



wwPDB X-ray Structure Validation Summary Report ⓘ

May 26, 2020 – 08:42 pm BST

PDB ID : 4YTX
Title : Crystal structure of Ups1-Mdm35 complex with PA
Authors : Watanabe, Y.; Tamura, Y.; Kawano, S.; Endo, T.
Deposited on : 2015-03-18
Resolution : 3.20 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

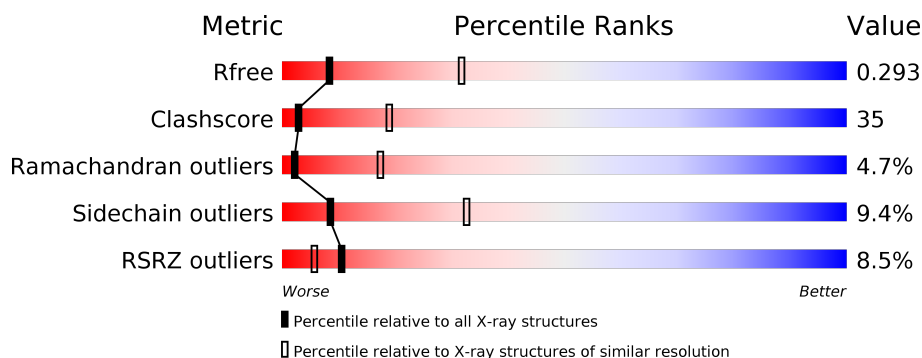
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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	81	<div> <div>43%</div> <div>41%</div> <div>10%</div> </div>
1	C	81	<div> <div>46%</div> <div>43%</div> <div>10%</div> </div>
1	E	81	<div> <div>44%</div> <div>38%</div> <div>7%</div> <div>10%</div> </div>
1	G	81	<div> <div>46%</div> <div>32%</div> <div>9%</div> <div>10%</div> </div>
1	I	81	<div> <div>30%</div> <div>48%</div> <div>11%</div> <div>10%</div> </div>
1	K	81	<div> <div>35%</div> <div>54%</div> <div>10%</div> </div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	M	81	
1	O	81	
2	B	184	
2	D	184	
2	F	184	
2	H	184	
2	J	184	
2	L	184	
2	N	184	
2	P	184	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 15084 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 Mitochondrial distribution and morphology protein 35.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	73	Total	C	N	O	S	0	0	0
			584	372	91	116	5			
1	C	73	Total	C	N	O	S	0	0	0
			580	370	91	114	5			
1	E	73	Total	C	N	O	S	0	0	0
			584	372	91	116	5			
1	G	73	Total	C	N	O	S	0	0	0
			584	372	91	116	5			
1	I	73	Total	C	N	O	S	0	0	0
			584	372	91	116	5			
1	K	73	Total	C	N	O	S	0	0	0
			584	372	91	116	5			
1	M	73	Total	C	N	O	S	0	0	0
			584	372	91	116	5			
1	O	68	Total	C	N	O	S	0	0	0
			551	352	86	109	4			

- Molecule 2 is a protein called Protein UPS1, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	160	Total	C	N	O	S	0	0	0
			1278	811	222	241	4			
2	D	170	Total	C	N	O	S	0	0	0
			1344	849	233	256	6			
2	F	167	Total	C	N	O	S	0	0	0
			1325	838	230	253	4			
2	H	162	Total	C	N	O	S	0	0	0
			1249	794	214	236	5			
2	J	169	Total	C	N	O	S	0	0	0
			1332	844	229	254	5			
2	L	169	Total	C	N	O	S	0	0	0
			1330	842	229	254	5			

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	N	157	Total	C	N	O	S	0	0	0
			1257	792	218	242	5			
2	P	159	Total	C	N	O	S	0	0	0
			1262	796	218	243	5			

There are 112 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-13	MET	-	expression tag	UNP Q05776
B	-12	GLY	-	expression tag	UNP Q05776
B	-11	SER	-	expression tag	UNP Q05776
B	-10	SER	-	expression tag	UNP Q05776
B	-9	HIS	-	expression tag	UNP Q05776
B	-8	HIS	-	expression tag	UNP Q05776
B	-7	HIS	-	expression tag	UNP Q05776
B	-6	HIS	-	expression tag	UNP Q05776
B	-5	HIS	-	expression tag	UNP Q05776
B	-4	HIS	-	expression tag	UNP Q05776
B	-3	SER	-	expression tag	UNP Q05776
B	-2	GLN	-	expression tag	UNP Q05776
B	-1	ASP	-	expression tag	UNP Q05776
B	0	PRO	-	expression tag	UNP Q05776
D	-13	MET	-	expression tag	UNP Q05776
D	-12	GLY	-	expression tag	UNP Q05776
D	-11	SER	-	expression tag	UNP Q05776
D	-10	SER	-	expression tag	UNP Q05776
D	-9	HIS	-	expression tag	UNP Q05776
D	-8	HIS	-	expression tag	UNP Q05776
D	-7	HIS	-	expression tag	UNP Q05776
D	-6	HIS	-	expression tag	UNP Q05776
D	-5	HIS	-	expression tag	UNP Q05776
D	-4	HIS	-	expression tag	UNP Q05776
D	-3	SER	-	expression tag	UNP Q05776
D	-2	GLN	-	expression tag	UNP Q05776
D	-1	ASP	-	expression tag	UNP Q05776
D	0	PRO	-	expression tag	UNP Q05776
F	-13	MET	-	expression tag	UNP Q05776
F	-12	GLY	-	expression tag	UNP Q05776
F	-11	SER	-	expression tag	UNP Q05776
F	-10	SER	-	expression tag	UNP Q05776
F	-9	HIS	-	expression tag	UNP Q05776
F	-8	HIS	-	expression tag	UNP Q05776

Continued on next page...

