



wwPDB X-ray Structure Validation Summary Report ⓘ

May 16, 2020 – 01:49 pm BST

PDB ID : 4HE8
Title : Crystal structure of the membrane domain of respiratory complex I from *Thermus thermophilus*
Authors : Baradaran, R.; Berrisford, J.M.; Minhas, G.S.; Sazanov, L.A.
Deposited on : 2012-10-03
Resolution : 3.30 Å(reported)

This is a wwPDB X-ray Structure 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/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

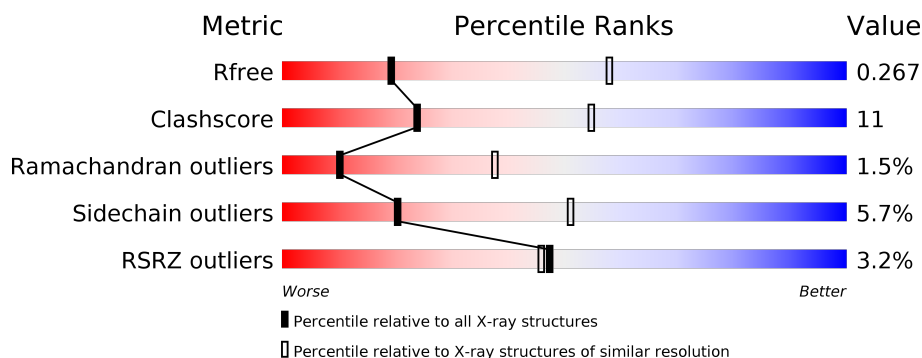
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 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.



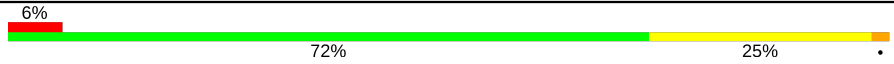



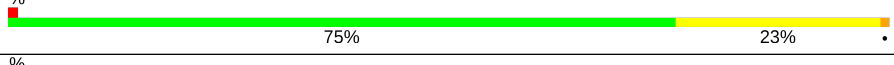
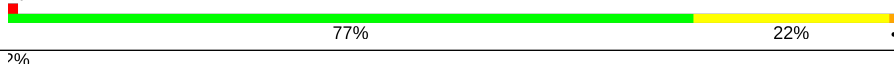
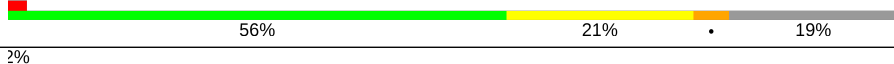

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1149 (3.34-3.26)
Clashscore	141614	1205 (3.34-3.26)
Ramachandran outliers	138981	1183 (3.34-3.26)
Sidechain outliers	138945	1182 (3.34-3.26)
RSRZ outliers	127900	1115 (3.34-3.26)

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 on 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	119	<div> <div>3%</div> <div> <div></div> <div>55%</div> <div>19%</div> <div>•</div> <div>23%</div> </div> </div>
1	B	119	<div> <div>2%</div> <div> <div></div> <div>55%</div> <div>20%</div> <div>•</div> <div>23%</div> </div> </div>
2	D	176	<div> <div>6%</div> <div> <div></div> <div>60%</div> <div>26%</div> <div>• •</div> <div>9%</div> </div> </div>
2	J	176	<div> <div>6%</div> <div> <div></div> <div>61%</div> <div>26%</div> <div>• •</div> <div>9%</div> </div> </div>
3	E	95	<div> <div>%</div> <div> <div></div> <div>71%</div> <div>27%</div> <div>•</div> </div> </div>
3	K	95	<div> <div>%</div> <div> <div></div> <div>72%</div> <div>26%</div> <div>•</div> </div> </div>

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Mol	Chain	Length	Quality of chain
4	F	606	
4	L	606	
5	G	469	
5	M	469	
6	I	427	
6	N	427	
7	C	365	
7	H	365	

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 32650 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 NADH-quinone oxidoreductase subunit 7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	92	Total	C	N	O	S	0	0	0
			724	508	103	110	3			
1	B	92	Total	C	N	O	S	0	0	0
			724	508	103	110	3			

- Molecule 2 is a protein called NADH-quinone oxidoreductase subunit 10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	J	160	Total	C	N	O	S	0	0	0
			1183	806	183	191	3			
2	D	160	Total	C	N	O	S	0	0	0
			1183	806	183	191	3			

- Molecule 3 is a protein called NADH-quinone oxidoreductase subunit 11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	K	95	Total	C	N	O	S	0	0	0
			703	456	118	126	3			
3	E	95	Total	C	N	O	S	0	0	0
			703	456	118	126	3			

- Molecule 4 is a protein called NADH-quinone oxidoreductase subunit 12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	L	605	Total	C	N	O	S	0	0	0
			4604	3089	740	756	19			
4	F	605	Total	C	N	O	S	0	0	0
			4604	3089	740	756	19			

- Molecule 5 is a protein called NADH-quinone oxidoreductase subunit 13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	M	467	Total	C	N	O	S	0	0	0
			3489	2363	546	572	8			
5	G	467	Total	C	N	O	S	0	0	0
			3489	2363	546	572	8			

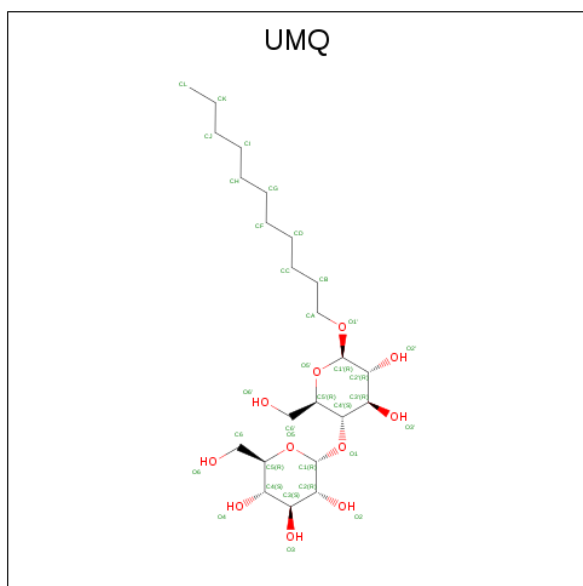
- Molecule 6 is a protein called NADH-quinone oxidoreductase subunit 14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	N	427	Total	C	N	O	S	0	0	0
			3154	2125	505	518	6			
6	I	427	Total	C	N	O	S	0	0	0
			3154	2125	505	518	6			

