



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 03:16 PM UTC

PDB ID : 2FUG / pdb_00002fug
Title : Crystal structure of the hydrophilic domain of respiratory complex I from
Thermus thermophilus
Authors : Sazanov, L.A.; Hinchliffe, P.
Deposited on : 2006-01-26
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 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

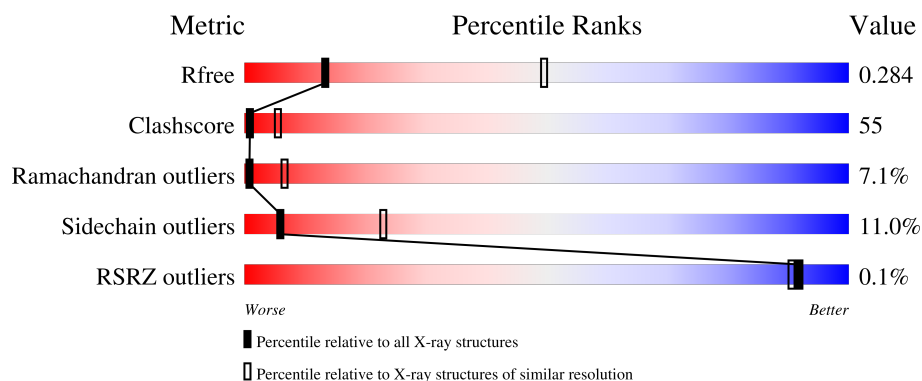
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 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.



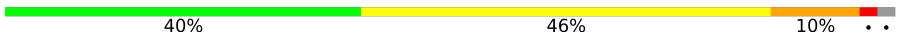
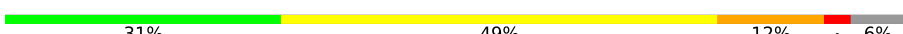
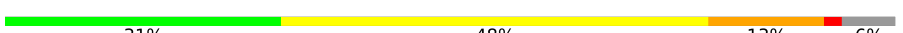
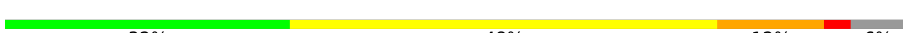
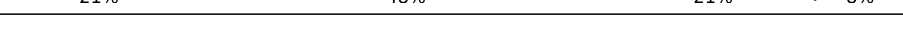
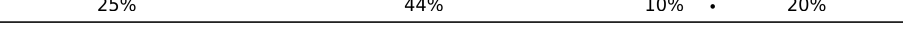
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1169 (3.32-3.28)
Clashscore	190562	1209 (3.32-3.28)
Ramachandran outliers	187476	1188 (3.32-3.28)
Sidechain outliers	187428	1187 (3.32-3.28)
RSRZ outliers	180081	1169 (3.32-3.28)

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	1	438	37% 51% 10% ..
1	A	438	36% 51% 11% ..
1	J	438	36% 50% 11% ..
1	S	438	35% 51% 11% ..
2	2	181	38% 48% 11% ..

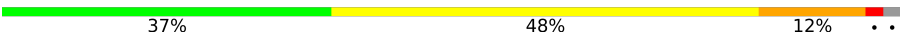
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Mol	Chain	Length	Quality of chain
2	B	181	
2	K	181	
2	T	181	
3	3	783	
3	C	783	
3	L	783	
3	U	783	
4	4	409	
4	D	409	
4	M	409	
4	V	409	
5	5	207	
5	E	207	
5	N	207	
5	W	207	
6	6	181	
6	F	181	
6	O	181	
6	X	181	
7	9	182	
7	G	182	
7	P	182	
7	Y	182	
8	7	129	
8	H	129	

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Mol	Chain	Length	Quality of chain
8	Q	129	
8	Z	129	

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
10	FES	2	182	-	-	X	-
10	FES	B	182	-	-	X	-
10	FES	K	182	-	-	X	-
9	SF4	3	786	-	-	X	-
9	SF4	C	786	-	-	X	-
9	SF4	L	786	-	-	X	-
9	SF4	U	786	-	-	X	-

2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 73916 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 chain 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	1	432	Total	C	N	O	S	0	0	0
			3383	2157	590	618	18			
1	A	432	Total	C	N	O	S	0	0	0
			3383	2157	590	618	18			
1	J	432	Total	C	N	O	S	0	0	0
			3383	2157	590	618	18			
1	S	432	Total	C	N	O	S	0	0	0
			3383	2157	590	618	18			

- Molecule 2 is a protein called NADH-quinone oxidoreductase chain 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	2	178	Total	C	N	O	S	0	0	0
			1406	895	238	265	8			
2	B	178	Total	C	N	O	S	0	0	0
			1406	895	238	265	8			
2	K	178	Total	C	N	O	S	0	0	0
			1406	895	238	265	8			
2	T	178	Total	C	N	O	S	0	0	0
			1406	895	238	265	8			

- Molecule 3 is a protein called NADH-quinone oxidoreductase chain 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	3	737	Total	C	N	O	S	0	0	0
			5746	3657	1031	1027	31			
3	C	737	Total	C	N	O	S	0	0	0
			5746	3657	1031	1027	31			
3	L	737	Total	C	N	O	S	0	0	0
			5746	3657	1031	1027	31			
3	U	737	Total	C	N	O	S	0	0	0
			5746	3657	1031	1027	31			

- Molecule 4 is a protein called NADH-quinone oxidoreductase chain 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	4	370	Total	C	N	O	S	0	0	0
			2953	1902	504	537	10			
4	D	370	Total	C	N	O	S	0	0	0
			2953	1902	504	537	10			
4	M	370	Total	C	N	O	S	0	0	0
			2953	1902	504	537	10			
4	V	370	Total	C	N	O	S	0	0	0
			2953	1902	504	537	10			

- Molecule 5 is a protein called NADH-quinone oxidoreductase chain 5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	5	191	Total	C	N	O	S	0	0	0
			1570	1018	267	282	3			
5	E	191	Total	C	N	O	S	0	0	0
			1570	1018	267	282	3			
5	N	191	Total	C	N	O	S	0	0	0
			1570	1018	267	282	3			
5	W	191	Total	C	N	O	S	0	0	0
			1570	1018	267	282	3			

- Molecule 6 is a protein called NADH-quinone oxidoreductase chain 6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	6	144	Total	C	N	O	S	0	0	0
			1102	700	192	197	13			
6	F	144	Total	C	N	O	S	0	0	0
			1102	700	192	197	13			
6	O	144	Total	C	N	O	S	0	0	0
			1102	700	192	197	13			
6	X	144	Total	C	N	O	S	0	0	0
			1102	700	192	197	13			

- Molecule 7 is a protein called NADH-quinone oxidoreductase chain 9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	9	154	Total	C	N	O	S	0	0	0
			1193	759	201	222	11			
7	G	154	Total	C	N	O	S	0	0	0
			1193	759	201	222	11			
7	P	154	Total	C	N	O	S	0	0	0
			1193	759	201	222	11			

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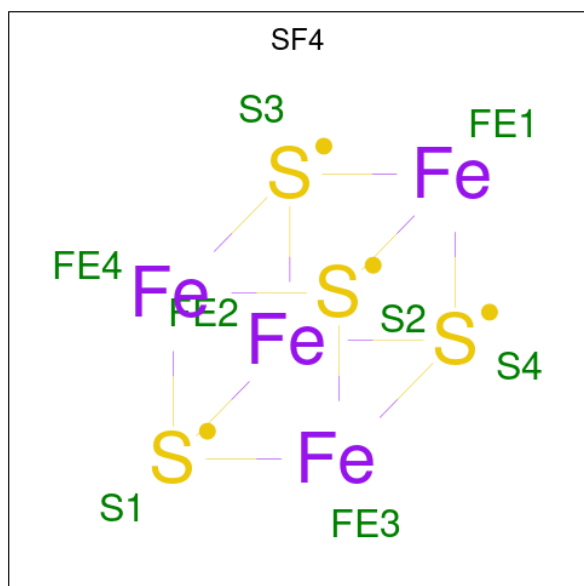
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	Y	154	Total	C	N	O	S	0	0	0
			1193	759	201	222	11			

- Molecule 8 is a protein called conserved hypothetical protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	7	127	Total	C	N	O	S	0	0	0
			1031	664	183	181	3			
8	H	127	Total	C	N	O	S	0	0	0
			1031	664	183	181	3			
8	Q	127	Total	C	N	O	S	0	0	0
			1031	664	183	181	3			
8	Z	127	Total	C	N	O	S	0	0	0
			1031	664	183	181	3			

- Molecule 9 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	1	1	Total	Fe	S	0	0
			8	4	4		
9	3	1	Total	Fe	S	0	0
			8	4	4		
9	3	1	Total	Fe	S	0	0
			8	4	4		
9	3	1	Total	Fe	S	0	0
			8	4	4		

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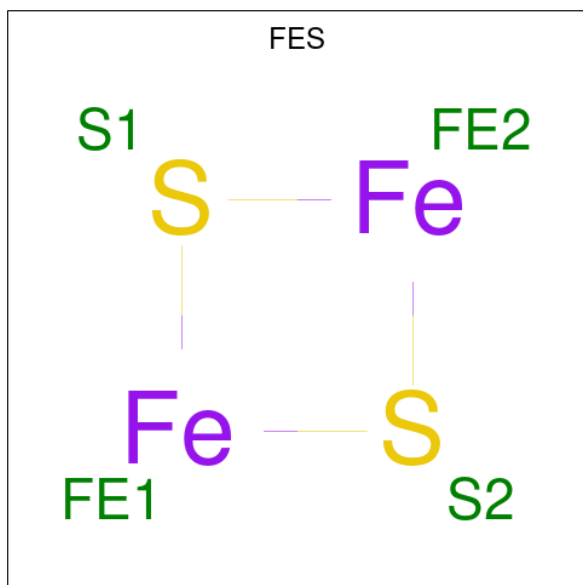
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	6	1	Total 8	Fe 4	S 4	0	0
9	9	1	Total 8	Fe 4	S 4	0	0
9	9	1	Total 8	Fe 4	S 4	0	0
9	A	1	Total 8	Fe 4	S 4	0	0
9	C	1	Total 8	Fe 4	S 4	0	0
9	C	1	Total 8	Fe 4	S 4	0	0
9	C	1	Total 8	Fe 4	S 4	0	0
9	F	1	Total 8	Fe 4	S 4	0	0
9	G	1	Total 8	Fe 4	S 4	0	0
9	G	1	Total 8	Fe 4	S 4	0	0
9	J	1	Total 8	Fe 4	S 4	0	0
9	L	1	Total 8	Fe 4	S 4	0	0
9	L	1	Total 8	Fe 4	S 4	0	0
9	L	1	Total 8	Fe 4	S 4	0	0
9	O	1	Total 8	Fe 4	S 4	0	0
9	P	1	Total 8	Fe 4	S 4	0	0
9	P	1	Total 8	Fe 4	S 4	0	0
9	S	1	Total 8	Fe 4	S 4	0	0
9	U	1	Total 8	Fe 4	S 4	0	0
9	U	1	Total 8	Fe 4	S 4	0	0
9	U	1	Total 8	Fe 4	S 4	0	0

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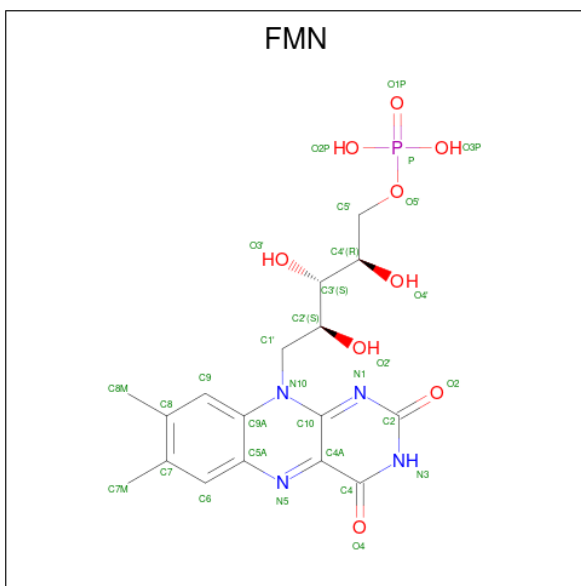
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	X	1	Total	Fe	S	0	0
			8	4	4		
9	Y	1	Total	Fe	S	0	0
			8	4	4		
9	Y	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 10 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe_2S_2).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	2	1	Total	Fe	S	0	0
			4	2	2		
10	3	1	Total	Fe	S	0	0
			4	2	2		
10	B	1	Total	Fe	S	0	0
			4	2	2		
10	C	1	Total	Fe	S	0	0
			4	2	2		
10	K	1	Total	Fe	S	0	0
			4	2	2		
10	L	1	Total	Fe	S	0	0
			4	2	2		
10	T	1	Total	Fe	S	0	0
			4	2	2		
10	U	1	Total	Fe	S	0	0
			4	2	2		

- Molecule 11 is FLAVIN MONONUCLEOTIDE (CCD ID: FMN) (formula: $C_{17}H_{21}N_4O_9P$).