Continued from previous page...

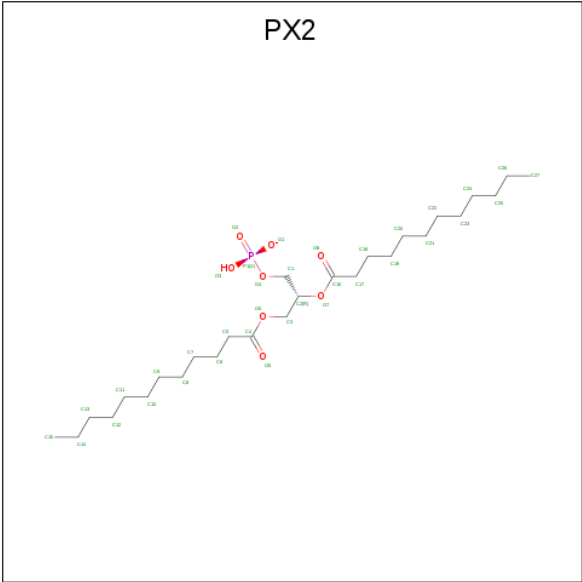
Chain	Residue	Modelled	Actual	Comment	Reference
F	-7	HIS	-	expression tag	UNP Q05776
F	-6	HIS	-	expression tag	UNP Q05776
F	-5	HIS	-	expression tag	UNP Q05776
F	-4	HIS	-	expression tag	UNP Q05776
F	-3	SER	-	expression tag	UNP Q05776
F	-2	GLN	-	expression tag	UNP Q05776
F	-1	ASP	-	expression tag	UNP Q05776
F	0	PRO	-	expression tag	UNP Q05776
H	-13	MET	-	expression tag	UNP Q05776
H	-12	GLY	-	expression tag	UNP Q05776
H	-11	SER	-	expression tag	UNP Q05776
H	-10	SER	-	expression tag	UNP Q05776
H	-9	HIS	-	expression tag	UNP Q05776
H	-8	HIS	-	expression tag	UNP Q05776
H	-7	HIS	-	expression tag	UNP Q05776
H	-6	HIS	-	expression tag	UNP Q05776
H	-5	HIS	-	expression tag	UNP Q05776
H	-4	HIS	-	expression tag	UNP Q05776
H	-3	SER	-	expression tag	UNP Q05776
H	-2	GLN	-	expression tag	UNP Q05776
H	-1	ASP	-	expression tag	UNP Q05776
H	0	PRO	-	expression tag	UNP Q05776
J	-13	MET	-	expression tag	UNP Q05776
J	-12	GLY	-	expression tag	UNP Q05776
J	-11	SER	-	expression tag	UNP Q05776
J	-10	SER	-	expression tag	UNP Q05776
J	-9	HIS	-	expression tag	UNP Q05776
J	-8	HIS	-	expression tag	UNP Q05776
J	-7	HIS	-	expression tag	UNP Q05776
J	-6	HIS	-	expression tag	UNP Q05776
J	-5	HIS	-	expression tag	UNP Q05776
J	-4	HIS	-	expression tag	UNP Q05776
J	-3	SER	-	expression tag	UNP Q05776
J	-2	GLN	-	expression tag	UNP Q05776
J	-1	ASP	-	expression tag	UNP Q05776
J	0	PRO	-	expression tag	UNP Q05776
L	-13	MET	-	expression tag	UNP Q05776
L	-12	GLY	-	expression tag	UNP Q05776
L	-11	SER	-	expression tag	UNP Q05776
L	-10	SER	-	expression tag	UNP Q05776
L	-9	HIS	-	expression tag	UNP Q05776
L	-8	HIS	-	expression tag	UNP Q05776

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
L	-7	HIS	-	expression tag	UNP Q05776
L	-6	HIS	-	expression tag	UNP Q05776
L	-5	HIS	-	expression tag	UNP Q05776
L	-4	HIS	-	expression tag	UNP Q05776
L	-3	SER	-	expression tag	UNP Q05776
L	-2	GLN	-	expression tag	UNP Q05776
L	-1	ASP	-	expression tag	UNP Q05776
L	0	PRO	-	expression tag	UNP Q05776
N	-13	MET	-	expression tag	UNP Q05776
N	-12	GLY	-	expression tag	UNP Q05776
N	-11	SER	-	expression tag	UNP Q05776
N	-10	SER	-	expression tag	UNP Q05776
N	-9	HIS	-	expression tag	UNP Q05776
N	-8	HIS	-	expression tag	UNP Q05776
N	-7	HIS	-	expression tag	UNP Q05776
N	-6	HIS	-	expression tag	UNP Q05776
N	-5	HIS	-	expression tag	UNP Q05776
N	-4	HIS	-	expression tag	UNP Q05776
N	-3	SER	-	expression tag	UNP Q05776
N	-2	GLN	-	expression tag	UNP Q05776
N	-1	ASP	-	expression tag	UNP Q05776
N	0	PRO	-	expression tag	UNP Q05776
P	-13	MET	-	expression tag	UNP Q05776
P	-12	GLY	-	expression tag	UNP Q05776
P	-11	SER	-	expression tag	UNP Q05776
P	-10	SER	-	expression tag	UNP Q05776
P	-9	HIS	-	expression tag	UNP Q05776
P	-8	HIS	-	expression tag	UNP Q05776
P	-7	HIS	-	expression tag	UNP Q05776
P	-6	HIS	-	expression tag	UNP Q05776
P	-5	HIS	-	expression tag	UNP Q05776
P	-4	HIS	-	expression tag	UNP Q05776
P	-3	SER	-	expression tag	UNP Q05776
P	-2	GLN	-	expression tag	UNP Q05776
P	-1	ASP	-	expression tag	UNP Q05776
P	0	PRO	-	expression tag	UNP Q05776