- Molecule 7 is a protein called NADH-quinone oxidoreductase subunit 8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	H	297	Total	C	N	O	S	0	0	0
			2400	1662	357	375	6			
7	C	297	Total	C	N	O	S	0	0	0
			2400	1662	357	375	6			

- Molecule 8 is UNDECYL-MALTOSIDE (three-letter code: UMQ) (formula: C₂₃H₄₄O₁₁).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	J	1	Total	C	O	0	0
			34	23	11		

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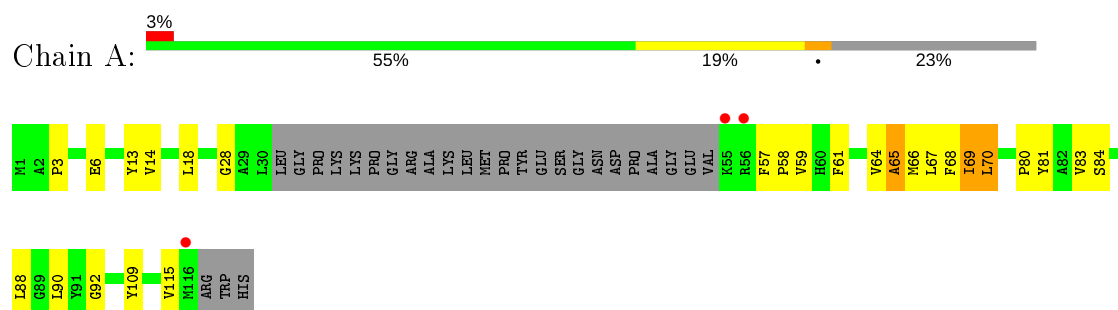
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	L	1	Total	C	O	0	0
			34	23	11		
8	D	1	Total	C	O	0	0
			34	23	11		
8	F	1	Total	C	O	0	0
			34	23	11		

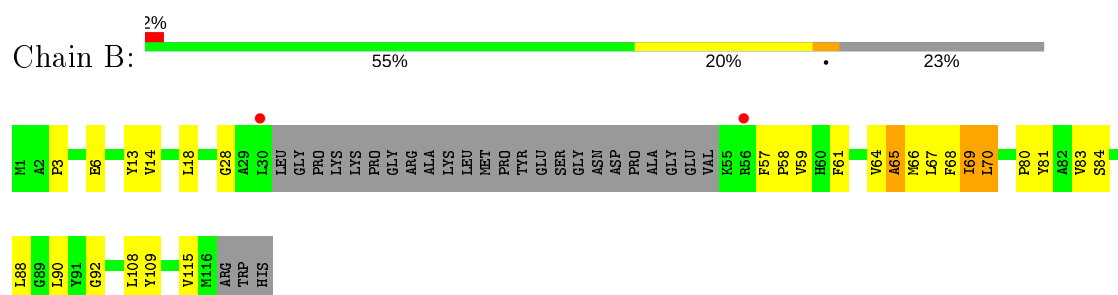
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

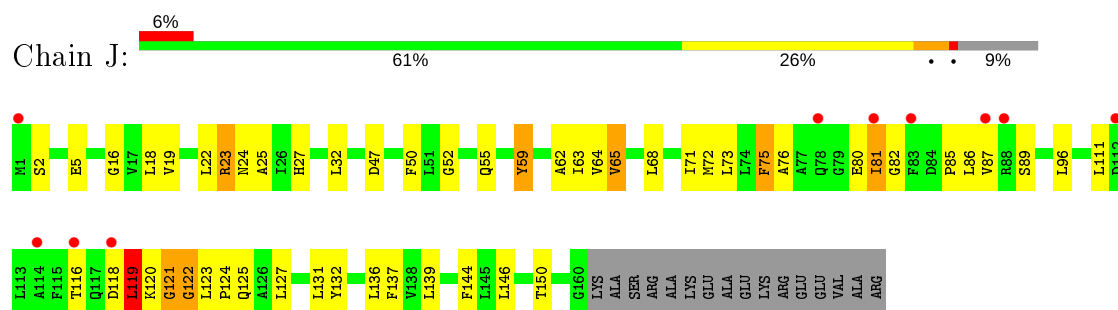
• Molecule 1: NADH-quinone oxidoreductase subunit 7



• Molecule 1: NADH-quinone oxidoreductase subunit 7

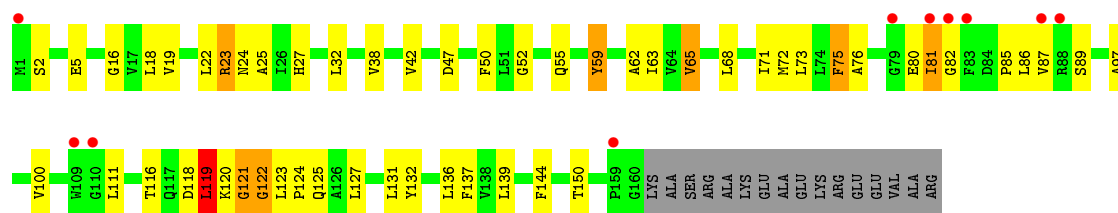


• Molecule 2: NADH-quinone oxidoreductase subunit 10

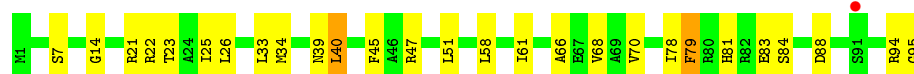
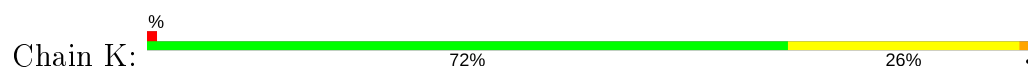