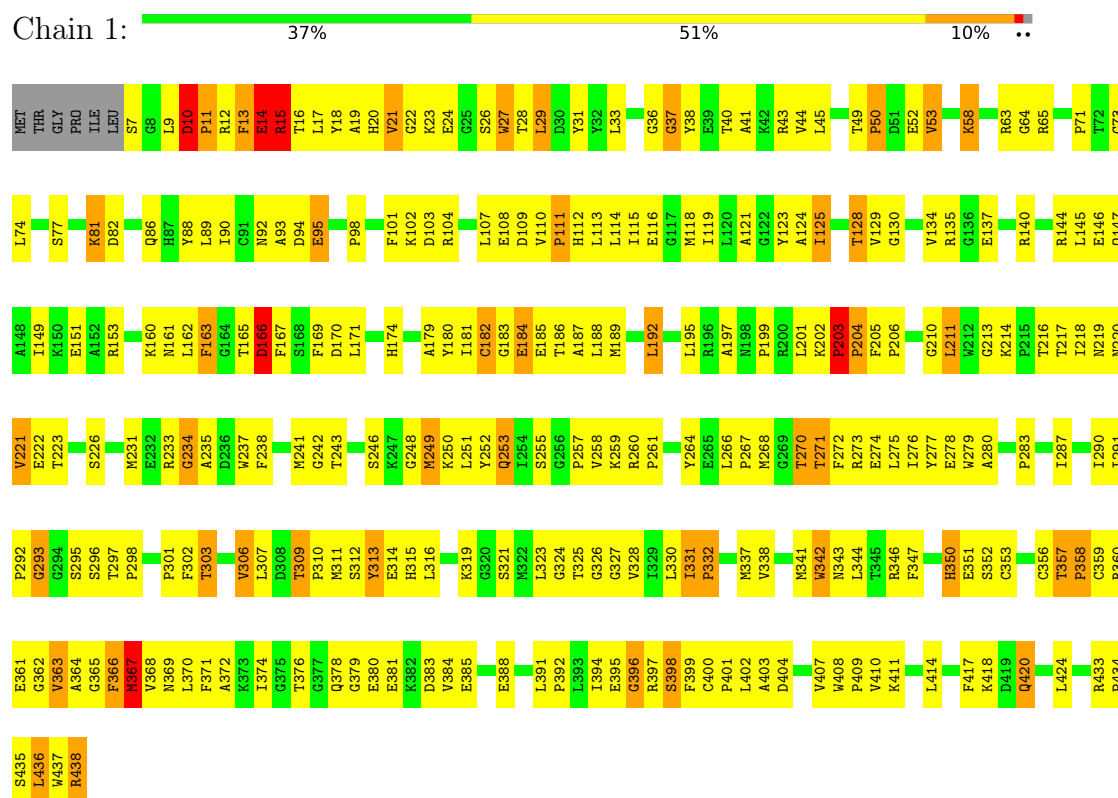


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
11	7	1	Total 31	C 17	N 4	O 9	P 1	0	0
11	H	1	Total 31	C 17	N 4	O 9	P 1	0	0
11	Q	1	Total 31	C 17	N 4	O 9	P 1	0	0
11	Z	1	Total 31	C 17	N 4	O 9	P 1	0	0

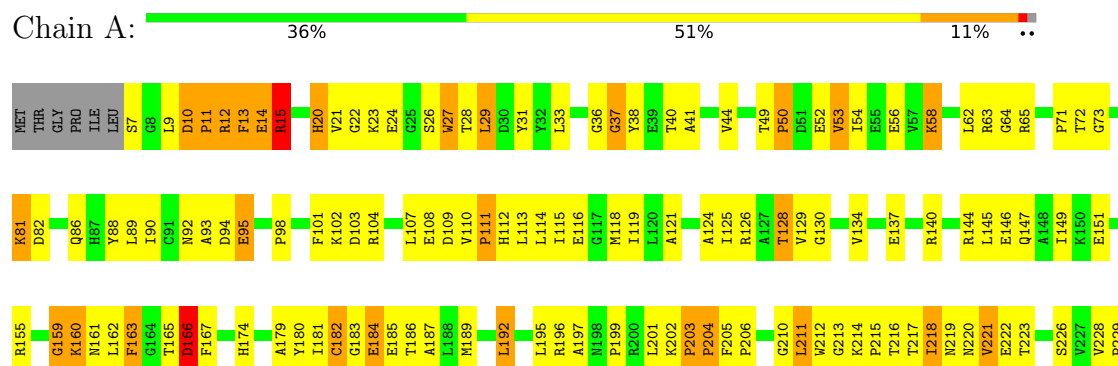
3 Residue-property plots

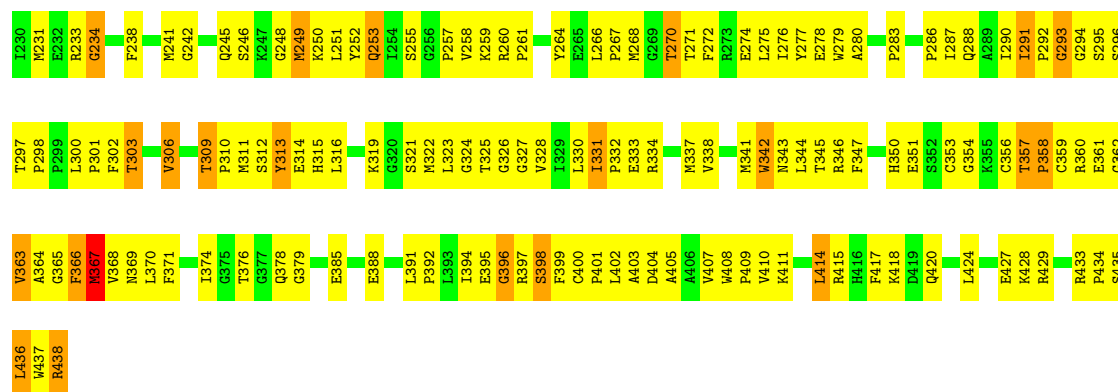
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: NADH-quinone oxidoreductase chain 1



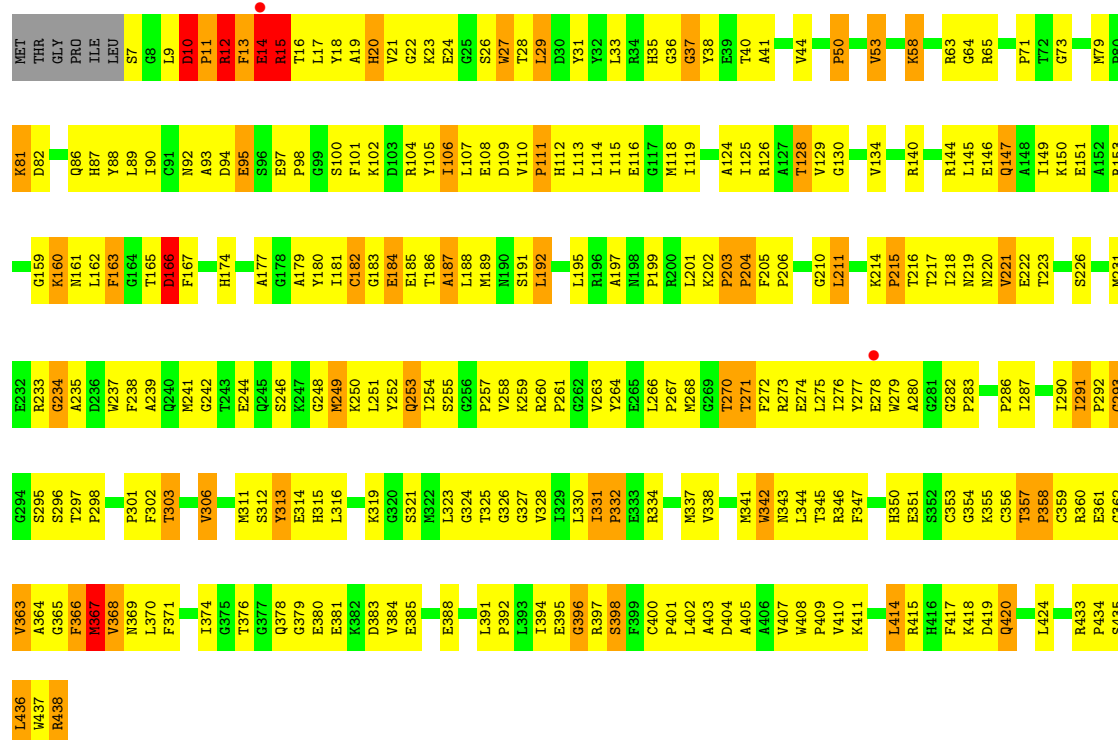
• Molecule 1: NADH-quinone oxidoreductase chain 1





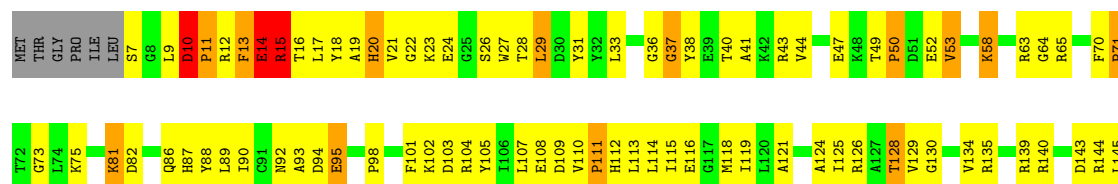
• Molecule 1: NADH-quinone oxidoreductase chain 1

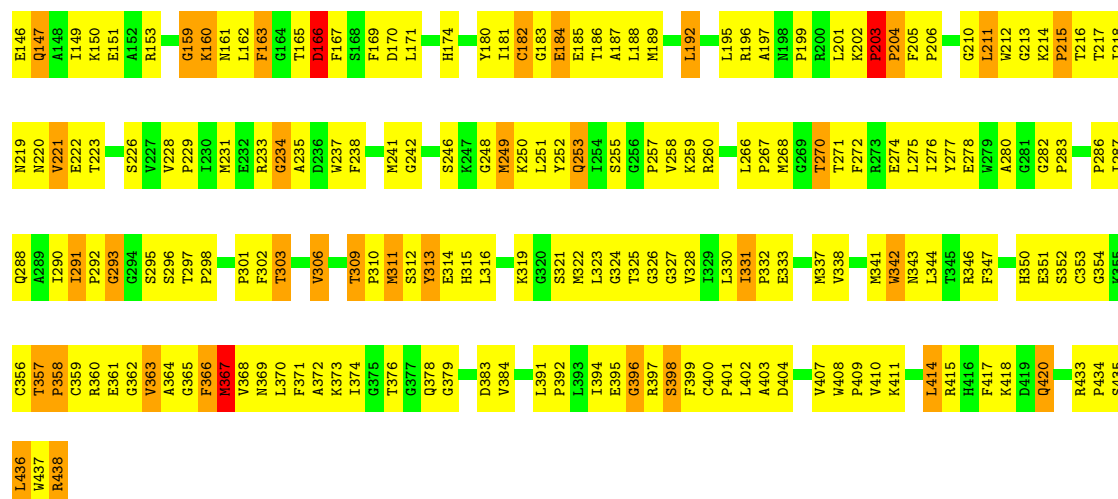
Chain J: 36% 50% 11% ..



• Molecule 1: NADH-quinone oxidoreductase chain 1

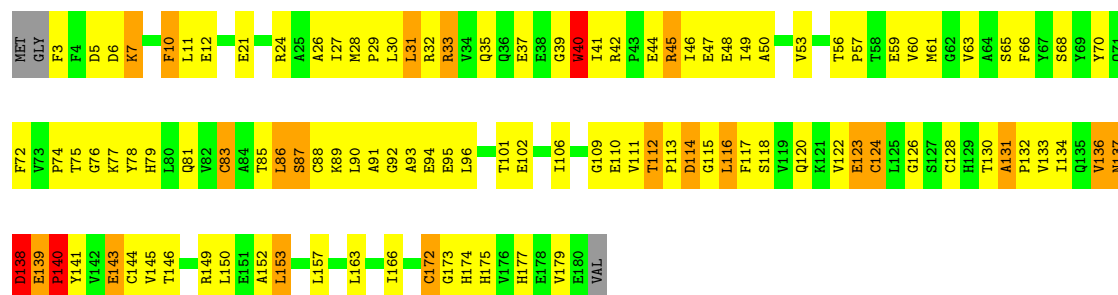
Chain S: 35% 51% 11% ..





• Molecule 2: NADH-quinone oxidoreductase chain 2

Chain 2: 38% 48% 11% ..



• Molecule 2: NADH-quinone oxidoreductase chain 2

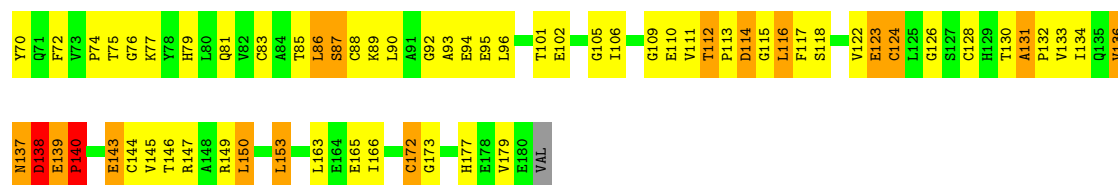
Chain B: 43% 44% 10% ..



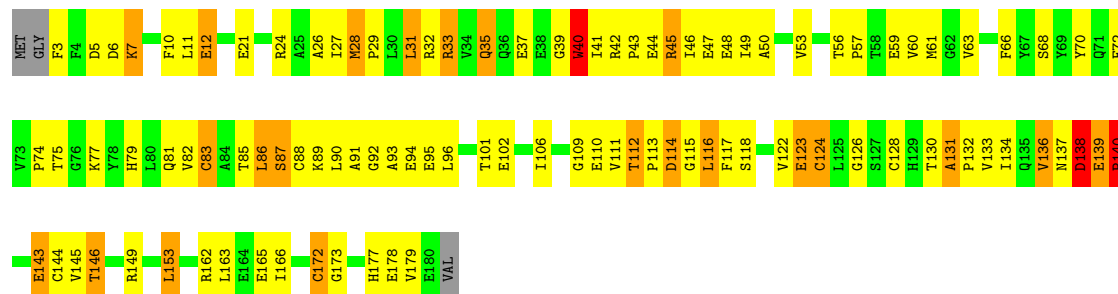
• Molecule 2: NADH-quinone oxidoreductase chain 2

Chain K: 40% 46% 10% ..