- Molecule 3 is 1,2-DILAUIROYL-SN-GLYCERO-3-PHOSPHATE (three-letter code: PX2) (formula: C₂₇H₅₂O₈P).



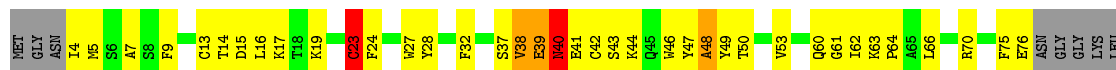
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	O	P	0	0
			36	27	8	1		
3	F	1	Total	C	O	P	0	0
			36	27	8	1		

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: Mitochondrial distribution and morphology protein 35

Chain A: 

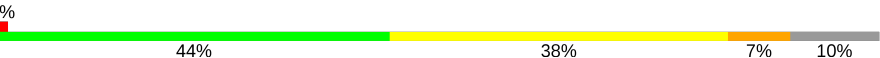


• Molecule 1: Mitochondrial distribution and morphology protein 35

Chain C: 



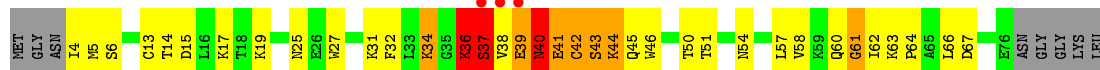
• Molecule 1: Mitochondrial distribution and morphology protein 35

Chain E: 



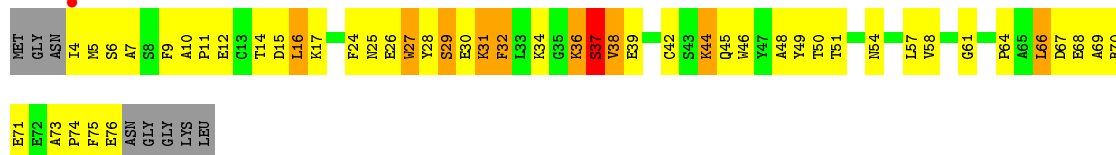
• Molecule 1: Mitochondrial distribution and morphology protein 35

Chain G: 

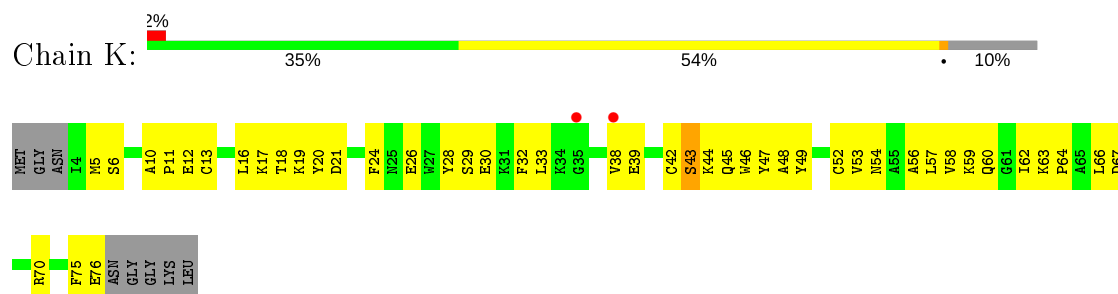


• Molecule 1: Mitochondrial distribution and morphology protein 35

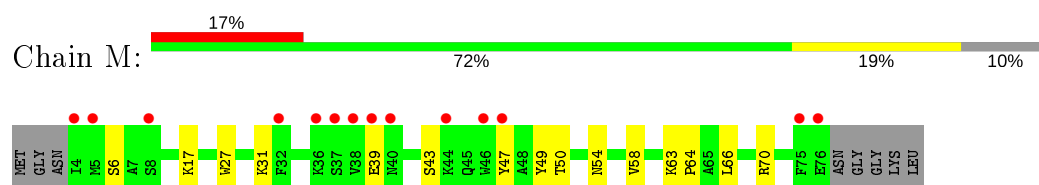
Chain I: 



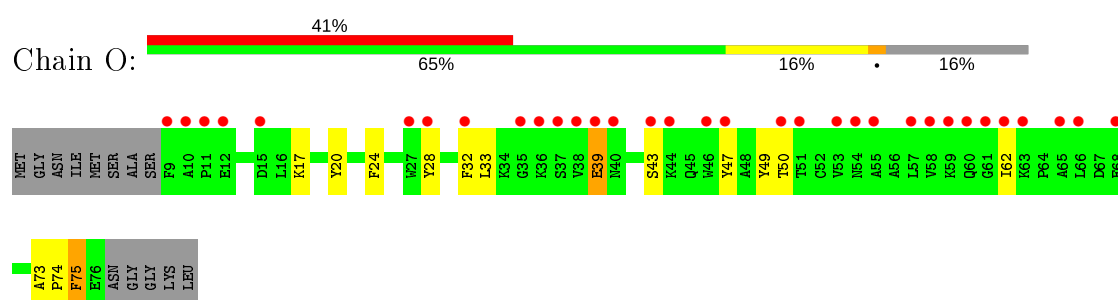
- Molecule 1: Mitochondrial distribution and morphology protein 35