• Molecule 2: NADH-quinone oxidoreductase subunit 10





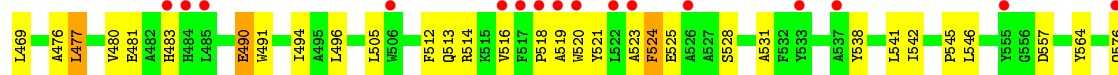
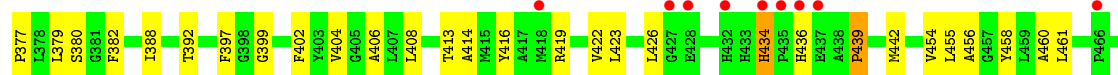
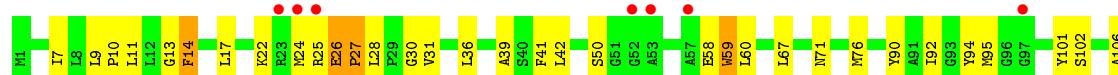
• Molecule 3: NADH-quinone oxidoreductase subunit 11



• Molecule 3: NADH-quinone oxidoreductase subunit 11

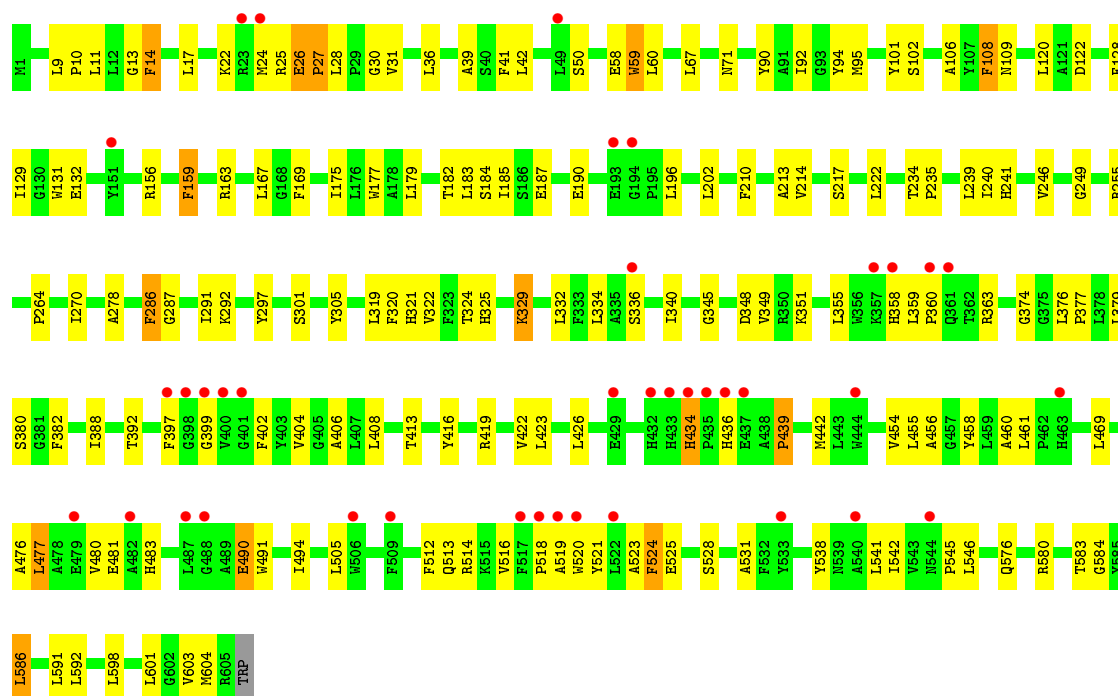


• Molecule 4: NADH-quinone oxidoreductase subunit 12

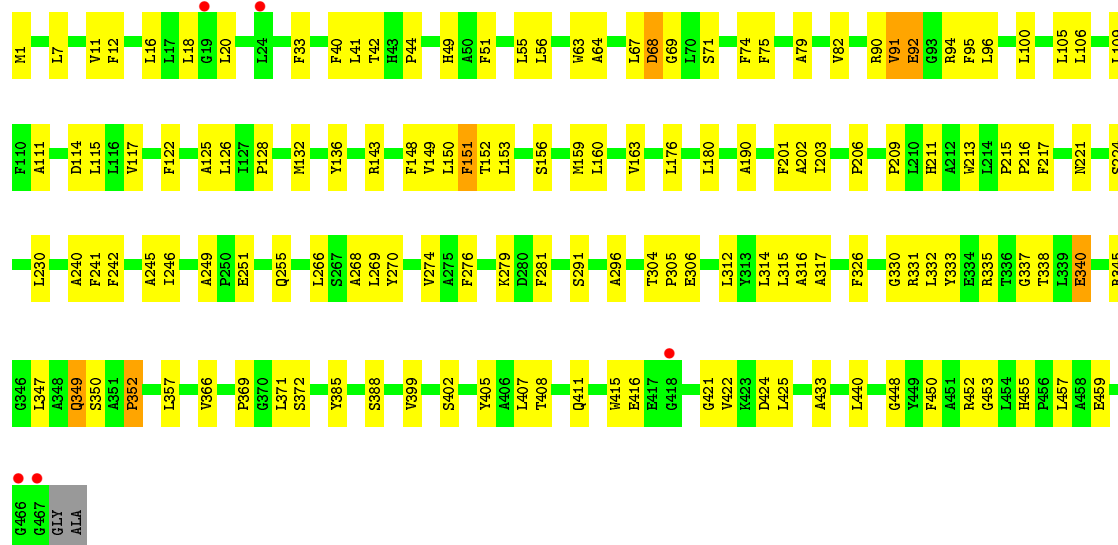


• Molecule 4: NADH-quinone oxidoreductase subunit 12



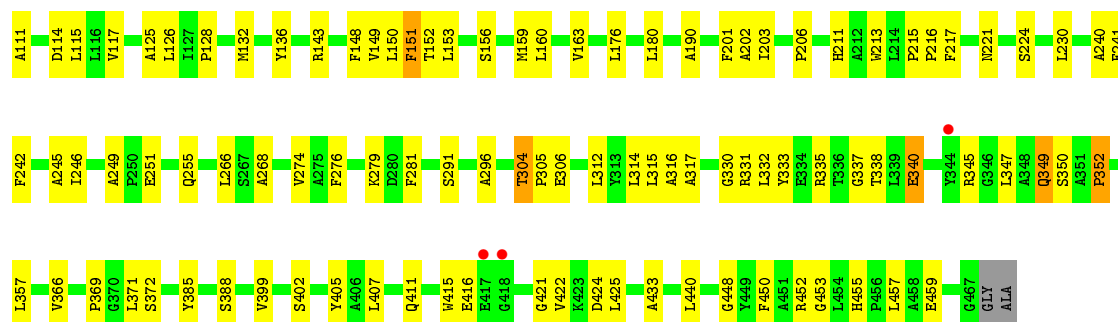


• Molecule 5: NADH-quinone oxidoreductase subunit 13

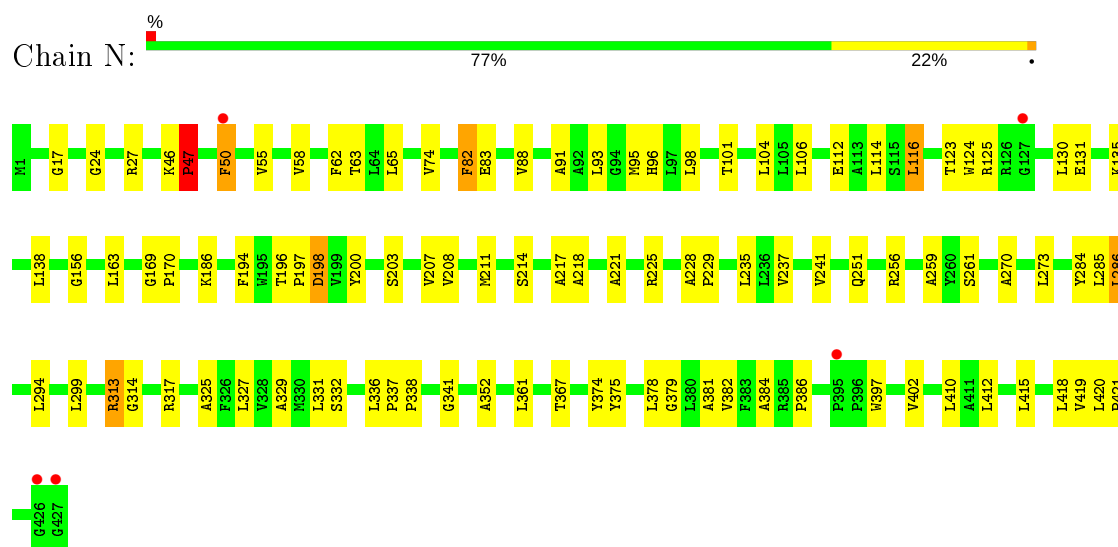


• Molecule 5: NADH-quinone oxidoreductase subunit 13

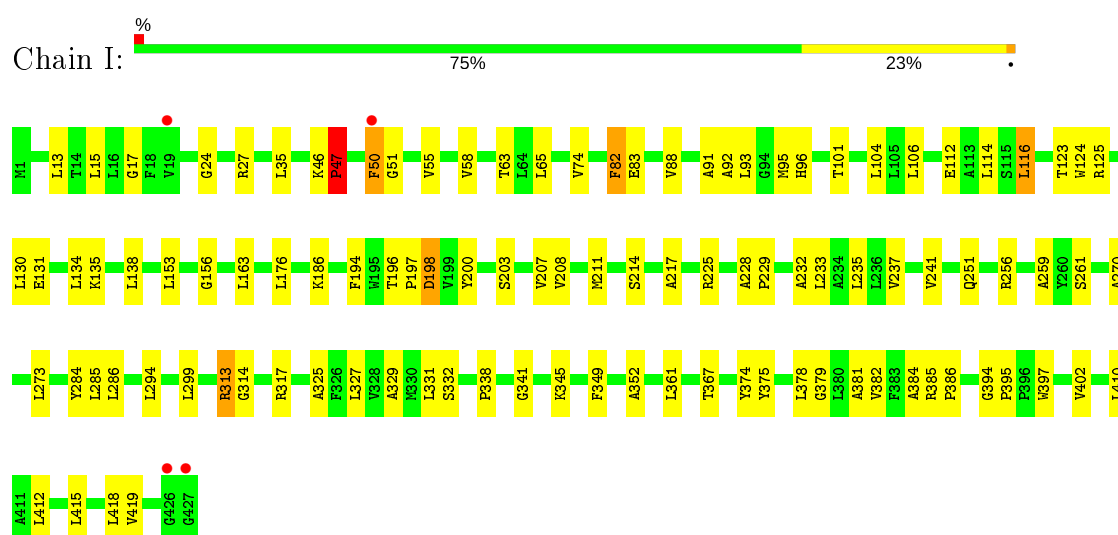




• Molecule 6: NADH-quinone oxidoreductase subunit 14

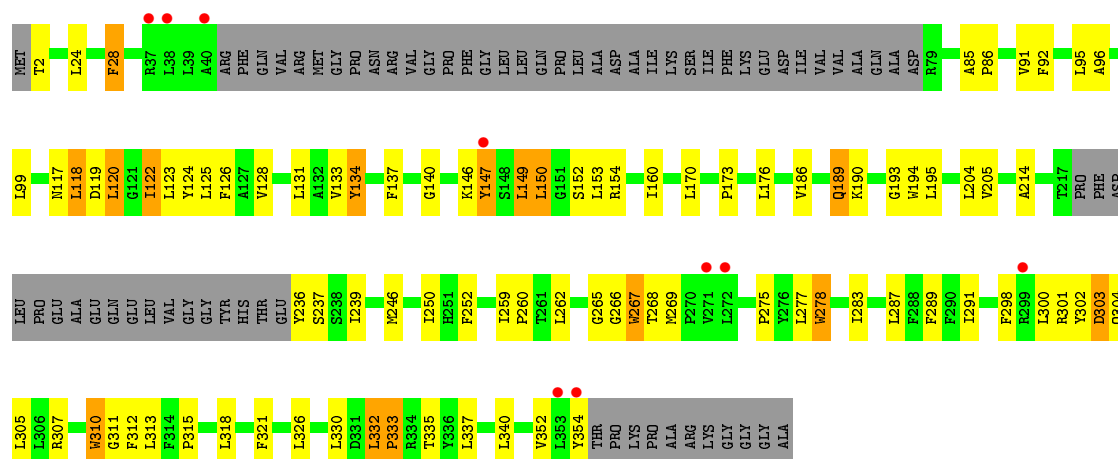


• Molecule 6: NADH-quinone oxidoreductase subunit 14

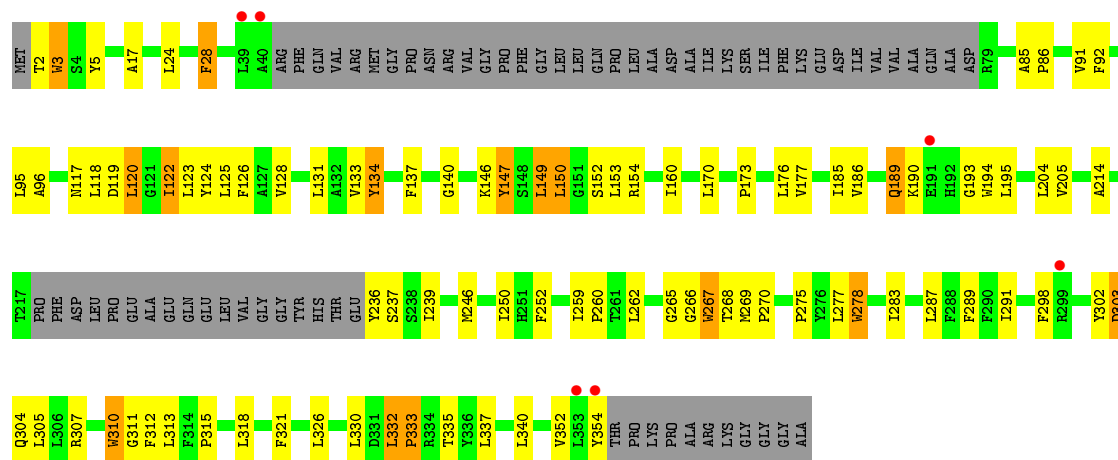


• Molecule 7: NADH-quinone oxidoreductase subunit 8





• Molecule 7: NADH-quinone oxidoreductase subunit 8



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	85.26Å 120.54Å 176.66Å 91.91° 95.73° 101.41°	Depositor
Resolution (Å)	25.73 – 3.30 25.73 – 3.30	Depositor EDS
% Data completeness (in resolution range)	86.7 (25.73-3.30) 86.8 (25.73-3.30)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.57 (at 3.31Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1041)	Depositor