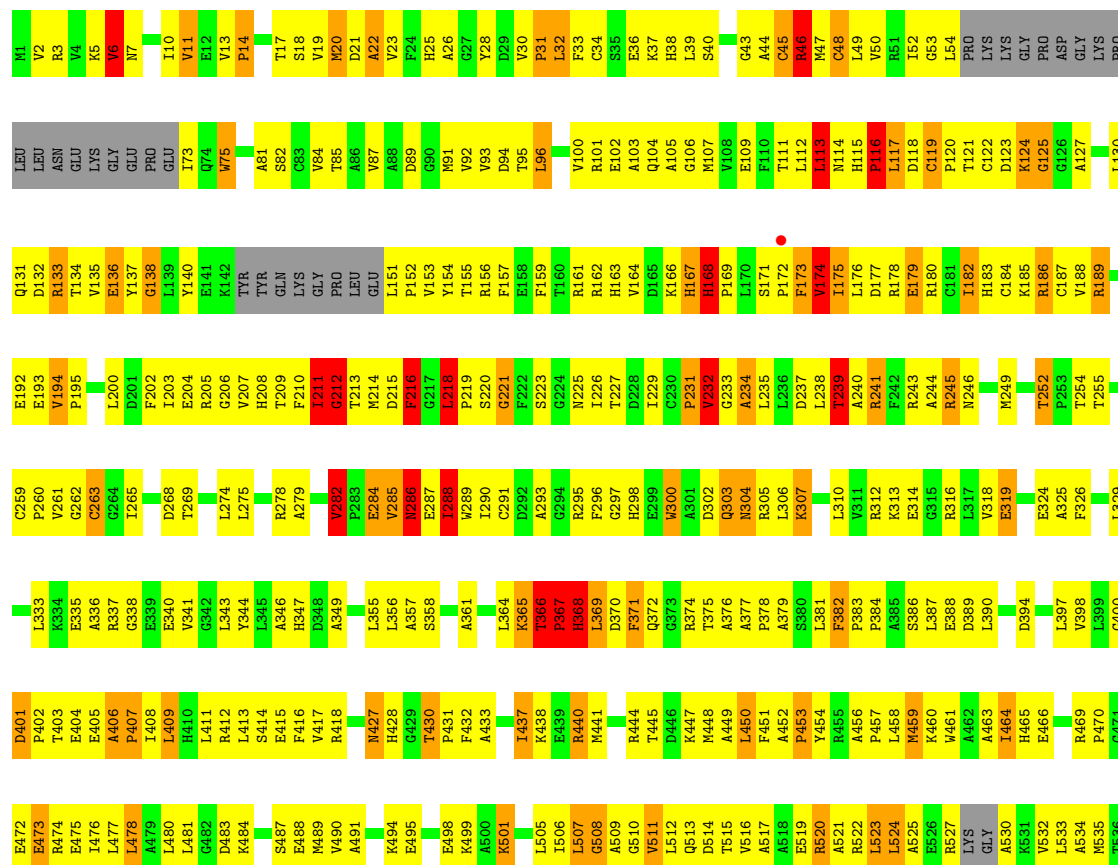


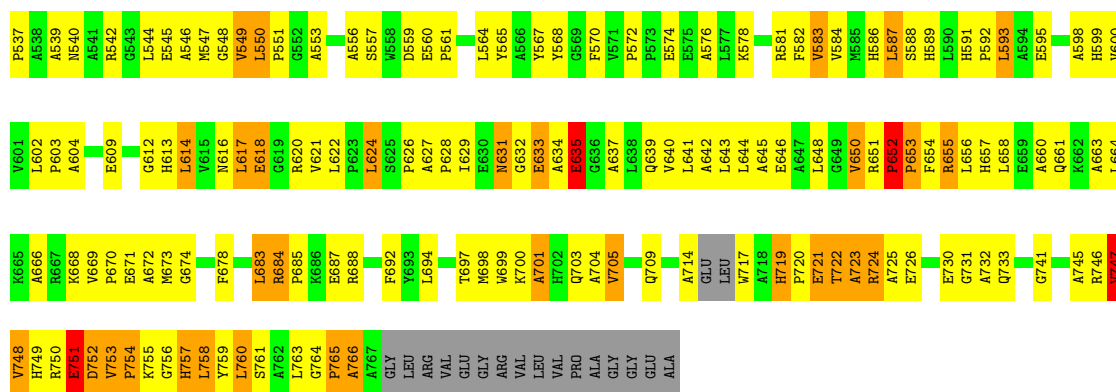


• Molecule 2: NADH-quinone oxidoreductase chain 2



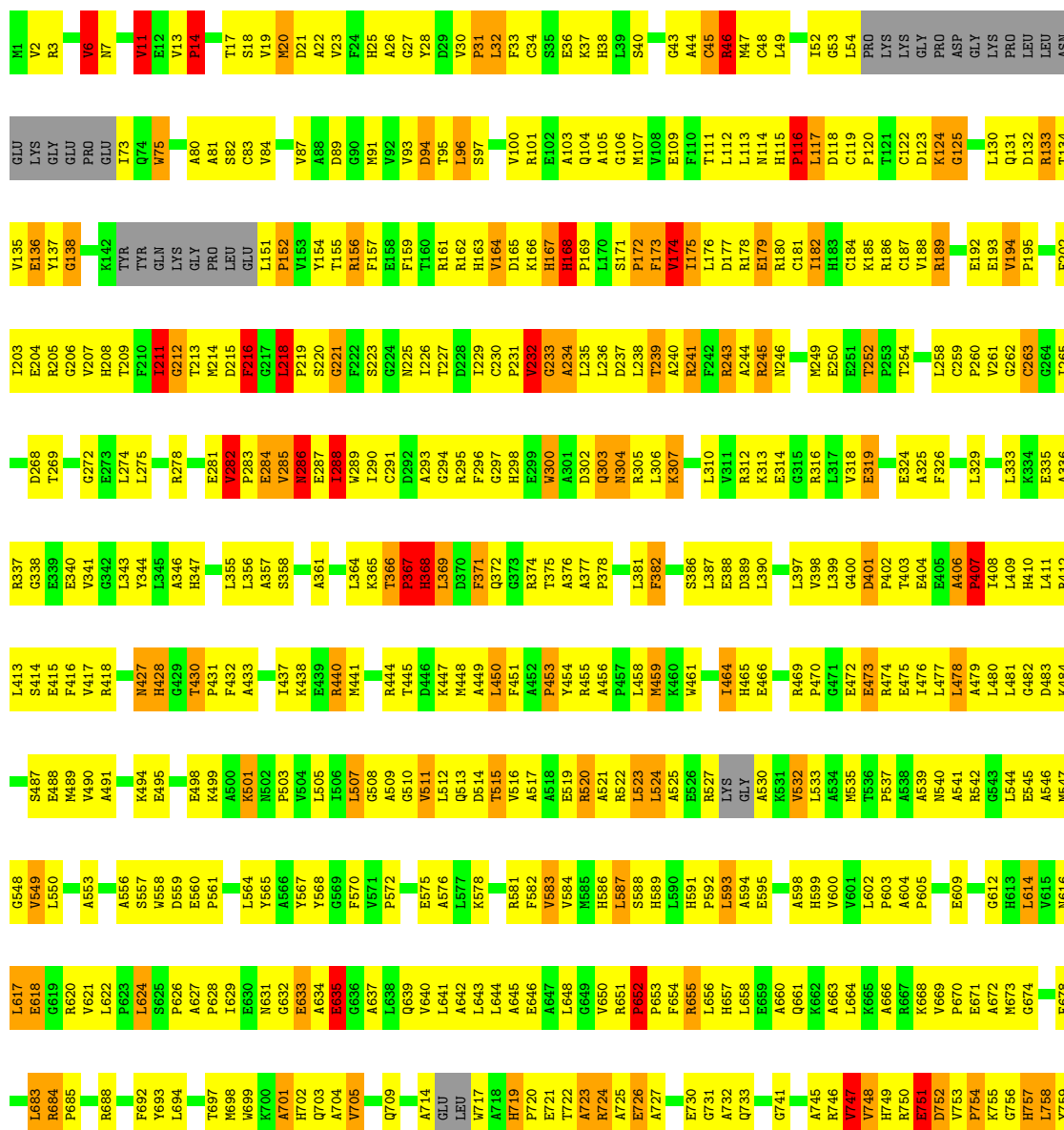
• Molecule 3: NADH-quinone oxidoreductase chain 3

