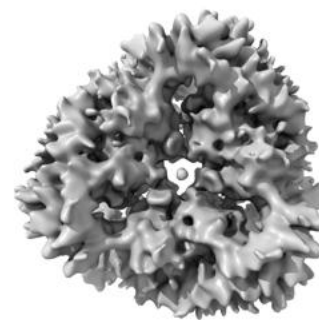
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 125.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

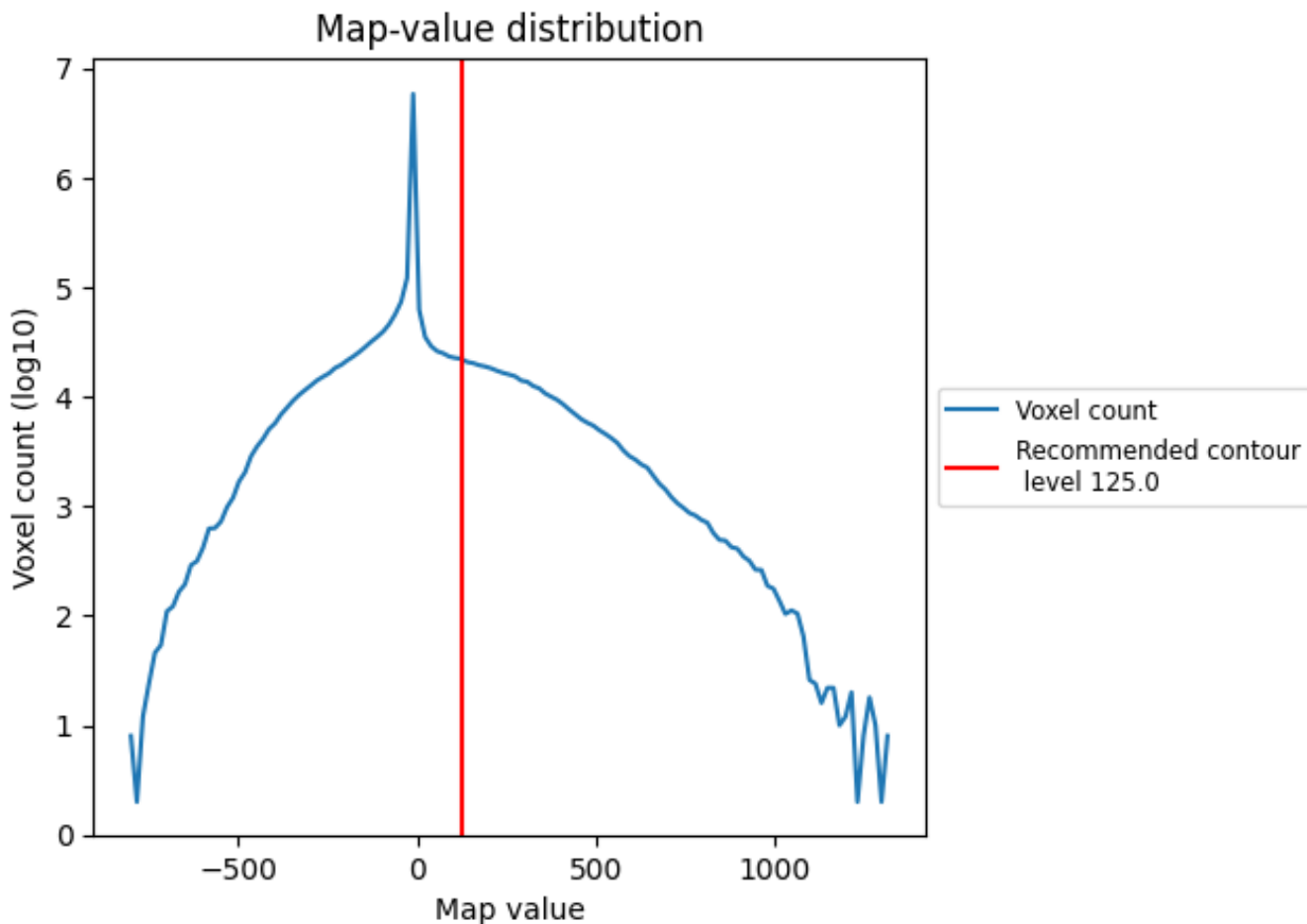