R, R_{free}	0.209 , 0.263 0.210 , 0.267	Depositor DCC
R_{free} test set	1819 reflections (2.04%)	wwPDB-VP
Wilson B-factor (Å ²)	84.3	Xtriage
Anisotropy	0.007	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 74.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	32650	wwPDB-VP
Average B, all atoms (Å ²)	93.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.21% 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: UMQ

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	0.32	0/748	0.53	0/1020
1	B	0.32	0/748	0.53	0/1020
2	D	0.29	0/1206	0.52	0/1649
2	J	0.28	0/1206	0.52	0/1649
3	E	0.31	0/710	0.53	0/962
3	K	0.30	0/710	0.53	0/962
4	F	0.27	0/4741	0.50	0/6460
4	L	0.27	0/4741	0.49	0/6460
5	G	0.29	0/3591	0.53	0/4896
5	M	0.29	0/3591	0.53	0/4896
6	I	0.29	0/3238	0.50	0/4434
6	N	0.29	0/3238	0.50	0/4434
7	C	0.30	0/2484	0.51	0/3398
7	H	0.29	0/2484	0.52	0/3398
All	All	0.29	0/33436	0.51	0/45638

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
4	F	0	1
4	L	0	1
6	I	0	1
6	N	0	1
7	C	0	1
7	H	0	1
All	All	0	6

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	F	434	HIS	Peptide
7	H	332	LEU	Peptide
6	I	46	LYS	Peptide
4	L	434	HIS	Peptide
6	N	46	LYS	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	724	0	747	27	0
1	B	724	0	747	29	0
2	D	1183	0	1286	46	0
2	J	1183	0	1286	50	0
3	E	703	0	747	25	0
3	K	703	0	747	26	0
4	F	4604	0	4734	106	0
4	L	4604	0	4734	115	0