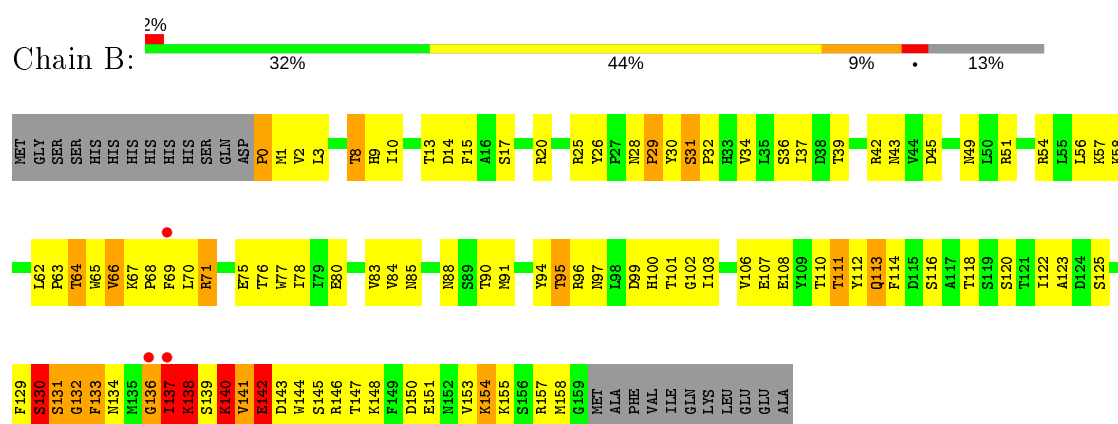
- Molecule 1: Mitochondrial distribution and morphology protein 35



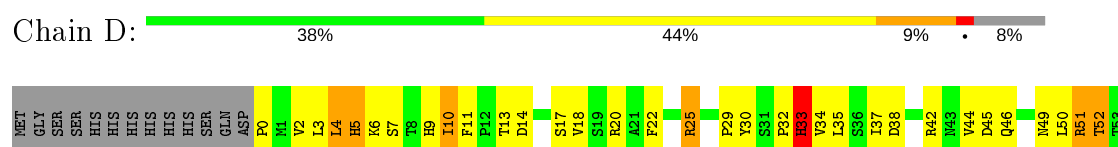
- Molecule 1: Mitochondrial distribution and morphology protein 35