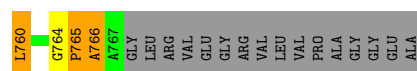




• Molecule 3: NADH-quinone oxidoreductase chain 3

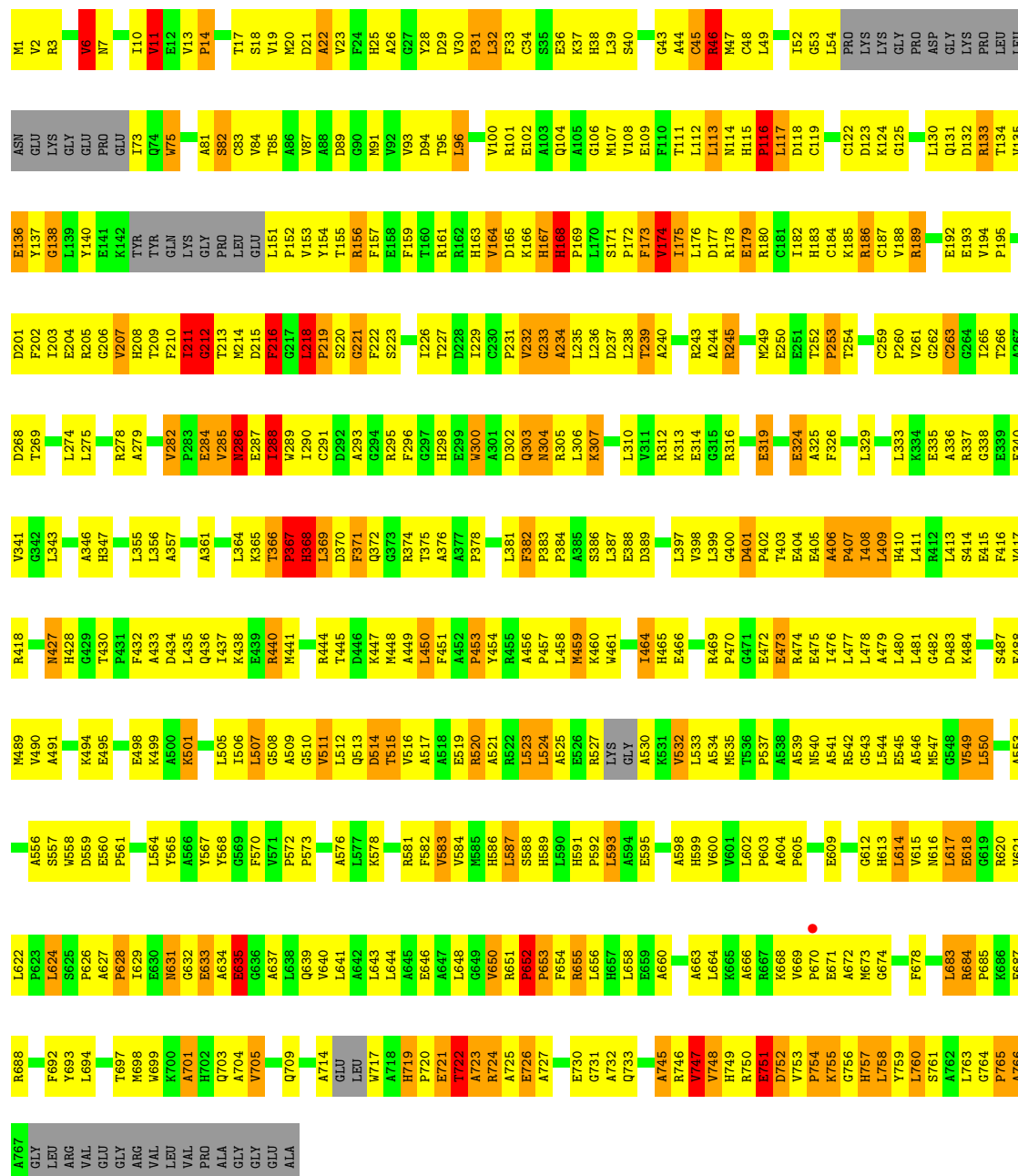
Chain C: 31% 49% 12% 6%





• Molecule 3: NADH-quinone oxidoreductase chain 3

Chain L: 31% 48% 13% 6%

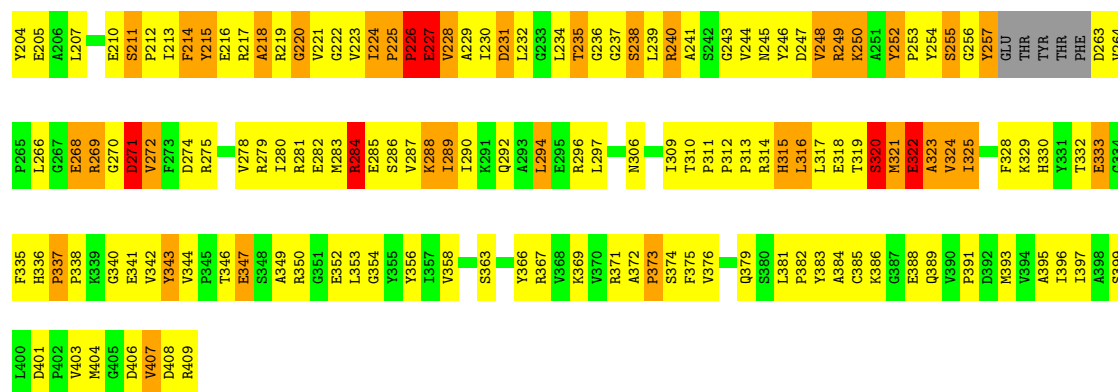


• Molecule 3: NADH-quinone oxidoreductase chain 3

Chain U: 32% 48% 12% 6%

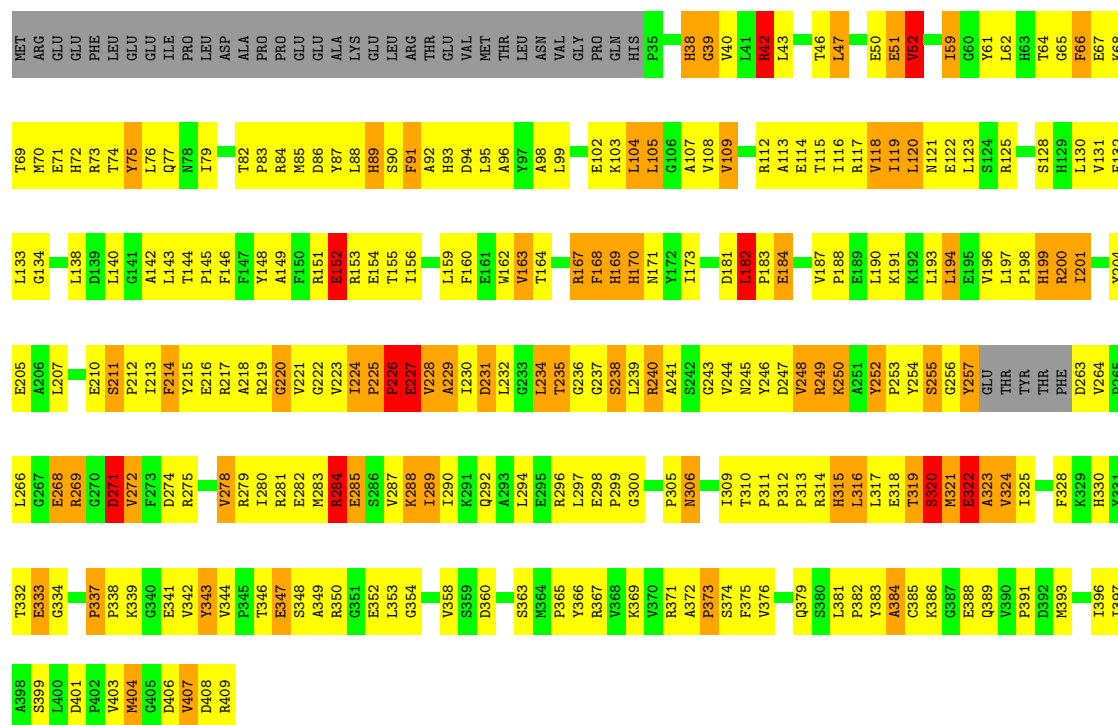


V131	K68	MET
F132	T69	ARG
L133	M70	GLU
	E71	PHE
L138	H72	LEU
D139	R73	GLU
L140	T74	GLU
G141	Y75	IIE
A142	L76	P80
L143	Q77	LEU
T144	W78	ASP
P145	I79	ALA
F146		P80
Y148	T82	GLU
A149	P83	P80
F150	R84	GLU
R151	M85	GLU
E152	D86	ALA
R153	Y87	LYS
E154	L88	GLU
T155	H89	LEU
I156	S90	ARG
	F91	THR
	A92	GLU
L159	H93	VAL
F160	D94	MET
E161	L95	THR
W162	A96	LEU
V163	Y97	ASN
T164	A98	VAL
	L99	GLY
		P80
R167	E102	GLN
H168	K103	HIS
H169	L104	P35
H170	L105	
M171	G106	H38
Y172	A107	G39
I173	I108	V40
	V109	L41
D181	P110	R42
L182	F111	
P183	R112	T46
E184	A113	L47
V187	E114	S48
P188	T115	G49
F189	I116	E50
L190	R117	E51
K191	V118	V52
R192	I119	L53
L193	L120	
L194	N121	T59
F195	E122	G60
V196	L123	Y61
L197	S124	L62
P198	R125	H63
H199		T64
R200	S128	G65
I201	H129	F66
	L130	F67



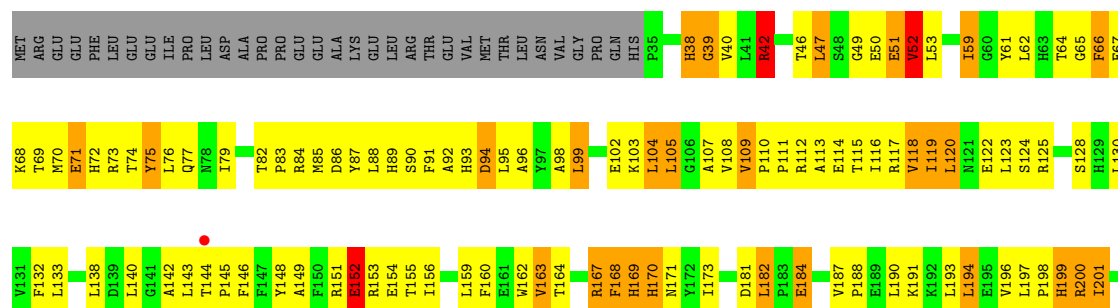
• Molecule 4: NADH-quinone oxidoreductase chain 4

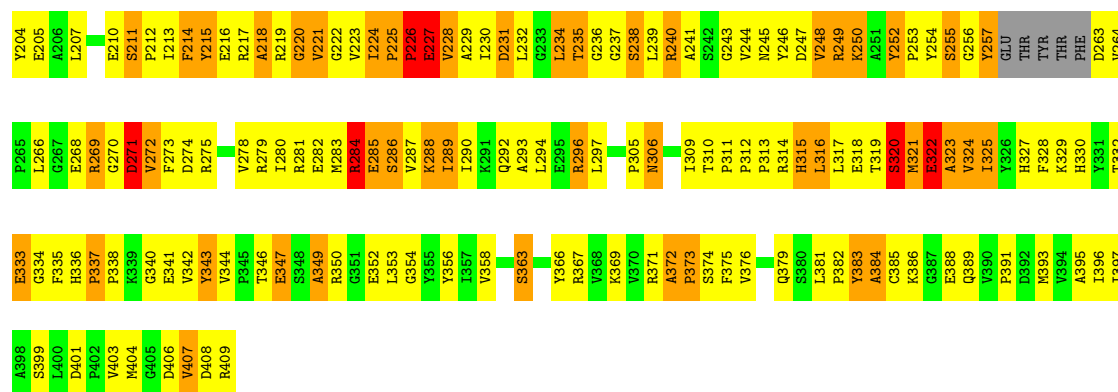
Chain D: 26% 46% 16% 10%



• Molecule 4: NADH-quinone oxidoreductase chain 4

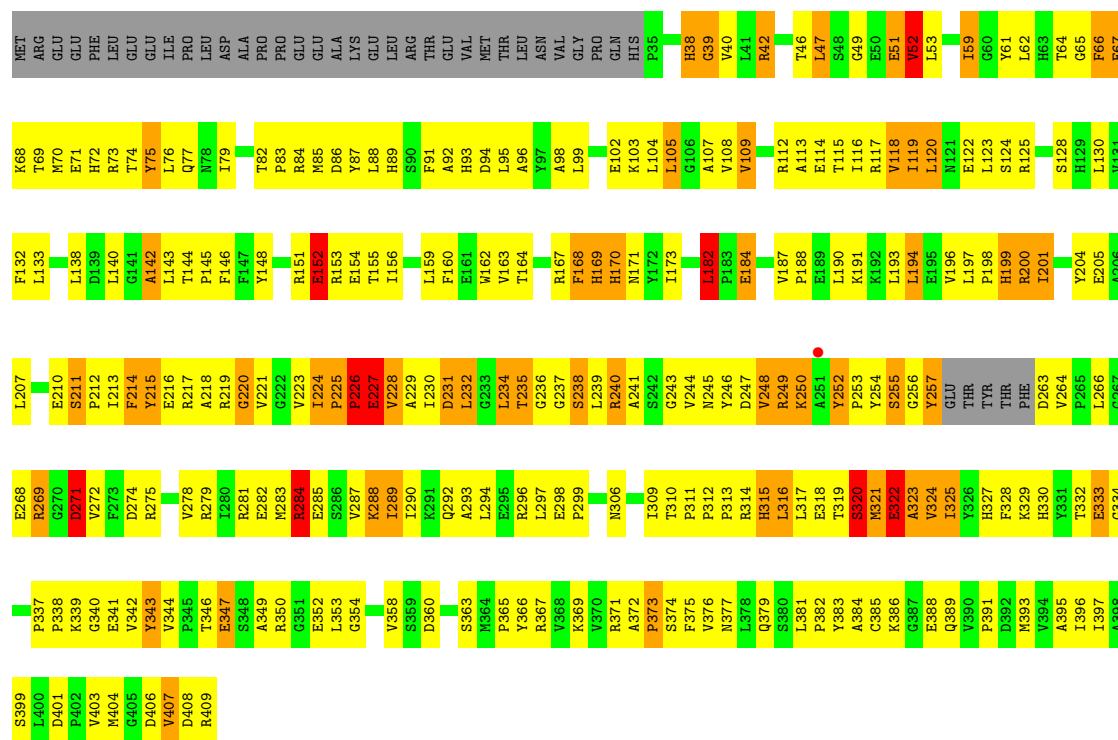
Chain M: 25% 45% 18% 10%





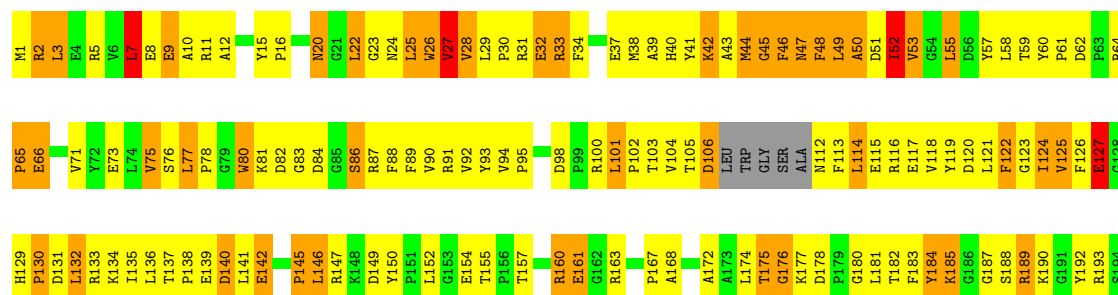
• Molecule 4: NADH-quinone oxidoreductase chain 4

Chain V: 28% 47% 14% • 10%



• Molecule 5: NADH-quinone oxidoreductase chain 5

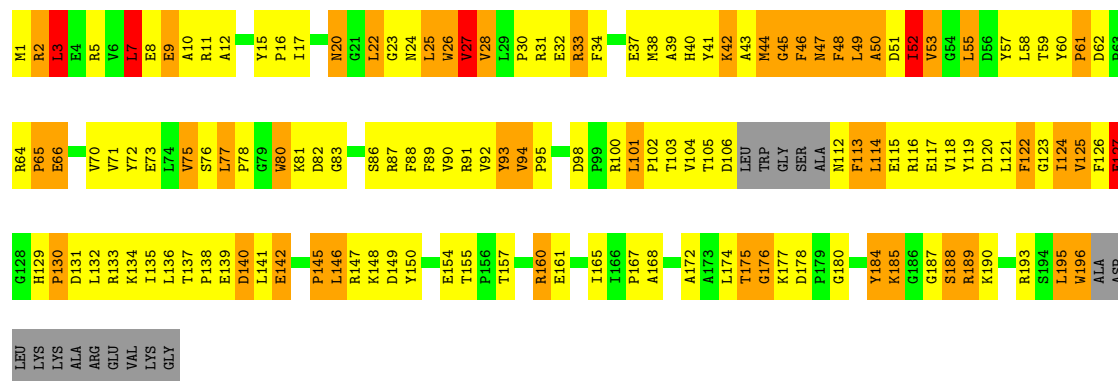
Chain 5: 22% 46% 23% • 8%



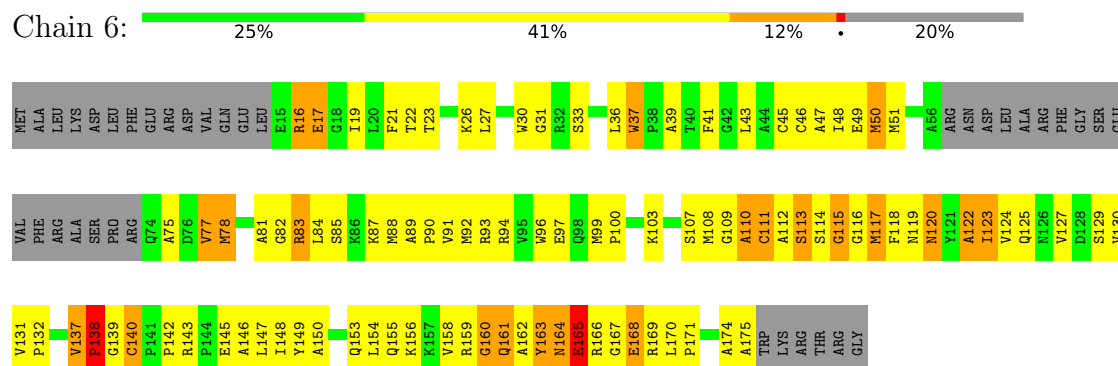
L195
W196
ALA
ASP
LEU
LYS
LYS
ALA
ARG
GLU
VAL
LYS
GLY