5	G	3489	0	3606	77	0
5	M	3489	0	3606	78	0
6	I	3154	0	3343	76	0
6	N	3154	0	3343	67	0
7	C	2400	0	2471	63	0
7	H	2400	0	2471	62	0
8	D	34	0	43	3	0
8	F	34	0	43	2	0
8	J	34	0	43	3	0
8	L	34	0	43	2	0
All	All	32650	0	34040	740	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 11.

The worst 5 of 740 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)
7:H:302:TYR:HA	7:H:305:LEU:HB3	1.52	0.90
1:B:3:PRO:HD2	7:C:2:THR:HB	1.55	0.88
7:C:302:TYR:HA	7:C:305:LEU:HB3	1.54	0.87
2:J:121:GLY:O	2:J:123:LEU:N	2.08	0.86
5:M:115:LEU:HD13	5:M:163:VAL:HG23	1.55	0.85

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 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	88/119 (74%)	82 (93%)	4 (4%)	2 (2%)	6	29
1	B	88/119 (74%)	82 (93%)	4 (4%)	2 (2%)	6	29
2	D	158/176 (90%)	142 (90%)	11 (7%)	5 (3%)	4	22
2	J	158/176 (90%)	141 (89%)	12 (8%)	5 (3%)	4	22
3	E	93/95 (98%)	88 (95%)	4 (4%)	1 (1%)	14	45
3	K	93/95 (98%)	88 (95%)	4 (4%)	1 (1%)	14	45
4	F	603/606 (100%)	553 (92%)	44 (7%)	6 (1%)	15	46
4	L	603/606 (100%)	553 (92%)	45 (8%)	5 (1%)	19	51
5	G	465/469 (99%)	425 (91%)	32 (7%)	8 (2%)	9	35
5	M	465/469 (99%)	427 (92%)	30 (6%)	8 (2%)	9	35
6	I	425/427 (100%)	389 (92%)	33 (8%)	3 (1%)	22	54
6	N	425/427 (100%)	386 (91%)	36 (8%)	3 (1%)	22	54
7	C	291/365 (80%)	261 (90%)	22 (8%)	8 (3%)	5	26
7	H	291/365 (80%)	261 (90%)	22 (8%)	8 (3%)	5	26
All	All	4246/4514 (94%)	3878 (91%)	303 (7%)	65 (2%)	10	38