6.5 Mask visualisation

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

7 Map analysis [i](#)

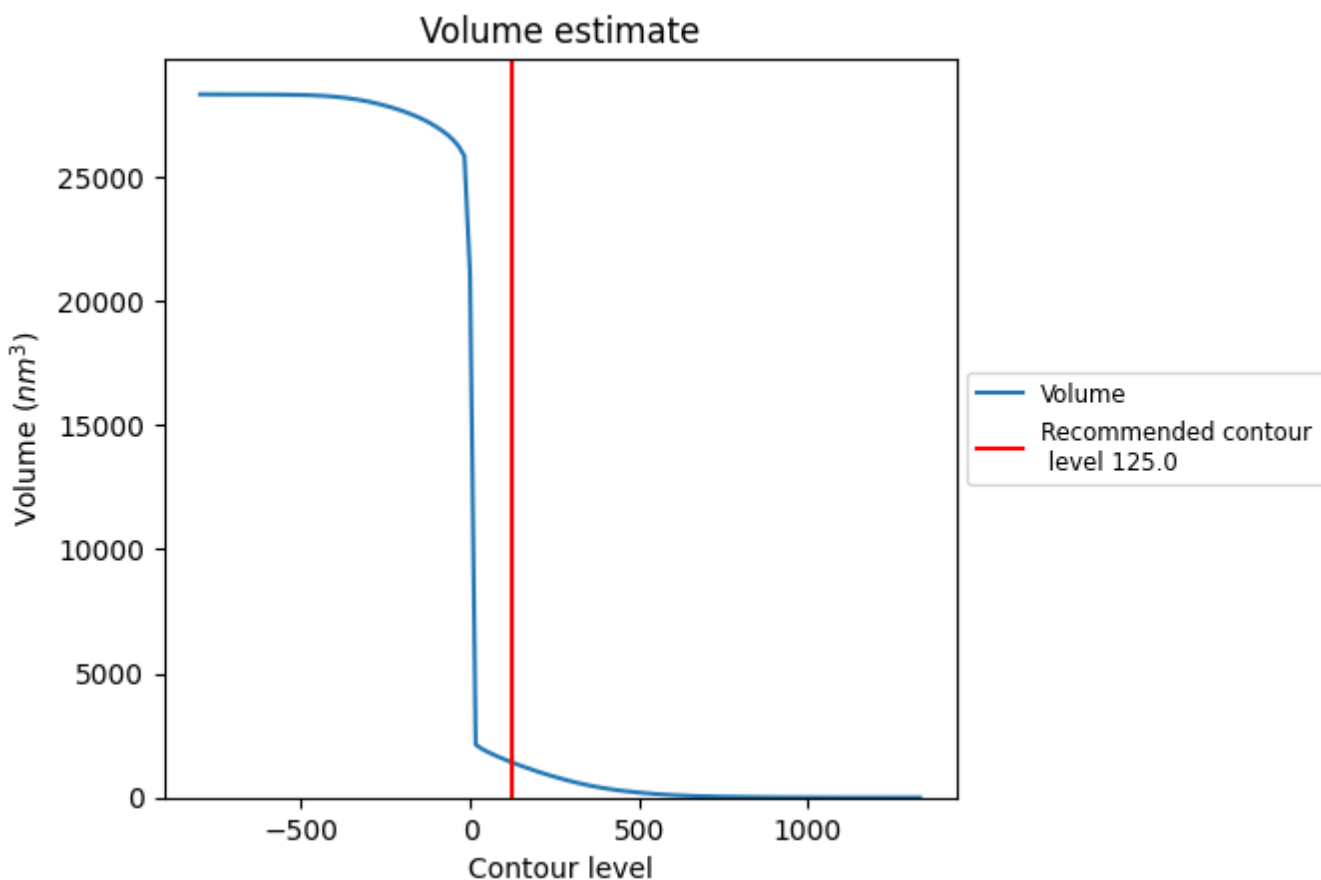
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