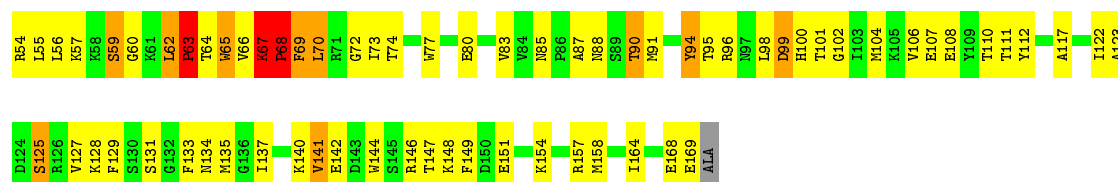


- Molecule 2: Protein UPS1, mitochondrial

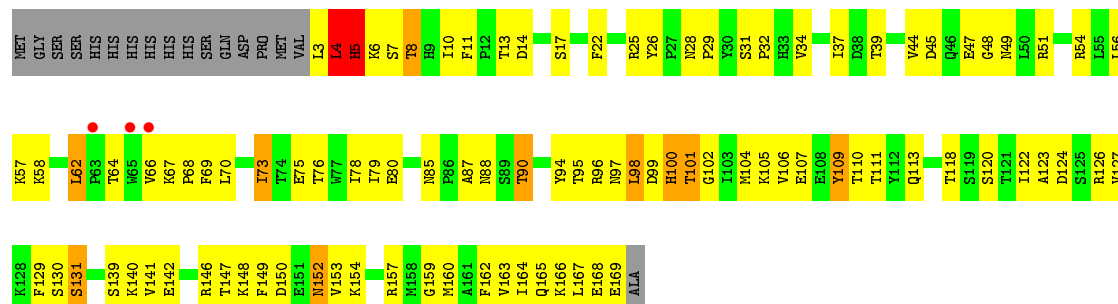


- Molecule 2: Protein UPS1, mitochondrial

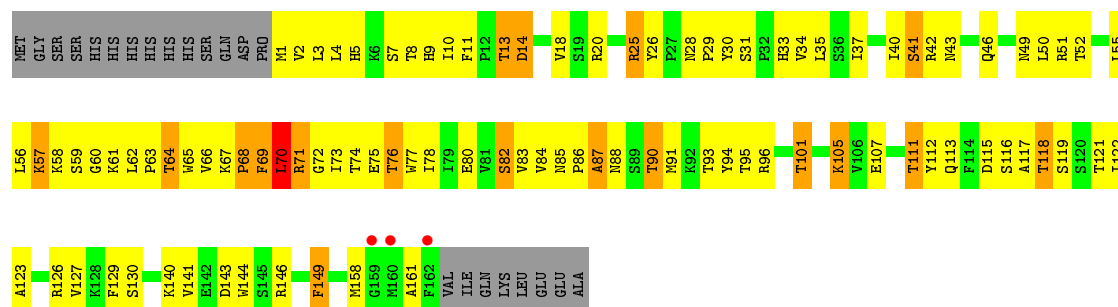




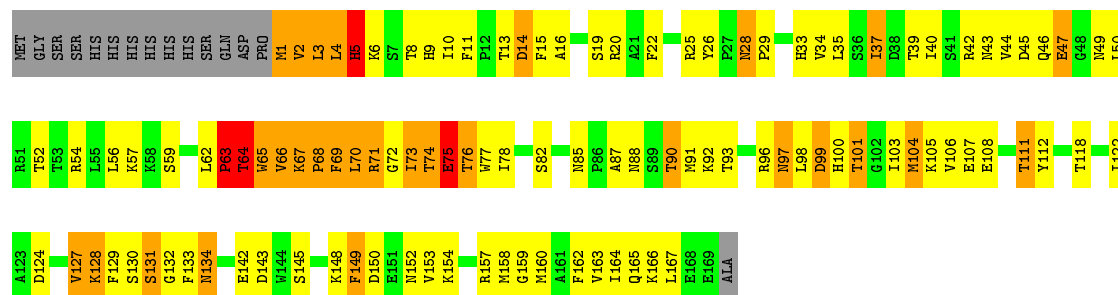
• Molecule 2: Protein UPS1, mitochondrial



• Molecule 2: Protein UPS1, mitochondrial

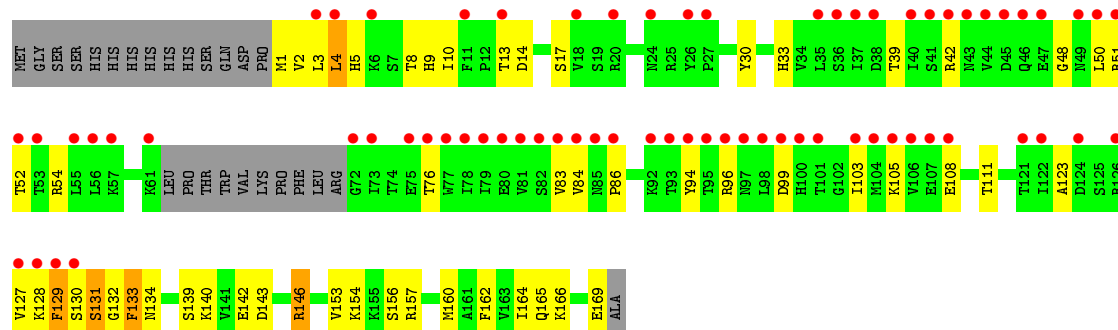


• Molecule 2: Protein UPS1, mitochondrial



• Molecule 2: Protein UPS1, mitochondrial





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	208.64Å 154.67Å 99.01Å 90.00° 104.42° 90.00°	Depositor
Resolution (Å)	43.23 – 3.20 43.23 – 3.19	Depositor EDS
% Data completeness (in resolution range)	94.7 (43.23-3.20) 94.2 (43.23-3.19)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.29 (at 3.19Å)	Xtriage
Refinement program	CNS 1.3	Depositor
R, R_{free}	0.251 , 0.300 0.245 , 0.293	Depositor DCC
R_{free} test set	4772 reflections (9.44%)	wwPDB-VP
Wilson B-factor (Å ²)	68.9	Xtriage
Anisotropy	0.391	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 63.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	15084	wwPDB-VP
Average B, all atoms (Å ²)	94.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.43% 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: PX2

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	0.48	0/598	0.76	1/807 (0.1%)
1	C	0.53	0/594	0.70	0/802
1	E	0.44	0/598	0.63	0/807
1	G	1.26	12/598 (2.0%)	1.03	6/807 (0.7%)
1	I	0.41	0/598	0.79	1/807 (0.1%)
1	K	0.34	0/598	0.56	0/807
1	M	0.39	0/598	0.57	0/807
1	O	0.32	0/565	0.54	0/763
2	B	1.07	15/1308 (1.1%)	0.95	10/1771 (0.6%)
2	D	0.59	0/1373	0.92	4/1858 (0.2%)
2	F	0.51	0/1355	0.77	1/1835 (0.1%)
2	H	0.47	0/1280	0.75	1/1742 (0.1%)
2	J	1.43	23/1362 (1.7%)	1.03	12/1847 (0.6%)
2	L	0.48	0/1359	0.83	2/1841 (0.1%)
2	N	0.45	0/1282	0.71	1/1729 (0.1%)
2	P	0.37	0/1287	0.60	0/1738
All	All	0.71	50/15353 (0.3%)	0.80	39/20768 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	G	0	3
2	B	0	5
2	F	0	1
2	J	0	4
All	All	0	13

The worst 5 of 50 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	J	77	TRP	CD2-CE2	-16.55	1.21	1.41
2	J	76	THR	C-O	-15.58	0.93	1.23
2	J	77	TRP	CZ3-CH2	-14.52	1.16	1.40
2	J	77	TRP	CE3-CZ3	-12.36	1.17	1.38
2	B	130	SER	CA-CB	-11.95	1.35	1.52

The worst 5 of 39 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	J	73	ILE	N-CA-C	-11.13	80.94	111.00
2	L	72	GLY	N-CA-C	-10.43	87.03	113.10
2	D	67	LYS	N-CA-C	-9.79	84.58	111.00
2	B	130	SER	CA-CB-OG	-9.02	86.83	111.20
2	B	140	LYS	CD-CE-NZ	8.46	131.15	111.70

There are no chirality outliers.