5 of 65 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	J	119	LEU
2	J	122	GLY
4	L	519	ALA
6	N	47	PRO
7	H	194	TRP

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	71/92 (77%)	69 (97%)	2 (3%)	43	70
1	B	71/92 (77%)	69 (97%)	2 (3%)	43	70
2	D	118/130 (91%)	110 (93%)	8 (7%)	16	44
2	J	118/130 (91%)	110 (93%)	8 (7%)	16	44
3	E	71/71 (100%)	65 (92%)	6 (8%)	10	35
3	K	71/71 (100%)	65 (92%)	6 (8%)	10	35
4	F	453/454 (100%)	430 (95%)	23 (5%)	24	54
4	L	453/454 (100%)	431 (95%)	22 (5%)	25	56
5	G	332/332 (100%)	311 (94%)	21 (6%)	18	47
5	M	332/332 (100%)	308 (93%)	24 (7%)	14	41
6	I	302/302 (100%)	293 (97%)	9 (3%)	41	68
6	N	302/302 (100%)	292 (97%)	10 (3%)	38	66
7	C	247/300 (82%)	226 (92%)	21 (8%)	10	35
7	H	247/300 (82%)	227 (92%)	20 (8%)	11	36
All	All	3188/3362 (95%)	3006 (94%)	182 (6%)	20	51

5 of 182 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	H	267	TRP
2	D	131	LEU
7	C	147	TYR

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Mol	Chain	Res	Type
7	H	278	TRP
1	B	69	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
6	N	245	ASN
6	N	279	GLN
5	G	43	HIS
5	M	255	GLN
5	G	49	HIS

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

4 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	$\# Z > 2$
8	UMQ	D	200	-	35,35,35	1.53	7 (20%)	46,46,46	1.46	9 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	UMQ	J	200	-	35,35,35	1.51	6 (17%)	46,46,46	1.46	7 (15%)
8	UMQ	F	700	-	35,35,35	1.51	6 (17%)	46,46,46	1.65	8 (17%)
8	UMQ	L	700	-	35,35,35	1.49	5 (14%)	46,46,46	1.66	9 (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
8	UMQ	D	200	-	-	8/20/60/60	0/2/2/2
8	UMQ	J	200	-	-	7/20/60/60	0/2/2/2
8	UMQ	F	700	-	-	11/20/60/60	0/2/2/2
8	UMQ	L	700	-	-	11/20/60/60	0/2/2/2

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	D	200	UMQ	C3'-C4'	-3.92	1.41	1.52
8	F	700	UMQ	C3'-C4'	-3.88	1.41	1.52
8	L	700	UMQ	C3'-C4'	-3.85	1.42	1.52
8	J	200	UMQ	C3'-C4'	-3.77	1.42	1.52
8	J	200	UMQ	C3-C4	-3.59	1.43	1.52

The worst 5 of 33 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	F	700	UMQ	CA-O1'-C1'	3.81	120.15	113.84
8	F	700	UMQ	O5-C5-C6	3.81	115.90	106.44
8	L	700	UMQ	CA-O1'-C1'	3.78	120.11	113.84
8	L	700	UMQ	O5-C5-C6	3.74	115.74	106.44
8	J	200	UMQ	CA-O1'-C1'	3.43	119.52	113.84

There are no chirality outliers.

5 of 37 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	D	200	UMQ	CB-CA-O1'-C1'
8	J	200	UMQ	CB-CA-O1'-C1'
8	F	700	UMQ	O5'-C1'-O1'-CA

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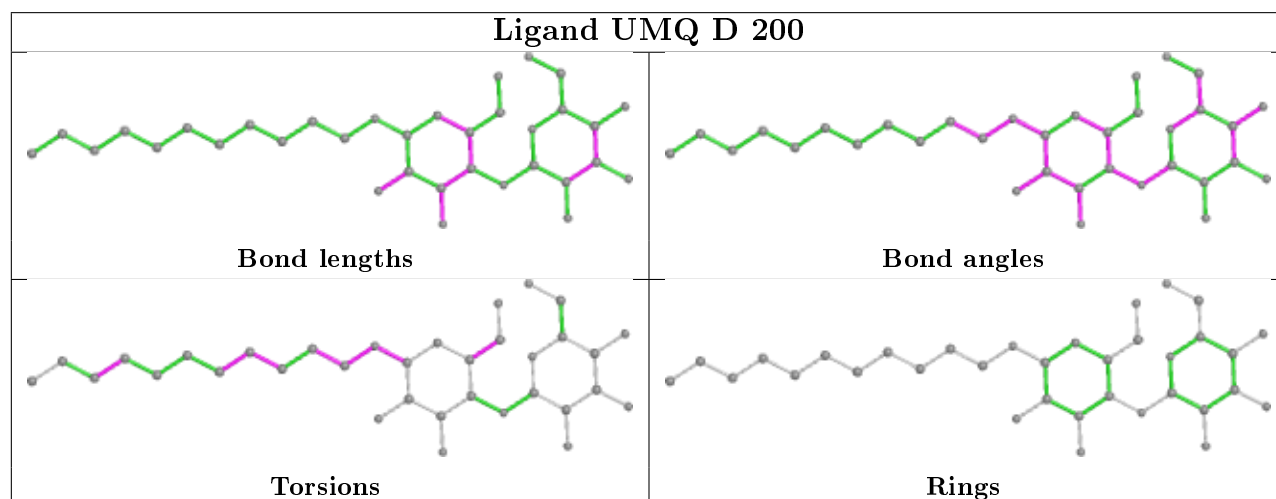
Mol	Chain	Res	Type	Atoms
8	L	700	UMQ	O5'-C1'-O1'-CA
8	D	200	UMQ	C4'-C5'-C6'-O6'