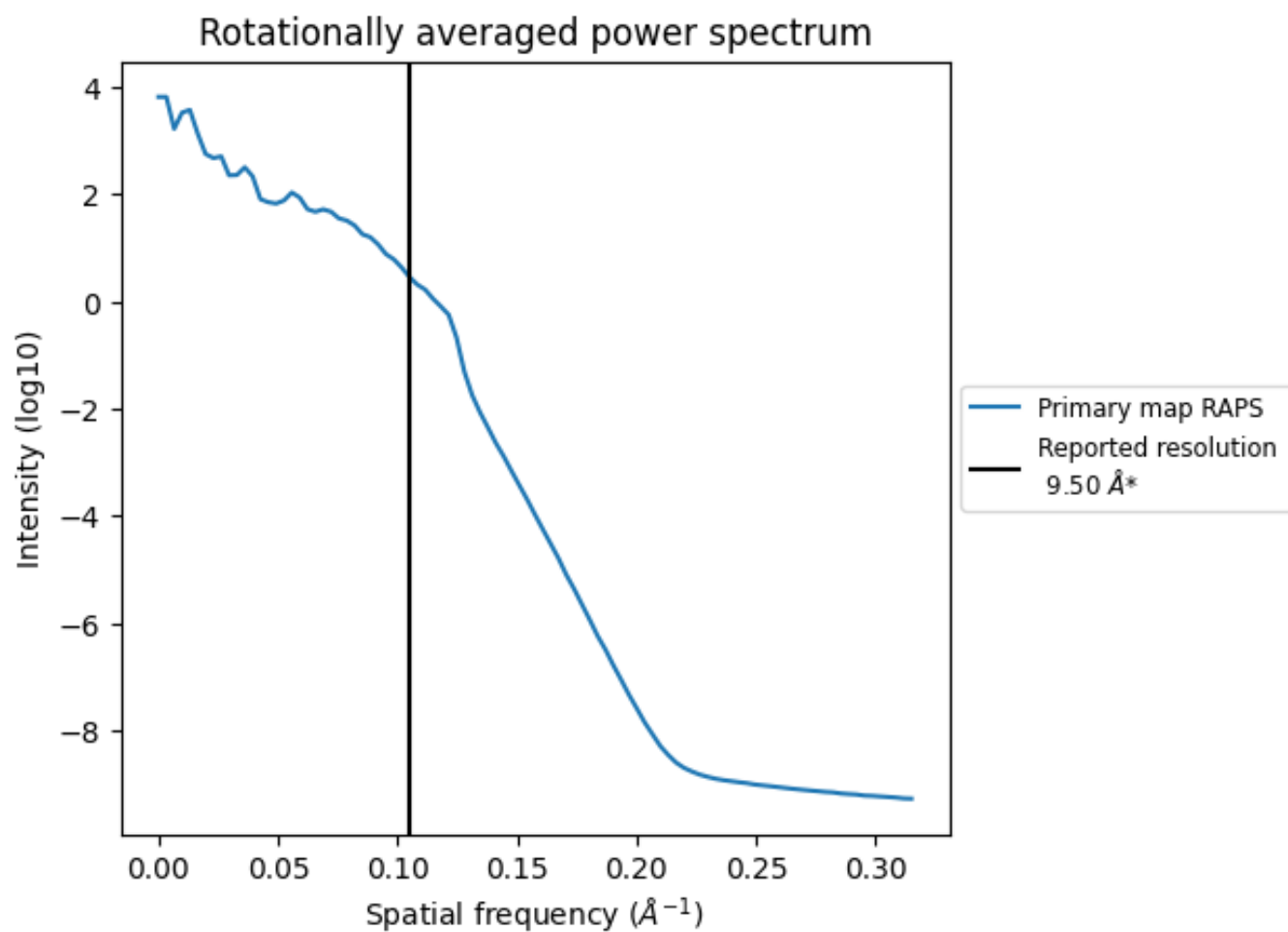
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1412 nm³; this corresponds to an approximate mass of 1276 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum [i](#)