• Molecule 5: NADH-quinone oxidoreductase chain 5

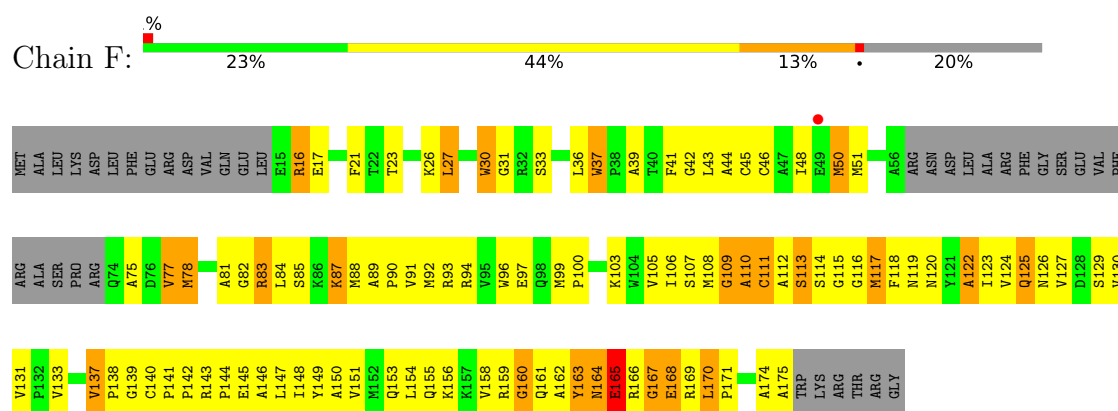
Chain E: 23% 44% 22% 8%



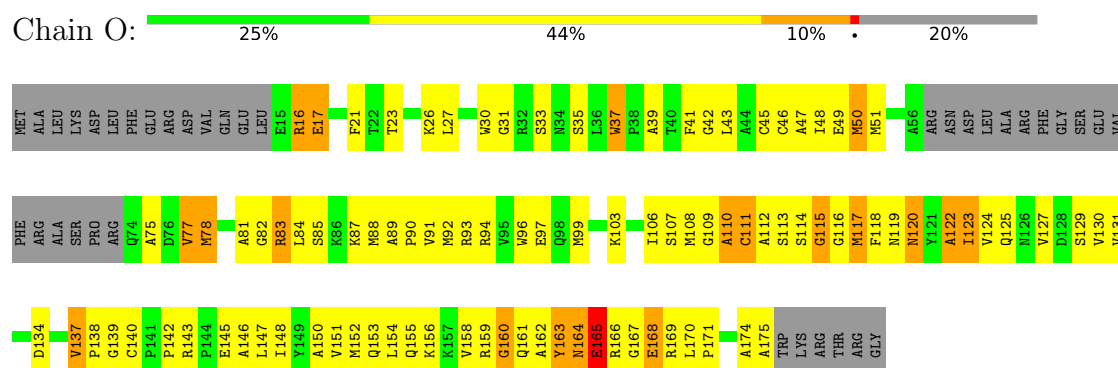
- Molecule 6: NADH-quinone oxidoreductase chain 6



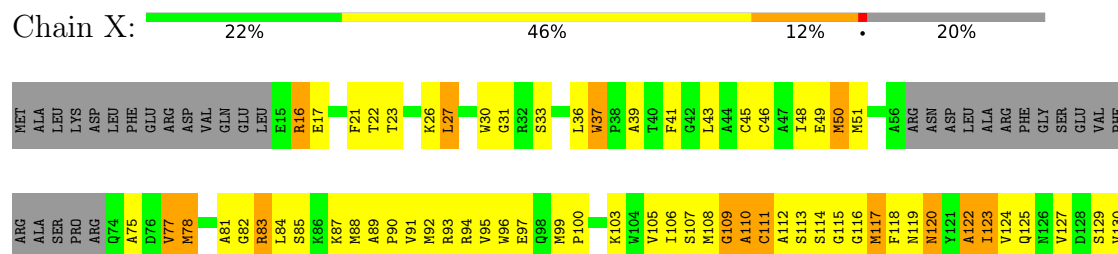
- Molecule 6: NADH-quinone oxidoreductase chain 6



- Molecule 6: NADH-quinone oxidoreductase chain 6



- Molecule 6: NADH-quinone oxidoreductase chain 6

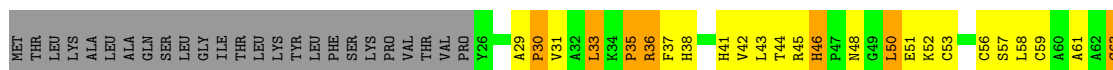
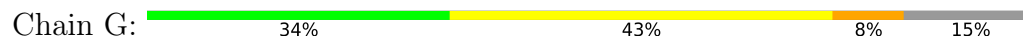




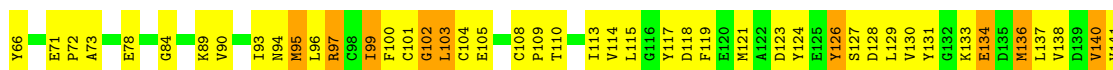
• Molecule 7: NADH-quinone oxidoreductase chain 9



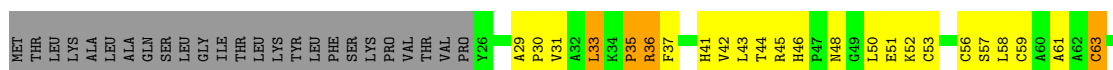
• Molecule 7: NADH-quinone oxidoreductase chain 9

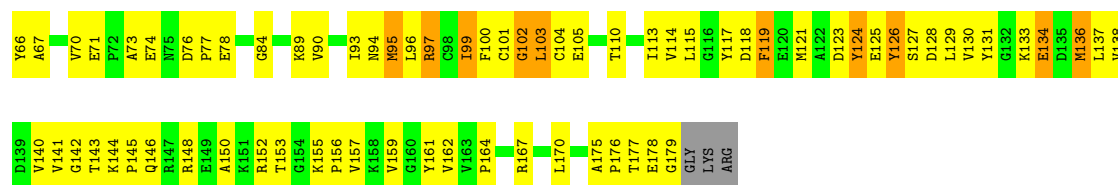


• Molecule 7: NADH-quinone oxidoreductase chain 9



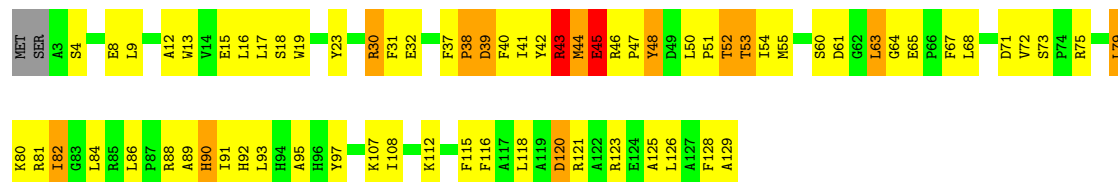
• Molecule 7: NADH-quinone oxidoreductase chain 9





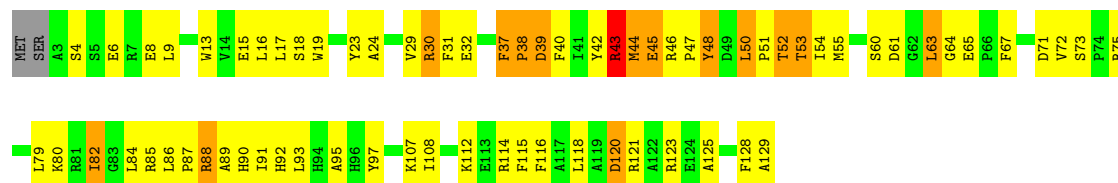
• Molecule 8: conserved hypothetical protein

Chain 7: 44% 43% 9% ..



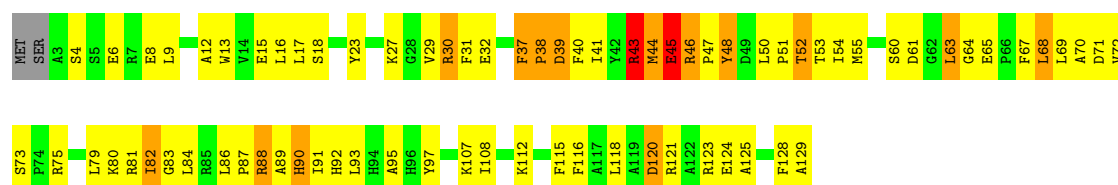
• Molecule 8: conserved hypothetical protein

Chain H: 43% 43% 11% ..



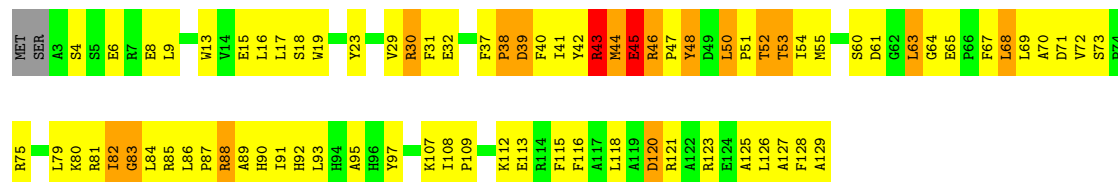
• Molecule 8: conserved hypothetical protein

Chain Q: 40% 46% 11% ..



• Molecule 8: conserved hypothetical protein

Chain Z: 37% 48% 12% ..



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	135.08Å 266.11Å 201.73Å 90.00° 104.71° 90.00°	Depositor
Resolution (Å)	20.00 – 3.30 20.00 – 3.30	Depositor EDS
% Data completeness (in resolution range)	95.3 (20.00-3.30) 74.5 (20.00-3.30)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	0.16	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.57 (at 3.31Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.265 , 0.298 0.252 , 0.284	Depositor DCC
R_{free} test set	3935 reflections (2.00%)	wwPDB-VP
Wilson B-factor (Å ²)	79.6	Xtriage
Anisotropy	0.495	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 32.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	73916	wwPDB-VP
Average B, all atoms (Å ²)	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.80% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: FES, FMN, SF4

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	1	0.61	1/3471 (0.0%)	1.08	21/4696 (0.4%)
1	A	0.56	0/3471	1.07	20/4696 (0.4%)
1	J	0.63	1/3471 (0.0%)	1.08	22/4696 (0.5%)
1	S	0.56	0/3471	1.08	24/4696 (0.5%)
2	2	0.61	0/1439	1.05	10/1953 (0.5%)
2	B	0.53	0/1439	1.04	7/1953 (0.4%)
2	K	0.60	0/1439	1.08	12/1953 (0.6%)
2	T	0.54	0/1439	1.04	10/1953 (0.5%)
3	3	0.59	1/5881 (0.0%)	1.16	58/7974 (0.7%)
3	C	0.57	0/5881	1.15	52/7974 (0.7%)
3	L	0.55	0/5881	1.15	55/7974 (0.7%)
3	U	0.55	0/5881	1.14	54/7974 (0.7%)
4	4	0.59	0/3031	1.21	32/4118 (0.8%)
4	D	0.59	0/3031	1.25	46/4118 (1.1%)
4	M	0.62	0/3031	1.22	40/4118 (1.0%)
4	V	0.52	0/3031	1.18	35/4118 (0.8%)
5	5	0.52	0/1616	1.21	21/2189 (1.0%)
5	E	0.54	0/1616	1.24	21/2189 (1.0%)
5	N	0.56	0/1616	1.22	16/2189 (0.7%)
5	W	0.46	0/1616	1.20	18/2189 (0.8%)
6	6	0.57	0/1126	1.28	14/1528 (0.9%)
6	F	0.62	0/1126	1.26	15/1528 (1.0%)
6	O	0.57	0/1126	1.25	13/1528 (0.9%)
6	X	0.52	0/1126	1.23	14/1528 (0.9%)
7	9	0.63	0/1224	1.11	6/1663 (0.4%)
7	G	0.66	0/1224	1.12	6/1663 (0.4%)
7	P	0.60	0/1224	1.12	5/1663 (0.3%)
7	Y	0.53	0/1224	1.07	7/1663 (0.4%)
8	7	0.53	0/1059	1.13	10/1429 (0.7%)
8	H	0.53	0/1059	1.11	10/1429 (0.7%)
8	Q	0.55	0/1059	1.12	10/1429 (0.7%)
8	Z	0.49	0/1059	1.11	12/1429 (0.8%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.57	3/75388 (0.0%)	1.15	696/102200 (0.7%)

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
7	9	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	3	747	VAL	CA-CB	5.72	1.62	1.54
1	J	331	ILE	CA-CB	-5.13	1.50	1.54
1	1	21	VAL	CA-CB	5.10	1.61	1.54

The worst 5 of 696 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	211	ILE	N-CA-C	13.34	128.14	112.80
3	L	211	ILE	N-CA-C	12.89	127.63	112.80
4	D	323	ALA	N-CA-C	-12.75	97.57	112.87
3	3	211	ILE	N-CA-C	12.60	127.30	112.80
5	E	44	MET	N-CA-C	-12.57	97.52	112.86

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	9	69	TYR	Sidechain

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	1	3383	0	3349	296	0
1	A	3383	0	3349	296	0
1	J	3383	0	3349	306	0
1	S	3383	0	3349	297	0
2	2	1406	0	1373	151	0
2	B	1406	0	1373	141	0
2	K	1406	0	1373	153	0
2	T	1406	0	1373	142	0
3	3	5746	0	5767	641	0
3	C	5746	0	5767	627	0
3	L	5746	0	5767	624	1
3	U	5746	0	5767	642	1
4	4	2953	0	2944	462	0
4	D	2953	0	2944	454	0
4	M	2953	0	2944	460	0
4	V	2953	0	2944	449	0
5	5	1570	0	1539	260	0
5	E	1570	0	1539	263	0
5	N	1570	0	1539	264	0
5	W	1570	0	1539	259	0
6	6	1102	0	1108	159	0
6	F	1102	0	1108	158	0
6	O	1102	0	1108	147	0
6	X	1102	0	1108	154	0
7	9	1193	0	1160	120	0
7	G	1193	0	1160	105	0
7	P	1193	0	1160	107	0
7	Y	1193	0	1160	119	0
8	7	1031	0	1029	77	0
8	H	1031	0	1029	84	0
8	Q	1031	0	1029	92	0
8	Z	1031	0	1029	89	0
9	1	8	0	0	0	0
9	3	24	0	0	3	0
9	6	8	0	0	1	0
9	9	16	0	0	2	0
9	A	8	0	0	0	0
9	C	24	0	0	3	0
9	F	8	0	0	1	0
9	G	16	0	0	2	0
9	J	8	0	0	0	0
9	L	24	0	0	3	0
9	O	8	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	P	16	0	0	1	0
9	S	8	0	0	0	0
9	U	24	0	0	3	0
9	X	8	0	0	1	0
9	Y	16	0	0	2	0
10	2	4	0	0	2	0
10	3	4	0	0	1	0
10	B	4	0	0	2	0
10	C	4	0	0	1	0
10	K	4	0	0	2	0
10	L	4	0	0	1	0
10	T	4	0	0	1	0
10	U	4	0	0	0	0
11	7	31	0	19	5	0
11	H	31	0	19	5	0
11	Q	31	0	19	7	0
11	Z	31	0	19	6	0
All	All	73916	0	73152	8020	1

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 55.