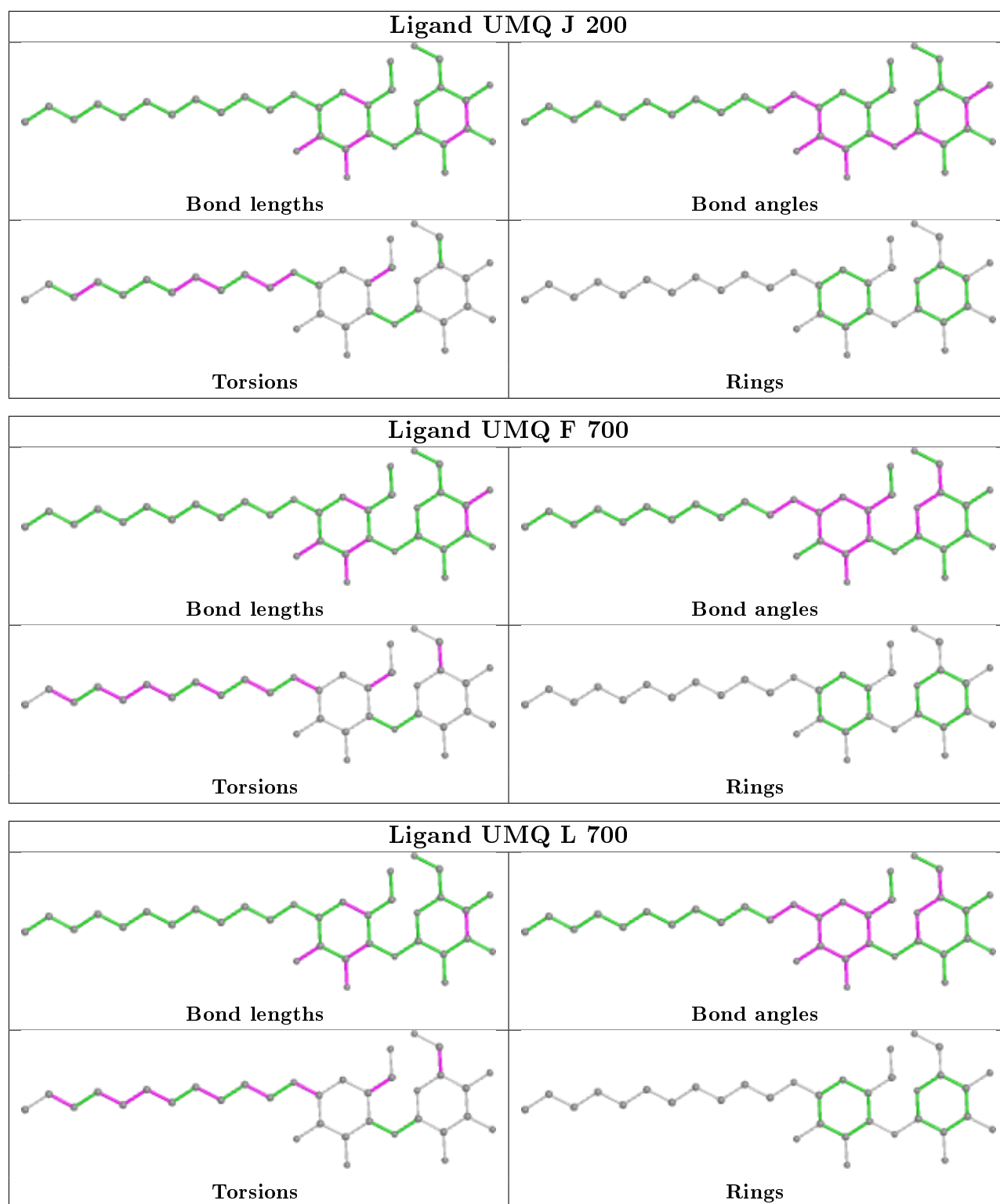
There are no ring outliers.

4 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	D	200	UMQ	3	0
8	J	200	UMQ	3	0
8	F	700	UMQ	2	0
8	L	700	UMQ	2	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 ⓘ

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	92/119 (77%)	-0.40	3 (3%) 46 44	49, 83, 152, 186	0
1	B	92/119 (77%)	-0.48	2 (2%) 62 60	52, 82, 152, 179	0
2	D	160/176 (90%)	-0.37	10 (6%) 20 20	44, 74, 165, 203	0
2	J	160/176 (90%)	-0.34	10 (6%) 20 20	47, 75, 165, 203	0
3	E	95/95 (100%)	-0.55	1 (1%) 80 81	48, 70, 132, 163	0
3	K	95/95 (100%)	-0.51	1 (1%) 80 81	46, 69, 131, 163	0
4	F	605/606 (99%)	0.01	39 (6%) 19 19	51, 112, 181, 329	0
4	L	605/606 (99%)	-0.07	36 (5%) 21 21	51, 111, 180, 329	0
5	G	467/469 (99%)	-0.55	6 (1%) 77 77	39, 74, 133, 175	0
5	M	467/469 (99%)	-0.56	5 (1%) 80 81	39, 74, 133, 174	0
6	I	427/427 (100%)	-0.60	4 (0%) 84 84	40, 65, 117, 195	0
6	N	427/427 (100%)	-0.57	5 (1%) 79 78	39, 65, 116, 196	0
7	C	297/365 (81%)	-0.29	6 (2%) 65 64	54, 95, 151, 205	0
7	H	297/365 (81%)	-0.33	9 (3%) 50 49	56, 96, 150, 205	0
All	All	4286/4514 (94%)	-0.36	137 (3%) 47 46	39, 84, 158, 329	0

The worst 5 of 137 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	L	435	PRO	14.9
4	F	435	PRO	13.2
4	L	434	HIS	11.8
4	F	436	HIS	9.8
4	L	436	HIS	8.4

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

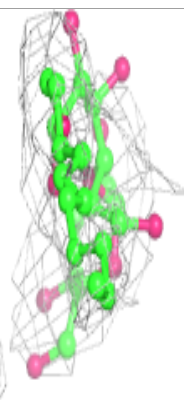
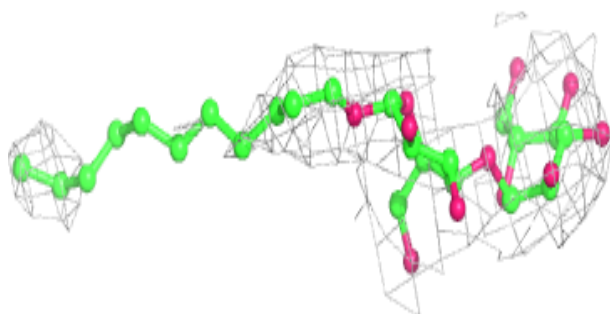
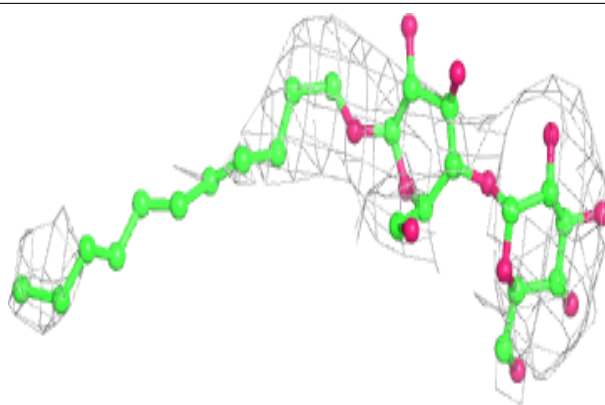
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
8	UMQ	F	700	34/34	0.83	0.28	52,122,193,206	0
8	UMQ	L	700	34/34	0.84	0.27	49,123,193,207	0
8	UMQ	J	200	34/34	0.89	0.26	32,84,118,140	0
8	UMQ	D	200	34/34	0.91	0.26	32,86,119,141	0