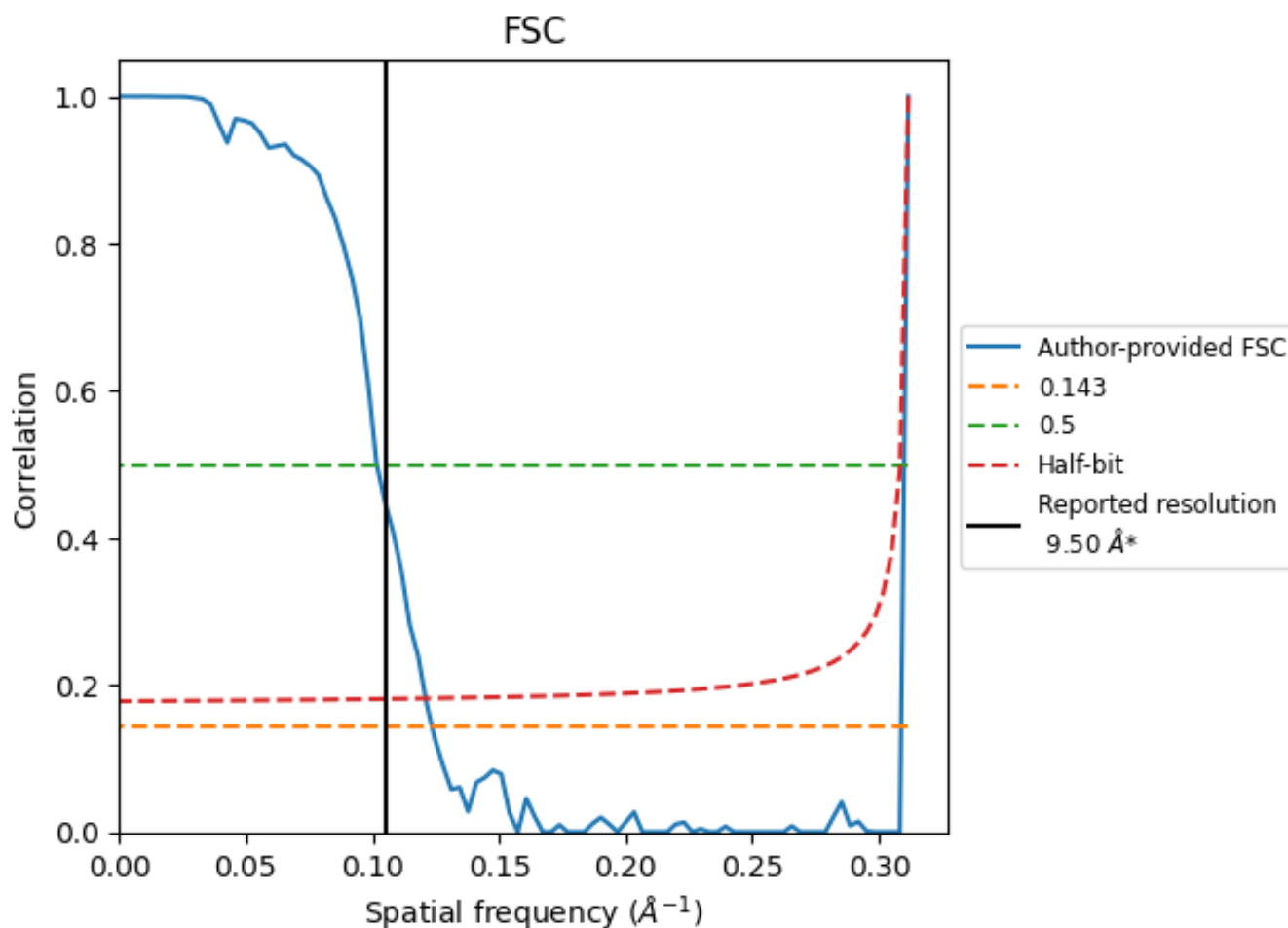


*Reported resolution corresponds to spatial frequency of 0.105 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.105 Å⁻¹

8.2 Resolution estimates [i](#)

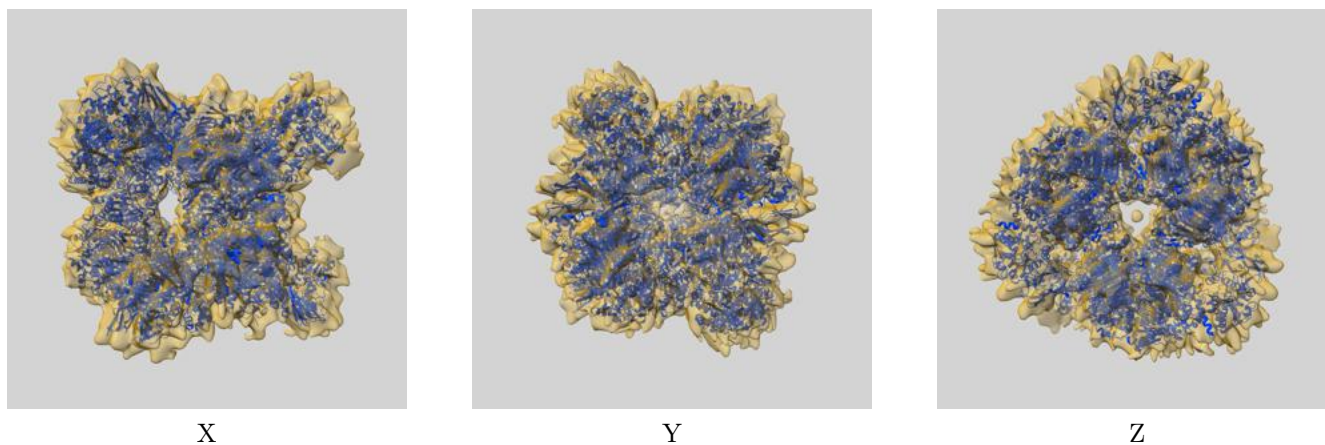
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	-	-	-
Author-provided FSC curve	8.10	9.83	8.26
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