The worst 5 of 8020 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)
2:K:139:GLU:HB2	2:K:140:PRO:HD2	1.25	1.19
4:M:249:ARG:HB3	4:M:249:ARG:HH11	1.08	1.18
1:S:10:ASP:HB3	1:S:11:PRO:HD2	1.19	1.17
1:J:11:PRO:HB3	1:J:270:THR:HB	1.20	1.17
1:S:11:PRO:HB3	1:S:270:THR:HB	1.26	1.17

All (1) 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)
3:L:1:MET:N	3:U:498:GLU:OE2[2_645]	2.01	0.19

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	1	430/438 (98%)	332 (77%)	68 (16%)	30 (7%)	1	7
1	A	430/438 (98%)	330 (77%)	70 (16%)	30 (7%)	1	7
1	J	430/438 (98%)	331 (77%)	70 (16%)	29 (7%)	1	7
1	S	430/438 (98%)	332 (77%)	65 (15%)	33 (8%)	1	5
2	2	176/181 (97%)	144 (82%)	24 (14%)	8 (4%)	2	13
2	B	176/181 (97%)	142 (81%)	26 (15%)	8 (4%)	2	13
2	K	176/181 (97%)	145 (82%)	23 (13%)	8 (4%)	2	13
2	T	176/181 (97%)	144 (82%)	24 (14%)	8 (4%)	2	13
3	3	727/783 (93%)	559 (77%)	117 (16%)	51 (7%)	1	7
3	C	727/783 (93%)	564 (78%)	116 (16%)	47 (6%)	1	8
3	L	727/783 (93%)	567 (78%)	109 (15%)	51 (7%)	1	7
3	U	727/783 (93%)	565 (78%)	110 (15%)	52 (7%)	1	6
4	4	366/409 (90%)	277 (76%)	64 (18%)	25 (7%)	1	7
4	D	366/409 (90%)	283 (77%)	57 (16%)	26 (7%)	1	6
4	M	366/409 (90%)	274 (75%)	63 (17%)	29 (8%)	1	5
4	V	366/409 (90%)	280 (76%)	63 (17%)	23 (6%)	1	8
5	5	187/207 (90%)	128 (68%)	34 (18%)	25 (13%)	0	1
5	E	187/207 (90%)	126 (67%)	35 (19%)	26 (14%)	0	1
5	N	187/207 (90%)	123 (66%)	38 (20%)	26 (14%)	0	1
5	W	187/207 (90%)	123 (66%)	39 (21%)	25 (13%)	0	1
6	6	140/181 (77%)	99 (71%)	31 (22%)	10 (7%)	1	6
6	F	140/181 (77%)	99 (71%)	33 (24%)	8 (6%)	1	9
6	O	140/181 (77%)	101 (72%)	31 (22%)	8 (6%)	1	9
6	X	140/181 (77%)	100 (71%)	33 (24%)	7 (5%)	1	11
7	9	152/182 (84%)	119 (78%)	24 (16%)	9 (6%)	1	9

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	G	152/182 (84%)	117 (77%)	25 (16%)	10 (7%)	1	7
7	P	152/182 (84%)	121 (80%)	22 (14%)	9 (6%)	1	9
7	Y	152/182 (84%)	116 (76%)	27 (18%)	9 (6%)	1	9
8	7	125/129 (97%)	110 (88%)	10 (8%)	5 (4%)	2	15
8	H	125/129 (97%)	110 (88%)	10 (8%)	5 (4%)	2	15
8	Q	125/129 (97%)	108 (86%)	11 (9%)	6 (5%)	2	12
8	Z	125/129 (97%)	107 (86%)	12 (10%)	6 (5%)	2	12
All	All	9212/10040 (92%)	7076 (77%)	1484 (16%)	652 (7%)	1	6

5 of 652 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1	14	GLU
1	1	28	THR
1	1	37	GLY
1	1	160	LYS
1	1	166	ASP

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	1	351/356 (99%)	321 (92%)	30 (8%)	10	33
1	A	351/356 (99%)	322 (92%)	29 (8%)	10	34
1	J	351/356 (99%)	320 (91%)	31 (9%)	9	32
1	S	351/356 (99%)	322 (92%)	29 (8%)	10	34
2	2	150/152 (99%)	128 (85%)	22 (15%)	3	14
2	B	150/152 (99%)	131 (87%)	19 (13%)	4	18
2	K	150/152 (99%)	129 (86%)	21 (14%)	3	15
2	T	150/152 (99%)	128 (85%)	22 (15%)	3	14
3	3	593/628 (94%)	517 (87%)	76 (13%)	4	18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	593/628 (94%)	518 (87%)	75 (13%)	4	18
3	L	593/628 (94%)	517 (87%)	76 (13%)	4	18
3	U	593/628 (94%)	521 (88%)	72 (12%)	5	20
4	4	319/355 (90%)	282 (88%)	37 (12%)	5	21
4	D	319/355 (90%)	284 (89%)	35 (11%)	6	23
4	M	319/355 (90%)	280 (88%)	39 (12%)	5	19
4	V	319/355 (90%)	284 (89%)	35 (11%)	6	23
5	5	164/175 (94%)	140 (85%)	24 (15%)	3	14
5	E	164/175 (94%)	140 (85%)	24 (15%)	3	14
5	N	164/175 (94%)	136 (83%)	28 (17%)	2	10
5	W	164/175 (94%)	139 (85%)	25 (15%)	3	13
6	6	117/149 (78%)	111 (95%)	6 (5%)	21	50
6	F	117/149 (78%)	111 (95%)	6 (5%)	21	50
6	O	117/149 (78%)	111 (95%)	6 (5%)	21	50
6	X	117/149 (78%)	111 (95%)	6 (5%)	21	50
7	9	126/150 (84%)	117 (93%)	9 (7%)	13	40
7	G	126/150 (84%)	116 (92%)	10 (8%)	11	36
7	P	126/150 (84%)	116 (92%)	10 (8%)	11	36
7	Y	126/150 (84%)	118 (94%)	8 (6%)	16	44
8	7	104/106 (98%)	94 (90%)	10 (10%)	8	29
8	H	104/106 (98%)	96 (92%)	8 (8%)	12	37
8	Q	104/106 (98%)	95 (91%)	9 (9%)	9	32
8	Z	104/106 (98%)	95 (91%)	9 (9%)	9	32
All	All	7696/8284 (93%)	6850 (89%)	846 (11%)	6	23

5 of 846 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	K	112	THR
4	M	249	ARG
5	W	3	LEU
3	L	46	ARG
2	K	87	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 163 such sidechains are listed below:

Mol	Chain	Res	Type
4	M	308	GLN
3	U	513	GLN
5	N	40	HIS
1	S	288	GLN
4	V	166	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

40 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	$\# Z > 2$
10	FES	T	182	2	0,4,4	-	-	-		
9	SF4	6	182	6	0,12,12	-	-	-		
11	FMN	7	500	-	33,33,33	1.45	5 (15%)	48,50,50	2.08	15 (31%)
9	SF4	P	184	7	0,12,12	-	-	-		
10	FES	C	787	3	0,4,4	-	-	-		
9	SF4	3	784	3	0,12,12	-	-	-		
10	FES	U	787	3	0,4,4	-	-	-		

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
10	FES	3	787	3	0,4,4	-	-	-		
9	SF4	J	439	1	0,12,12	-	-	-		
9	SF4	Y	184	7	0,12,12	-	-	-		
11	FMN	Q	500	-	33,33,33	1.31	4 (12%)	48,50,50	2.04	15 (31%)
9	SF4	U	786	3	0,12,12	-	-	-		
9	SF4	L	786	3	0,12,12	-	-	-		
9	SF4	Y	183	7	0,12,12	-	-	-		
9	SF4	A	439	1	0,12,12	-	-	-		
11	FMN	H	500	-	33,33,33	1.40	5 (15%)	48,50,50	2.08	15 (31%)
10	FES	L	787	3	0,4,4	-	-	-		
9	SF4	3	786	3	0,12,12	-	-	-		
9	SF4	9	184	7	0,12,12	-	-	-		
9	SF4	C	784	3	0,12,12	-	-	-		
9	SF4	C	786	3	0,12,12	-	-	-		
9	SF4	9	183	7	0,12,12	-	-	-		
9	SF4	F	182	6	0,12,12	-	-	-		
10	FES	K	182	2	0,4,4	-	-	-		
11	FMN	Z	500	-	33,33,33	1.30	3 (9%)	48,50,50	2.02	15 (31%)
9	SF4	S	439	1	0,12,12	-	-	-		
9	SF4	G	183	7	0,12,12	-	-	-		
9	SF4	L	785	3	0,12,12	-	-	-		
10	FES	B	182	2	0,4,4	-	-	-		
9	SF4	P	183	7	0,12,12	-	-	-		
9	SF4	C	785	3	0,12,12	-	-	-		
9	SF4	O	182	6	0,12,12	-	-	-		
9	SF4	X	182	6	0,12,12	-	-	-		
9	SF4	U	785	3	0,12,12	-	-	-		
9	SF4	L	784	3	0,12,12	-	-	-		
9	SF4	U	784	3	0,12,12	-	-	-		
9	SF4	1	439	1	0,12,12	-	-	-		
9	SF4	G	184	7	0,12,12	-	-	-		
10	FES	2	182	2	0,4,4	-	-	-		
9	SF4	3	785	3	0,12,12	-	-	-		

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
10	FES	T	182	2	-	-	0/1/1/1
11	FMN	7	500	-	-	1/18/18/18	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	SF4	6	182	6	-	-	0/6/5/5
9	SF4	P	184	7	-	-	0/6/5/5
10	FES	C	787	3	-	-	0/1/1/1
9	SF4	3	784	3	-	-	0/6/5/5
10	FES	U	787	3	-	-	0/1/1/1
10	FES	3	787	3	-	-	0/1/1/1
9	SF4	J	439	1	-	-	0/6/5/5
9	SF4	Y	184	7	-	-	0/6/5/5
11	FMN	Q	500	-	-	1/18/18/18	0/3/3/3
9	SF4	U	786	3	-	-	0/6/5/5
9	SF4	L	786	3	-	-	0/6/5/5
9	SF4	Y	183	7	-	-	0/6/5/5
9	SF4	A	439	1	-	-	0/6/5/5
11	FMN	H	500	-	-	0/18/18/18	0/3/3/3
10	FES	L	787	3	-	-	0/1/1/1
9	SF4	3	786	3	-	-	0/6/5/5
9	SF4	9	184	7	-	-	0/6/5/5
9	SF4	C	784	3	-	-	0/6/5/5
9	SF4	C	786	3	-	-	0/6/5/5
9	SF4	9	183	7	-	-	0/6/5/5
9	SF4	F	182	6	-	-	0/6/5/5
10	FES	K	182	2	-	-	0/1/1/1
11	FMN	Z	500	-	-	0/18/18/18	0/3/3/3
9	SF4	S	439	1	-	-	0/6/5/5
9	SF4	G	183	7	-	-	0/6/5/5
9	SF4	L	785	3	-	-	0/6/5/5
10	FES	B	182	2	-	-	0/1/1/1
9	SF4	P	183	7	-	-	0/6/5/5
9	SF4	C	785	3	-	-	0/6/5/5
9	SF4	O	182	6	-	-	0/6/5/5
9	SF4	X	182	6	-	-	0/6/5/5
9	SF4	U	785	3	-	-	0/6/5/5
9	SF4	L	784	3	-	-	0/6/5/5
9	SF4	U	784	3	-	-	0/6/5/5
9	SF4	1	439	1	-	-	0/6/5/5
9	SF4	G	184	7	-	-	0/6/5/5
10	FES	2	182	2	-	-	0/1/1/1
9	SF4	3	785	3	-	-	0/6/5/5

The worst 5 of 17 bond length outliers are listed below:

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	H	500	FMN	C9A-C5A	3.31	1.46	1.41
11	7	500	FMN	C6-C7	-2.95	1.35	1.39
11	7	500	FMN	C9A-C5A	2.92	1.45	1.41
11	Z	500	FMN	C9A-C5A	2.90	1.45	1.41
11	Q	500	FMN	C9A-C5A	2.81	1.45	1.41

The worst 5 of 60 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	Q	500	FMN	C5'-C4'-C3'	-6.15	100.61	112.22
11	H	500	FMN	C5'-C4'-C3'	-6.01	100.89	112.22
11	7	500	FMN	C5'-C4'-C3'	-5.89	101.11	112.22
11	Z	500	FMN	C5'-C4'-C3'	-5.71	101.45	112.22
11	7	500	FMN	C1'-N10-C9A	5.46	131.25	120.63

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
11	7	500	FMN	C2'-C1'-N10-C10
11	Q	500	FMN	C2'-C1'-N10-C10

There are no ring outliers.