5 of 13 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	133	PHE	Peptide
2	B	136	GLY	Peptide
2	B	138	LYS	Mainchain
2	B	140	LYS	Mainchain
2	B	142	GLU	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	584	0	551	27	0
1	C	580	0	547	21	0
1	E	584	0	551	34	0
1	G	584	0	551	36	0
1	I	584	0	551	60	0
1	K	584	0	551	55	0
1	M	584	0	551	9	0
1	O	551	0	516	14	0
2	B	1278	0	1265	131	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	1344	0	1313	116	0
2	F	1325	0	1296	123	0
2	H	1249	0	1178	107	0
2	J	1332	0	1300	145	0
2	L	1330	0	1298	132	0
2	N	1257	0	1241	71	0
2	P	1262	0	1240	68	0
3	B	36	0	52	8	0
3	F	36	0	52	7	0
All	All	15084	0	14604	1032	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 35.

The worst 5 of 1032 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:H:158:MET:SD	2:N:122:ILE:HD11	1.82	1.19
2:B:102:GLY:O	2:B:132:GLY:HA3	1.44	1.18
2:J:163:VAL:HG21	2:L:25:ARG:HA	1.37	1.06
2:D:9:HIS:HD2	2:J:8:THR:HG23	1.20	1.06
1:G:40:ASN:OD1	1:G:42:CYS:N	1.91	1.03

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	71/81 (88%)	54 (76%)	10 (14%)	7 (10%)	0 3
1	C	71/81 (88%)	54 (76%)	15 (21%)	2 (3%)	5 29

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	71/81 (88%)	52 (73%)	16 (22%)	3 (4%)	3	20
1	G	71/81 (88%)	54 (76%)	15 (21%)	2 (3%)	5	29
1	I	71/81 (88%)	52 (73%)	8 (11%)	11 (16%)	0	1
1	K	71/81 (88%)	50 (70%)	17 (24%)	4 (6%)	2	14
1	M	71/81 (88%)	69 (97%)	2 (3%)	0	100	100
1	O	66/81 (82%)	63 (96%)	3 (4%)	0	100	100
2	B	158/184 (86%)	133 (84%)	19 (12%)	6 (4%)	3	22
2	D	168/184 (91%)	137 (82%)	20 (12%)	11 (6%)	1	10
2	F	165/184 (90%)	129 (78%)	28 (17%)	8 (5%)	2	17
2	H	160/184 (87%)	130 (81%)	25 (16%)	5 (3%)	4	26
2	J	167/184 (91%)	130 (78%)	27 (16%)	10 (6%)	1	12
2	L	167/184 (91%)	128 (77%)	27 (16%)	12 (7%)	1	7
2	N	153/184 (83%)	139 (91%)	11 (7%)	3 (2%)	7	38
2	P	155/184 (84%)	144 (93%)	8 (5%)	3 (2%)	8	39
All	All	1856/2120 (88%)	1518 (82%)	251 (14%)	87 (5%)	2	17

5 of 87 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	71	ARG
1	C	40	ASN
2	D	5	HIS
2	D	63	PRO
2	D	64	THR

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	63/68 (93%)	59 (94%)	4 (6%)	18	52
1	C	62/68 (91%)	57 (92%)	5 (8%)	11	42

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	63/68 (93%)	58 (92%)	5 (8%)	12	43
1	G	63/68 (93%)	59 (94%)	4 (6%)	18	52
1	I	63/68 (93%)	58 (92%)	5 (8%)	12	43
1	K	63/68 (93%)	61 (97%)	2 (3%)	39	71
1	M	63/68 (93%)	61 (97%)	2 (3%)	39	71
1	O	59/68 (87%)	56 (95%)	3 (5%)	24	60
2	B	145/169 (86%)	132 (91%)	13 (9%)	9	34
2	D	150/169 (89%)	131 (87%)	19 (13%)	4	20
2	F	148/169 (88%)	141 (95%)	7 (5%)	26	62
2	H	133/169 (79%)	113 (85%)	20 (15%)	3	14
2	J	148/169 (88%)	123 (83%)	25 (17%)	2	10
2	L	148/169 (88%)	121 (82%)	27 (18%)	1	8
2	N	143/169 (85%)	133 (93%)	10 (7%)	15	48
2	P	142/169 (84%)	137 (96%)	5 (4%)	36	69
All	All	1656/1896 (87%)	1500 (91%)	156 (9%)	8	33

5 of 156 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	101	THR
2	J	28	ASN
2	N	137	ILE
2	H	111	THR
1	I	36	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
1	I	54	ASN
2	J	97	ASN
2	N	152	ASN
2	J	5	HIS
2	J	9	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
3	PX2	B	201	-	35,35,35	0.66	0	39,40,40	1.15	3 (7%)
3	PX2	F	201	-	35,35,35	0.69	0	39,40,40	1.12	1 (2%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PX2	B	201	-	-	9/37/37/37	-
3	PX2	F	201	-	-	10/37/37/37	-

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	201	PX2	C2-O7-C16	-3.53	109.11	117.79
3	B	201	PX2	C2-O7-C16	-2.62	111.33	117.79
3	B	201	PX2	C3-O5-C4	-2.31	108.55	117.12
3	B	201	PX2	O3-P1-O4	-2.17	100.97	106.73

There are no chirality outliers.