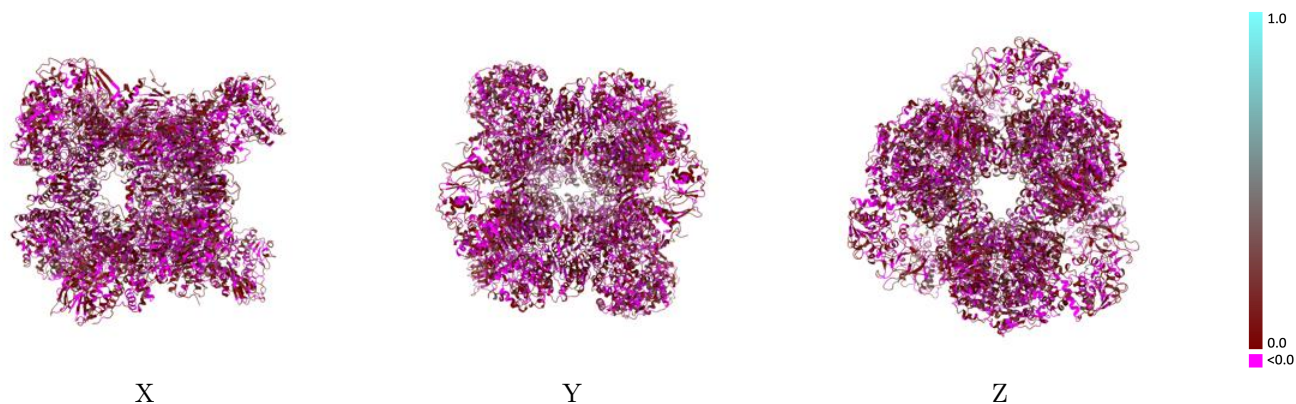
This section contains information regarding the fit between EMDB map EMD-1440 and PDB model 2VDC. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)



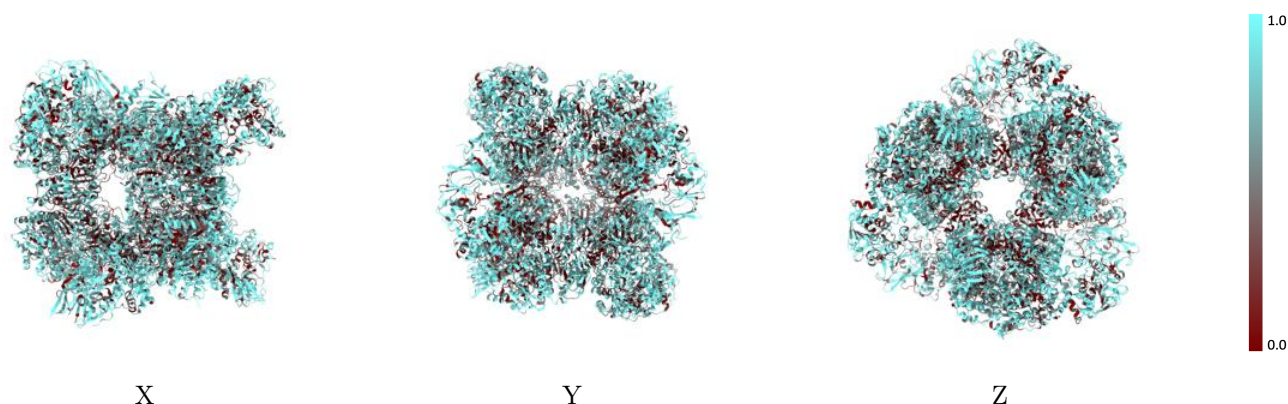
The images above show the 3D surface view of the map at the recommended contour level 125.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