30 monomers are involved in 56 short contacts:

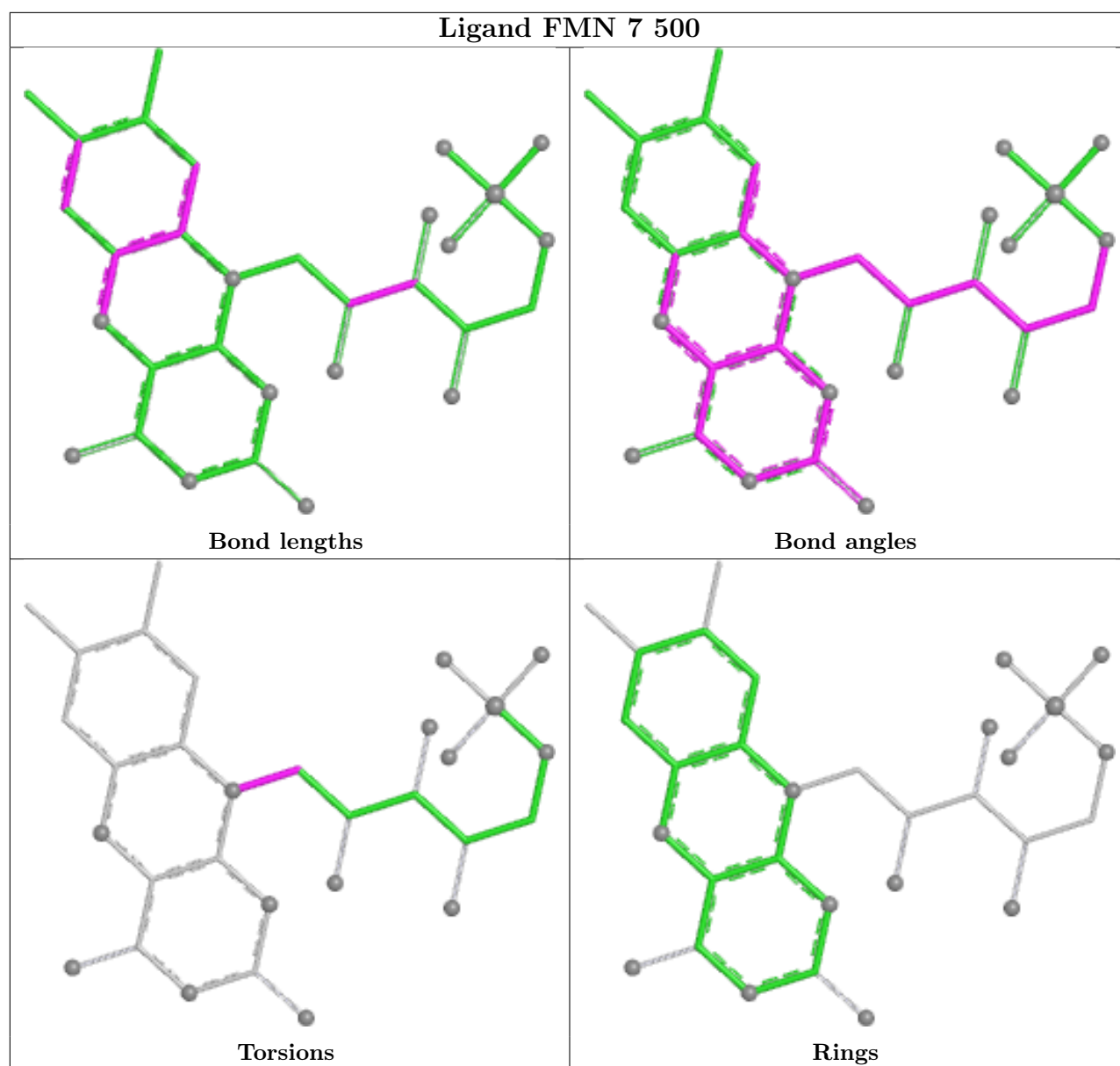
Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	T	182	FES	1	0
9	6	182	SF4	1	0
11	7	500	FMN	5	0
9	P	184	SF4	1	0
10	C	787	FES	1	0
9	3	784	SF4	1	0
10	3	787	FES	1	0
9	Y	184	SF4	1	0
11	Q	500	FMN	7	0
9	U	786	SF4	2	0
9	L	786	SF4	2	0
9	Y	183	SF4	1	0
11	H	500	FMN	5	0

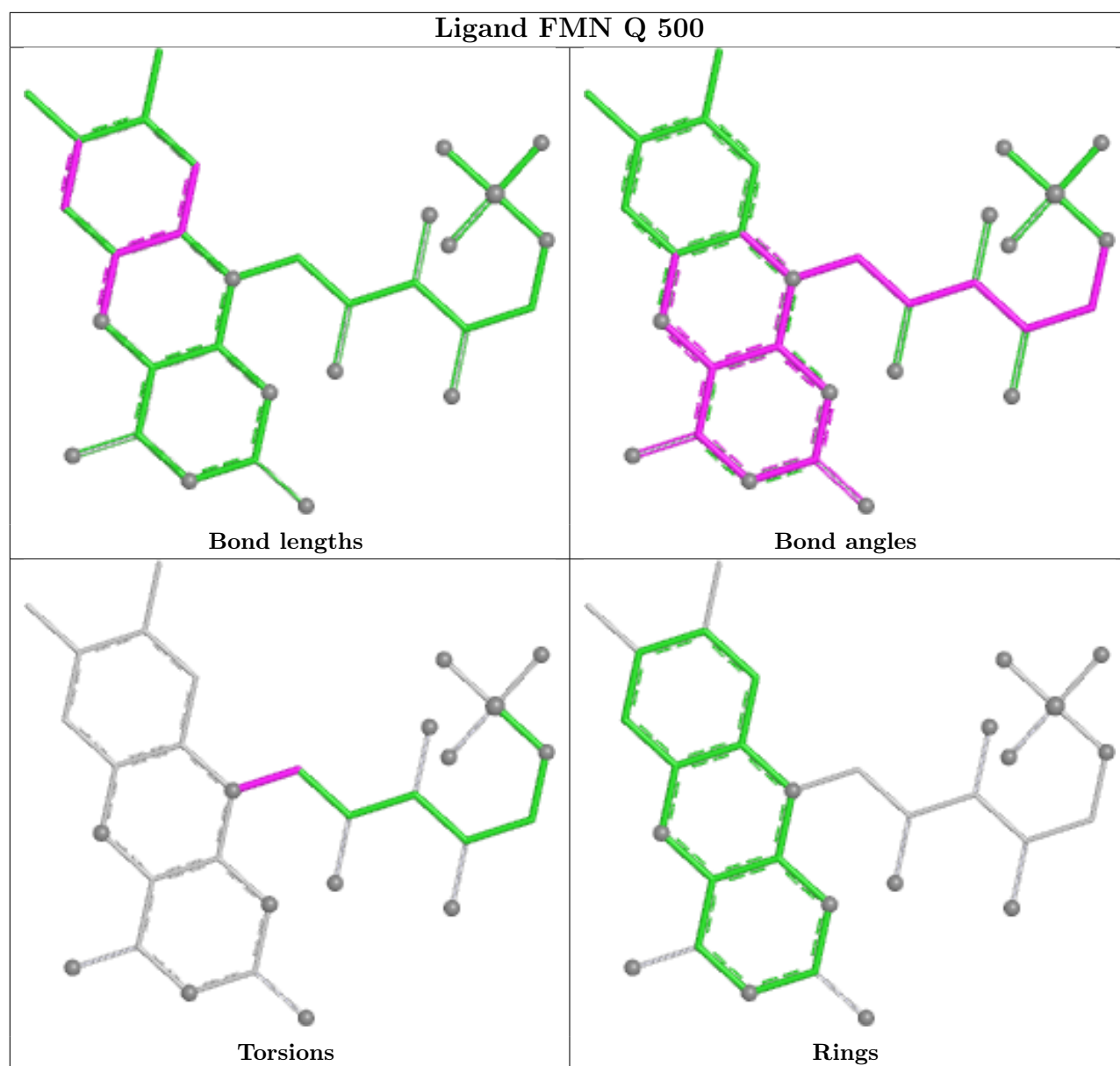
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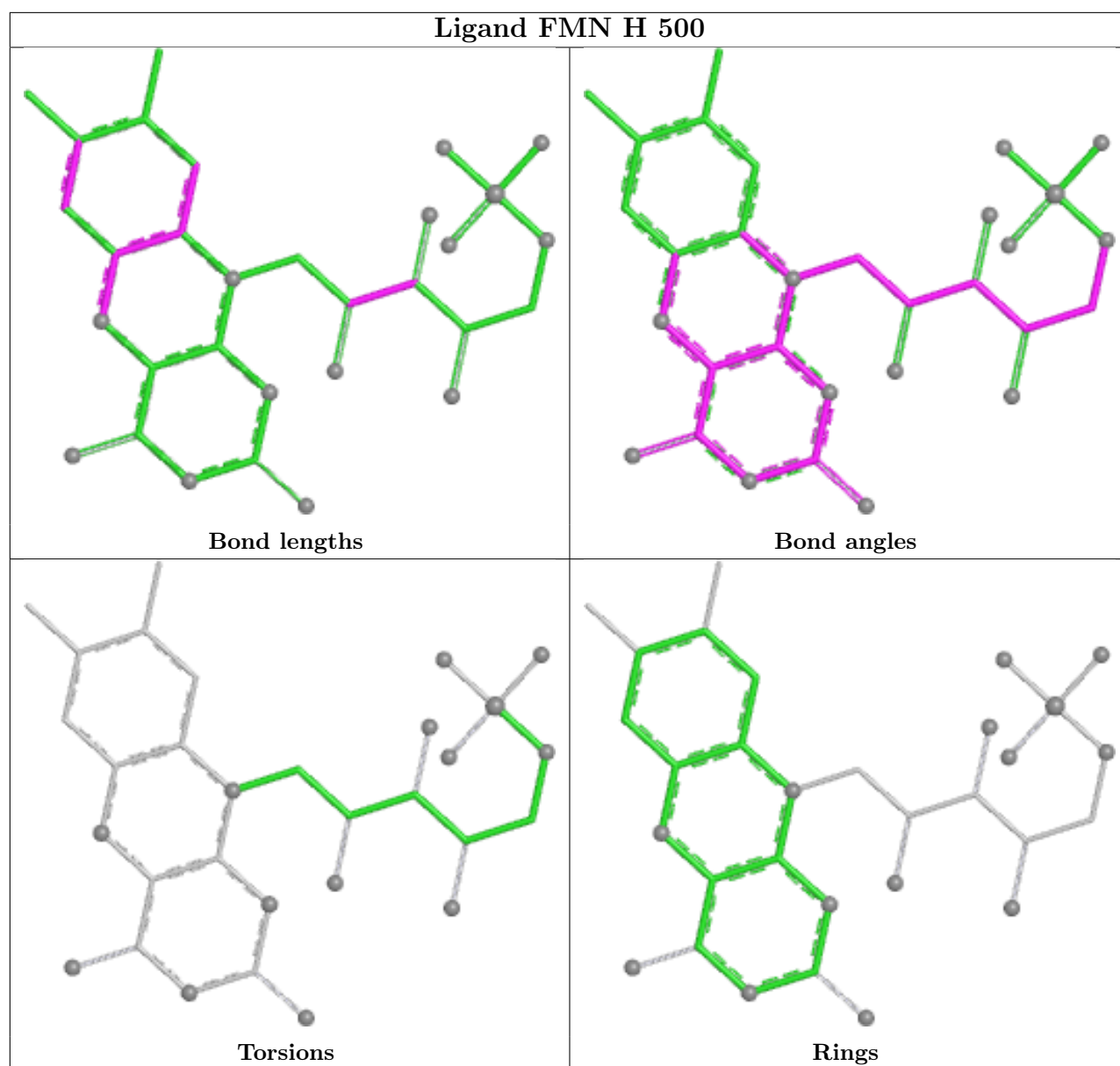
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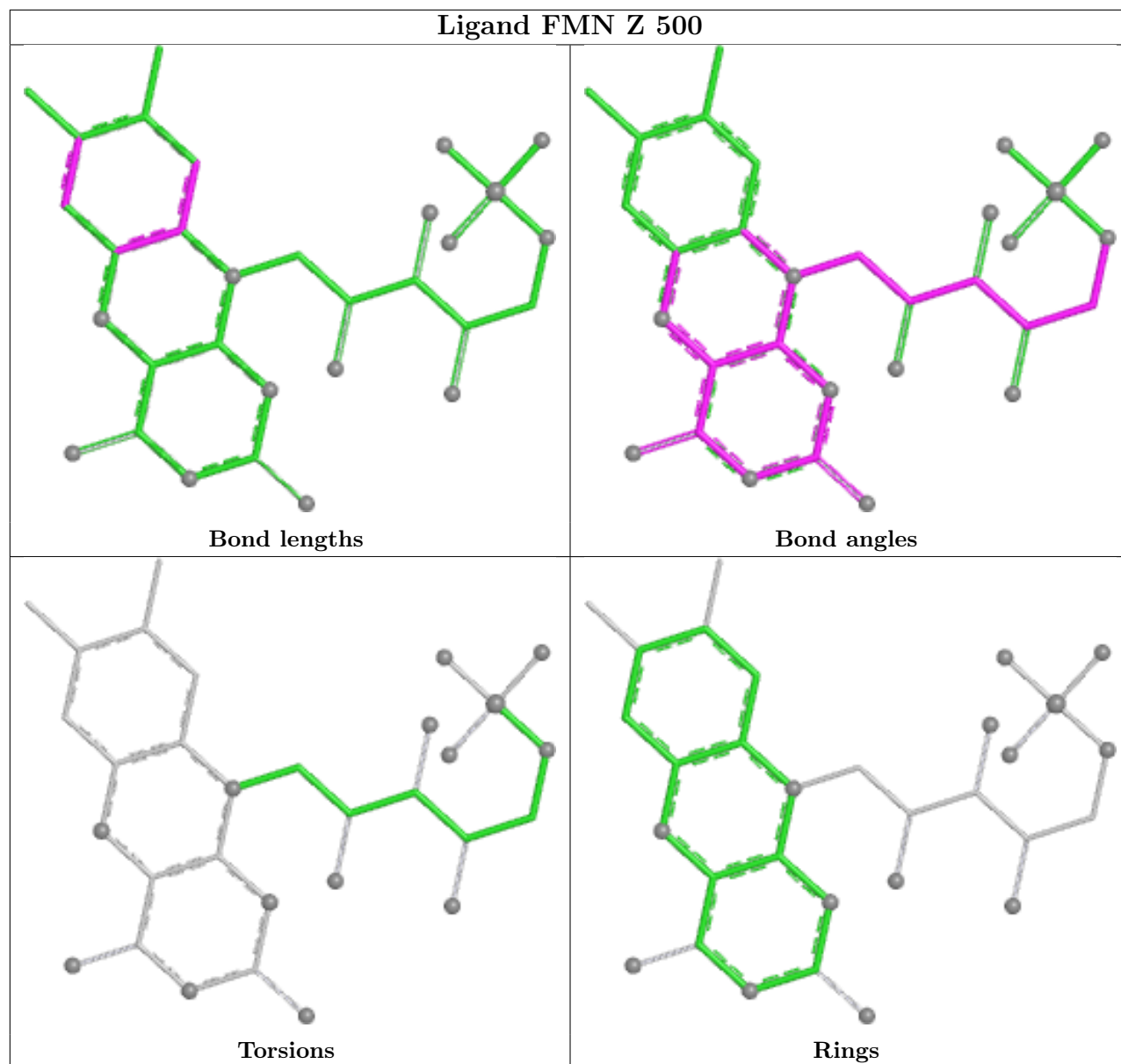
Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	L	787	FES	1	0
9	3	786	SF4	2	0
9	9	184	SF4	1	0
9	C	784	SF4	1	0
9	C	786	SF4	2	0
9	9	183	SF4	1	0
9	F	182	SF4	1	0
10	K	182	FES	2	0
11	Z	500	FMN	6	0
9	G	183	SF4	1	0
10	B	182	FES	2	0
9	O	182	SF4	1	0
9	X	182	SF4	1	0
9	L	784	SF4	1	0
9	U	784	SF4	1	0
9	G	184	SF4	1	0
10	2	182	FES	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 [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	1	432/438 (98%)	-1.11	0 100 100	14, 52, 90, 114	0
1	A	432/438 (98%)	-1.02	0 100 100	25, 57, 90, 115	0
1	J	432/438 (98%)	-1.07	2 (0%) 87 76	17, 52, 91, 113	0
1	S	432/438 (98%)	-1.03	0 100 100	23, 58, 93, 115	0
2	2	178/181 (98%)	-1.05	0 100 100	26, 59, 98, 140	0
2	B	178/181 (98%)	-1.02	0 100 100	29, 64, 100, 141	0
2	K	178/181 (98%)	-0.99	0 100 100	29, 60, 97, 143	0
2	T	178/181 (98%)	-1.02	0 100 100	32, 66, 100, 146	0
3	3	737/783 (94%)	-0.94	1 (0%) 92 90	20, 64, 110, 130	0
3	C	737/783 (94%)	-0.87	0 100 100	23, 67, 111, 137	0
3	L	737/783 (94%)	-0.85	1 (0%) 92 90	22, 69, 114, 137	0
3	U	737/783 (94%)	-0.88	0 100 100	23, 68, 112, 135	0
4	4	370/409 (90%)	-0.89	0 100 100	26, 67, 109, 167	0
4	D	370/409 (90%)	-0.86	0 100 100	26, 65, 109, 165	0
4	M	370/409 (90%)	-0.83	1 (0%) 90 82	24, 65, 109, 158	0
4	V	370/409 (90%)	-0.67	1 (0%) 90 82	32, 75, 113, 169	0
5	5	191/207 (92%)	-0.78	0 100 100	35, 76, 112, 144	0
5	E	191/207 (92%)	-0.75	0 100 100	36, 76, 117, 138	0
5	N	191/207 (92%)	-0.65	0 100 100	36, 75, 114, 141	0
5	W	191/207 (92%)	-0.65	1 (0%) 87 76	43, 83, 119, 143	0
6	6	144/181 (79%)	-0.95	0 100 100	34, 64, 110, 118	0
6	F	144/181 (79%)	-0.84	1 (0%) 84 70	31, 62, 110, 119	0
6	O	144/181 (79%)	-0.86	0 100 100	31, 62, 111, 116	0
6	X	144/181 (79%)	-0.66	0 100 100	45, 71, 113, 122	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
7	9	154/182 (84%)	-1.03	0 100 100	20, 56, 98, 118	0
7	G	154/182 (84%)	-0.98	0 100 100	26, 53, 95, 115	0
7	P	154/182 (84%)	-0.99	0 100 100	26, 56, 96, 117	0
7	Y	154/182 (84%)	-0.91	0 100 100	31, 63, 100, 122	0
8	7	127/129 (98%)	-1.09	0 100 100	33, 62, 101, 116	0
8	H	127/129 (98%)	-1.01	0 100 100	35, 62, 102, 119	0
8	Q	127/129 (98%)	-1.00	0 100 100	32, 63, 104, 116	0
8	Z	127/129 (98%)	-0.97	0 100 100	34, 68, 105, 119	0
All	All	9332/10040 (92%)	-0.91	8 (0%) 92 90	14, 64, 109, 169	0