5 of 19 torsion outliers are listed below:

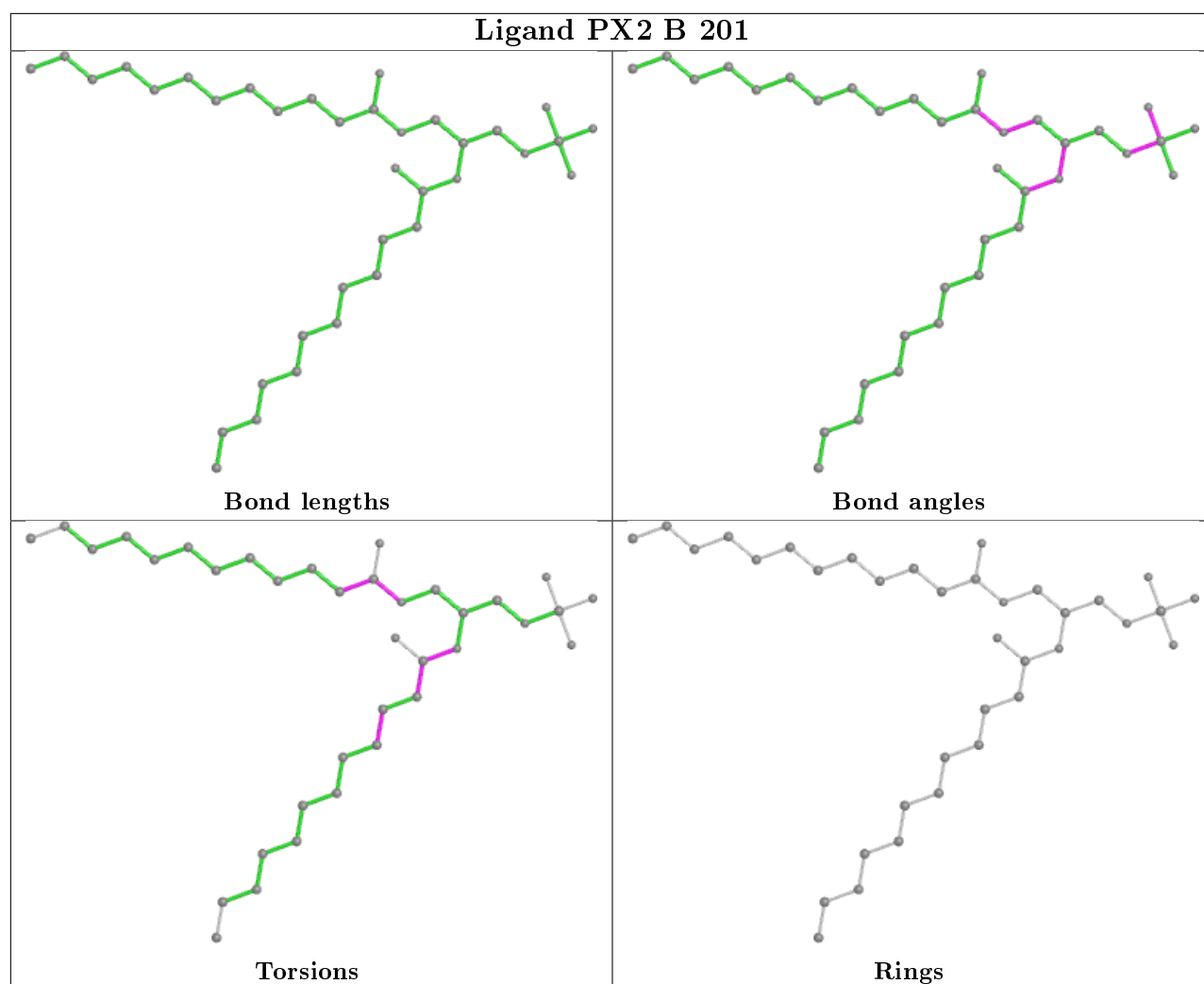
Mol	Chain	Res	Type	Atoms
3	F	201	PX2	C2-C1-O4-P1
3	B	201	PX2	C17-C16-O7-C2
3	F	201	PX2	C5-C4-O5-C3
3	F	201	PX2	O6-C4-O5-C3
3	B	201	PX2	O8-C16-O7-C2