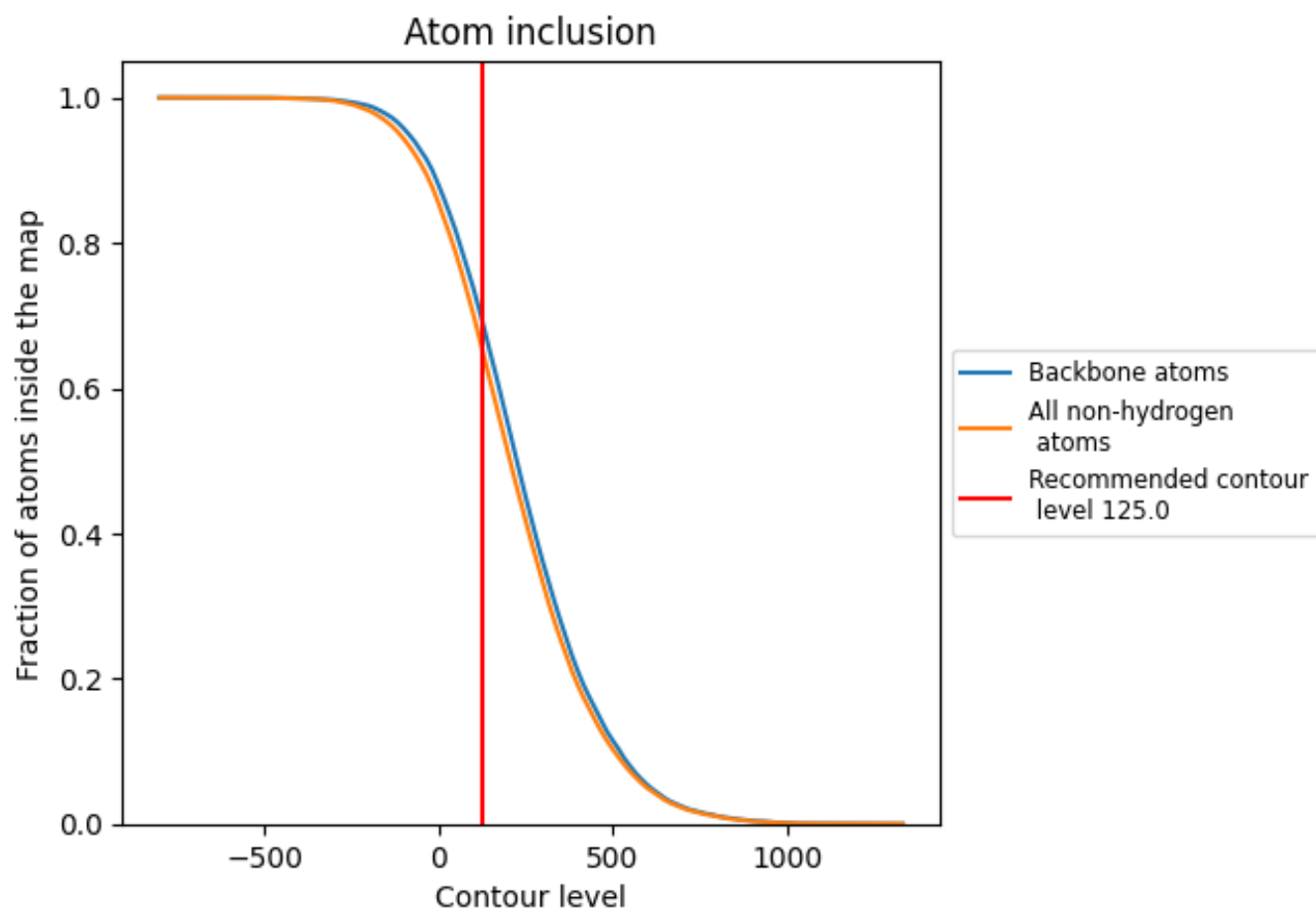
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (125.0).



























9.4 Atom inclusion [i](#)



At the recommended contour level, 69% of all backbone atoms, 66% 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 (125.0) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6561	 0.0430
A	 0.6473	 0.0430
B	 0.6458	 0.0430
C	 0.6349	 0.0400
D	 0.6351	 0.0430
E	 0.6361	 0.0450
F	 0.6348	 0.0410
G	 0.7248	 0.0470
H	 0.7080	 0.0430
I	 0.7011	 0.0470
J	 0.7248	 0.0490
K	 0.7011	 0.0470
L	 0.7080	 0.0430