The worst 5 of 8 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	L	670	PRO	3.4
4	V	251	ALA	2.9
5	W	50	ALA	2.6
1	J	14	GLU	2.2
4	M	144	THR	2.1

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 oligosaccharides 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(Å ²)	Q<0.9
11	FMN	H	500	31/31	0.98	0.10	80,87,88,90	0
11	FMN	7	500	31/31	0.99	0.09	75,80,83,87	0

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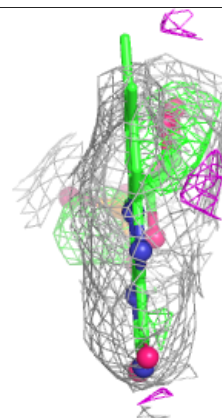
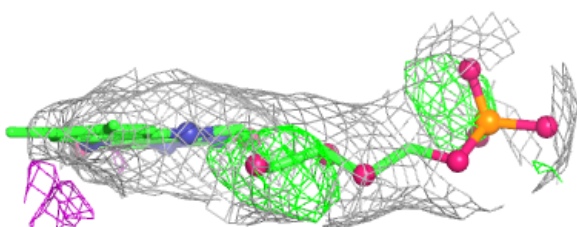
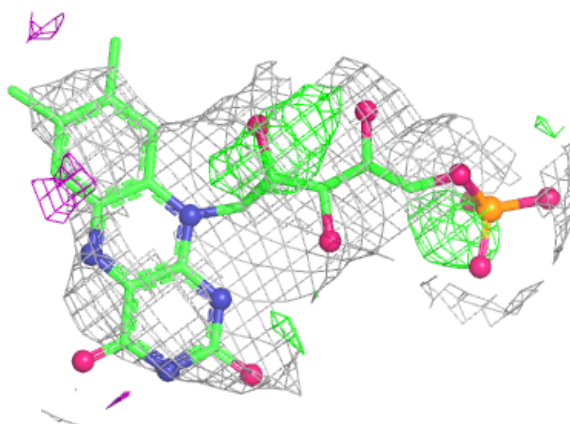
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
9	SF4	X	182	8/8	0.99	0.03	21,42,47,61	0
11	FMN	Q	500	31/31	0.99	0.10	79,86,88,91	0
11	FMN	Z	500	31/31	0.99	0.11	99,103,105,106	0
9	SF4	9	183	8/8	1.00	0.02	1,17,18,29	0
9	SF4	9	184	8/8	1.00	0.02	1,15,24,25	0
9	SF4	A	439	8/8	1.00	0.02	1,17,22,24	0
9	SF4	C	784	8/8	1.00	0.02	1,10,19,20	0
9	SF4	C	785	8/8	1.00	0.02	1,16,17,18	0
9	SF4	C	786	8/8	1.00	0.03	12,31,36,38	0
9	SF4	F	182	8/8	1.00	0.01	1,16,16,17	0
9	SF4	G	183	8/8	1.00	0.01	1,23,24,25	0
9	SF4	G	184	8/8	1.00	0.02	1,16,19,21	0
9	SF4	J	439	8/8	1.00	0.01	1,8,14,18	0
9	SF4	L	784	8/8	1.00	0.02	1,8,15,17	0
9	SF4	L	785	8/8	1.00	0.02	1,13,15,16	0
9	SF4	L	786	8/8	1.00	0.02	17,28,31,35	0
9	SF4	O	182	8/8	1.00	0.02	4,14,18,18	0
9	SF4	P	183	8/8	1.00	0.02	1,25,26,32	0
9	SF4	P	184	8/8	1.00	0.02	3,18,20,20	0
9	SF4	S	439	8/8	1.00	0.02	14,30,33,34	0
9	SF4	U	784	8/8	1.00	0.02	1,17,19,19	0
9	SF4	U	785	8/8	1.00	0.02	9,18,20,21	0
9	SF4	U	786	8/8	1.00	0.01	19,40,45,45	0
9	SF4	1	439	8/8	1.00	0.01	1,9,17,17	0
9	SF4	Y	183	8/8	1.00	0.02	20,27,29,44	0
9	SF4	Y	184	8/8	1.00	0.02	7,20,22,22	0
10	FES	2	182	4/4	1.00	0.04	1,4,19,19	0
10	FES	3	787	4/4	1.00	0.03	1,1,12,15	0
10	FES	B	182	4/4	1.00	0.04	2,13,32,33	0
10	FES	C	787	4/4	1.00	0.04	1,4,16,18	0
10	FES	K	182	4/4	1.00	0.04	2,5,21,23	0
10	FES	L	787	4/4	1.00	0.03	1,1,9,14	0
10	FES	T	182	4/4	1.00	0.05	2,9,29,30	0
10	FES	U	787	4/4	1.00	0.04	4,5,15,17	0
9	SF4	3	784	8/8	1.00	0.01	1,12,15,16	0
9	SF4	3	785	8/8	1.00	0.02	1,17,21,21	0
9	SF4	3	786	8/8	1.00	0.01	5,31,32,34	0
9	SF4	6	182	8/8	1.00	0.02	12,32,33,34	0

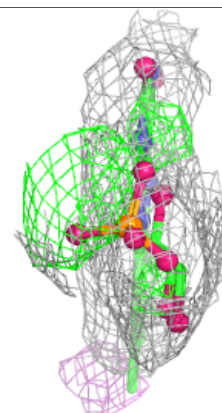
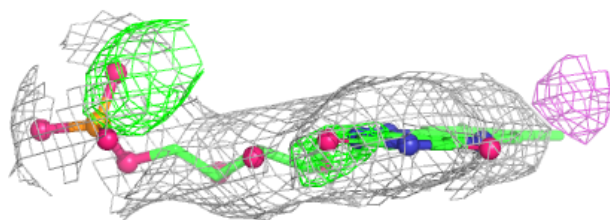
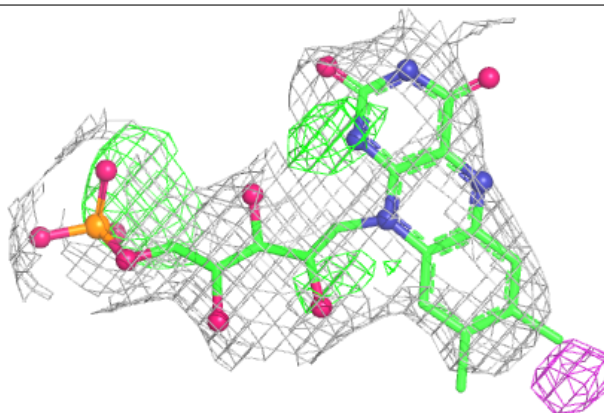
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around FMN H 500:

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

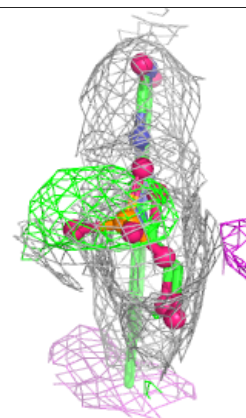
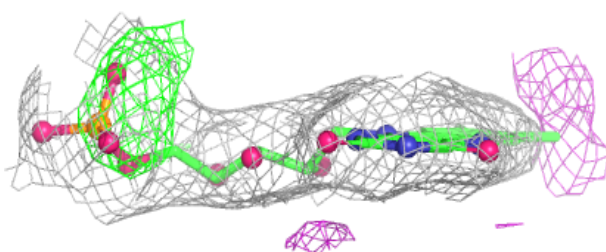
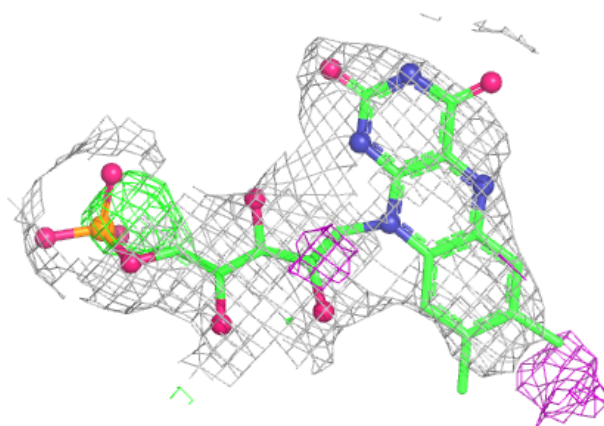
**Electron density around FMN 7 500:**

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



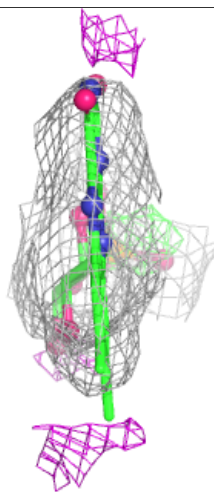
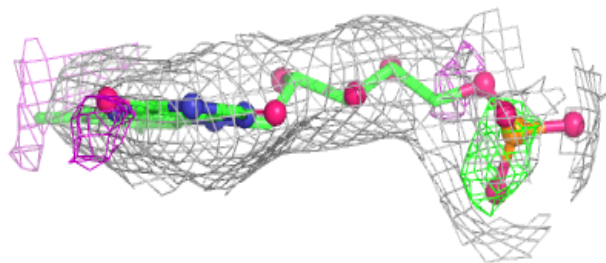
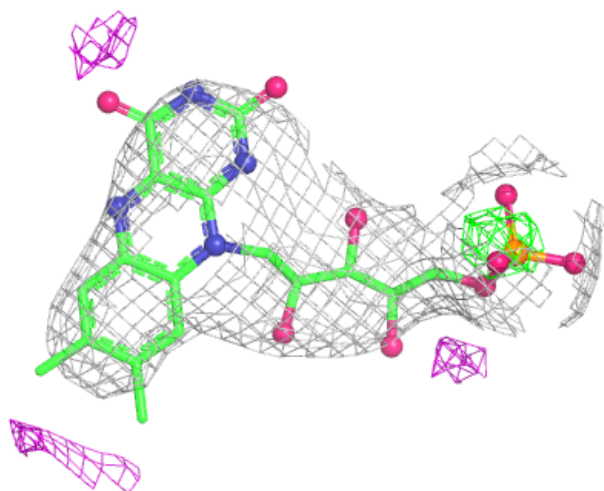
Electron density around FMN Q 500:

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



Electron density around FMN Z 500:

$2mF_o-DF_c$ (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.