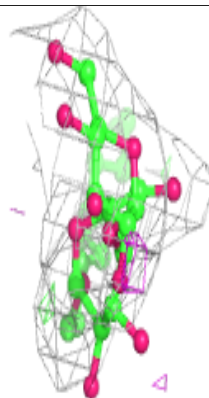
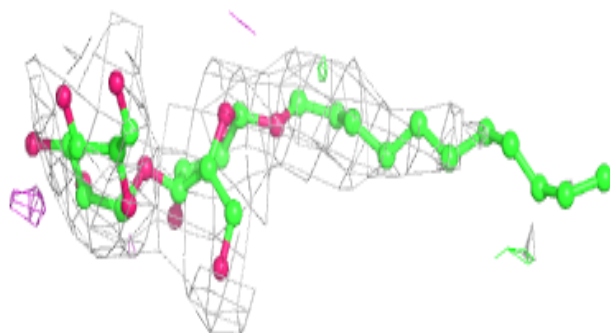
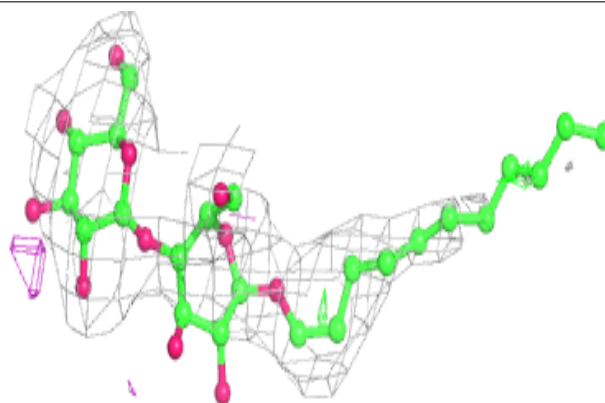
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around UMQ F 700:

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

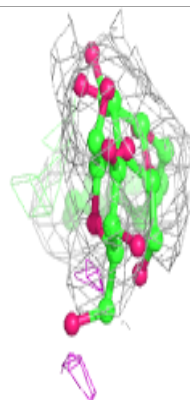
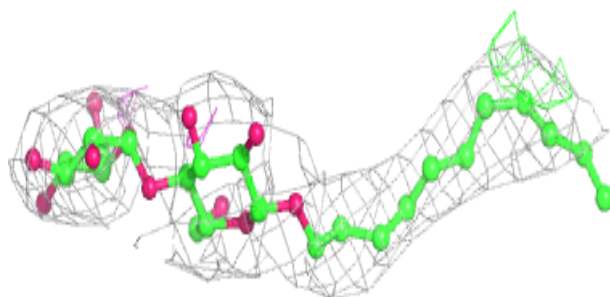
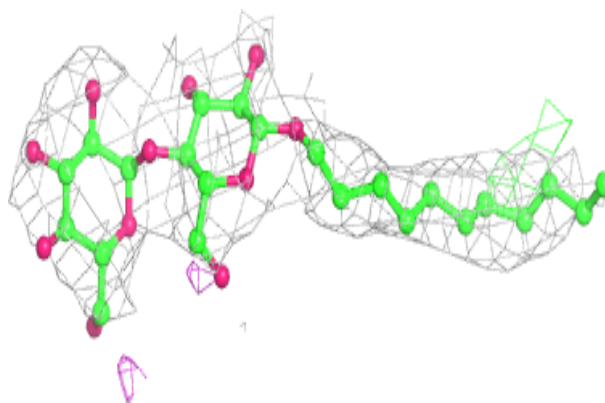
**Electron density around UMQ L 700:**

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

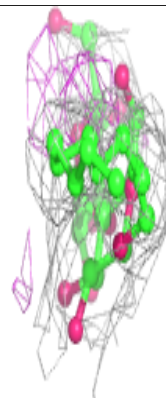
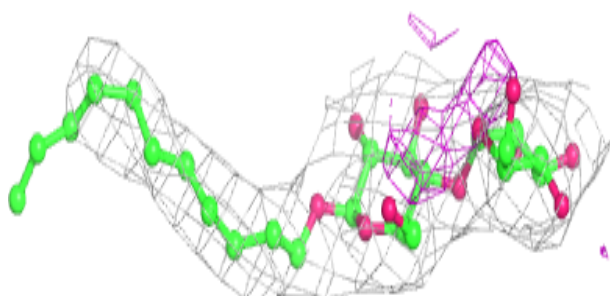
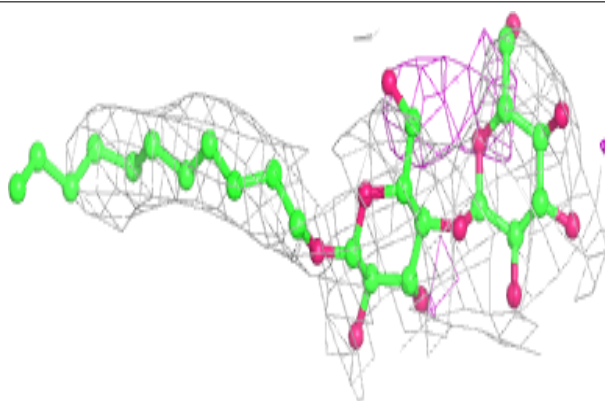


Electron density around UMQ J 200:

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

**Electron density around UMQ D 200:**

$2mF_o-DF_c$ (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.