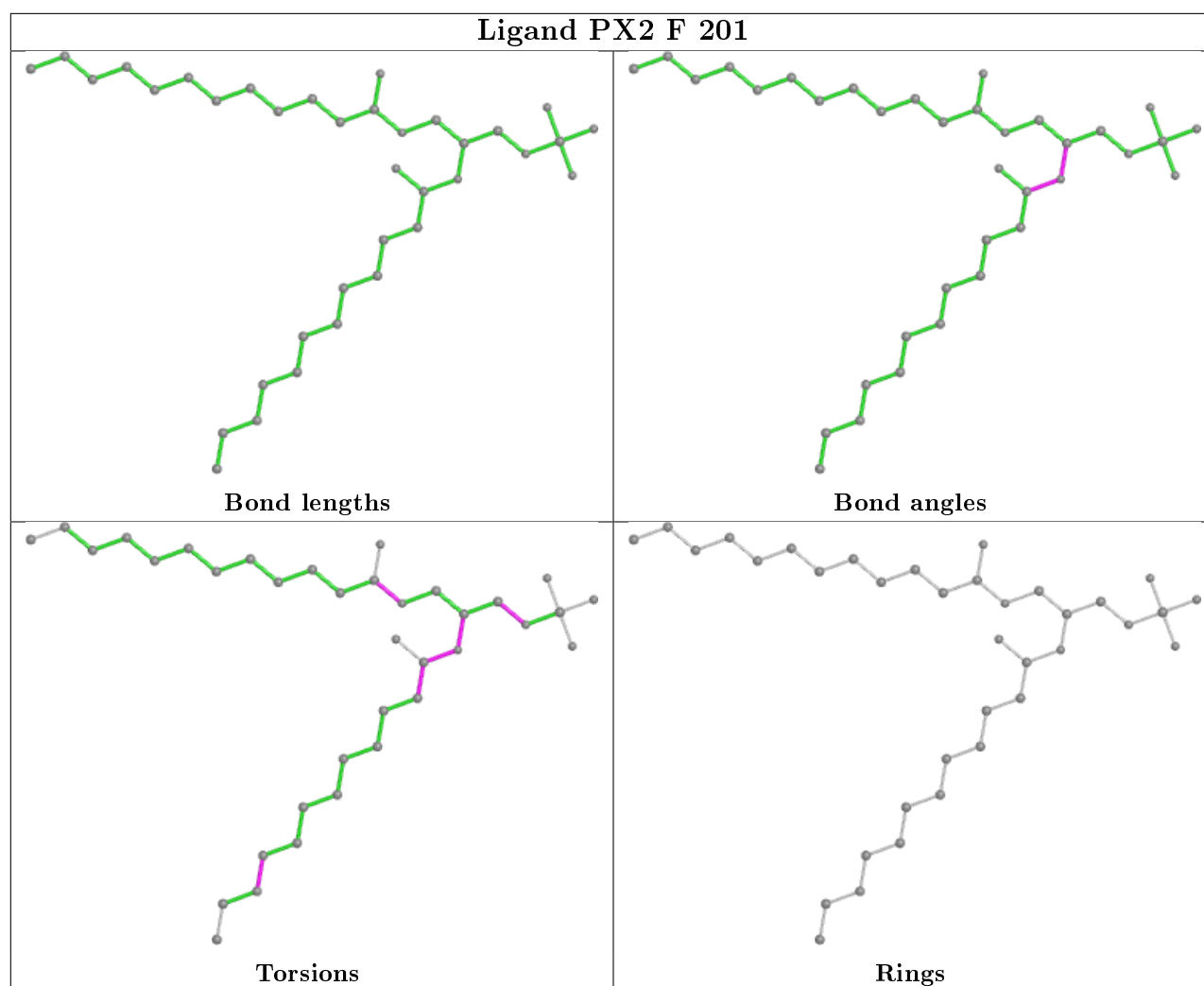
There are no ring outliers.

2 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	201	PX2	8	0
3	F	201	PX2	7	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	73/81 (90%)	-0.53	0 100 100	44, 64, 100, 113	0
1	C	73/81 (90%)	-0.37	0 100 100	34, 52, 92, 100	0
1	E	73/81 (90%)	-0.09	1 (1%) 75 63	52, 78, 112, 125	0
1	G	73/81 (90%)	-0.01	3 (4%) 37 24	54, 72, 107, 121	0
1	I	73/81 (90%)	-0.29	1 (1%) 75 63	69, 93, 117, 126	0
1	K	73/81 (90%)	0.32	2 (2%) 54 39	120, 139, 165, 171	0
1	M	73/81 (90%)	0.84	14 (19%) 1 1	142, 156, 167, 171	0
1	O	68/81 (83%)	2.73	33 (48%) 0 0	193, 208, 216, 216	0
2	B	160/184 (86%)	-0.20	3 (1%) 66 53	34, 59, 153, 157	0
2	D	170/184 (92%)	-0.28	0 100 100	30, 52, 89, 93	0
2	F	167/184 (90%)	-0.00	3 (1%) 68 55	35, 60, 112, 128	0
2	H	162/184 (88%)	-0.18	3 (1%) 66 53	42, 70, 142, 183	0
2	J	169/184 (91%)	-0.18	0 100 100	46, 64, 107, 117	0
2	L	169/184 (91%)	-0.08	1 (0%) 89 83	42, 76, 129, 147	0
2	N	157/184 (85%)	0.84	28 (17%) 1 1	43, 131, 151, 160	0
2	P	159/184 (86%)	2.38	69 (43%) 0 0	54, 189, 207, 213	0
All	All	1892/2120 (89%)	0.28	161 (8%) 10 6	30, 75, 200, 216	0

The worst 5 of 161 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	P	55	LEU	13.5
2	P	73	ILE	12.7
2	P	79	ILE	12.5
2	P	56	LEU	12.3
2	P	94	TYR	11.8

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](#)

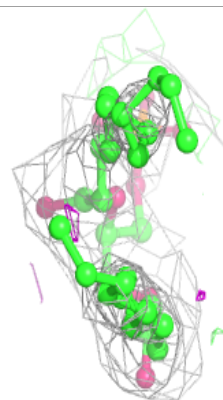
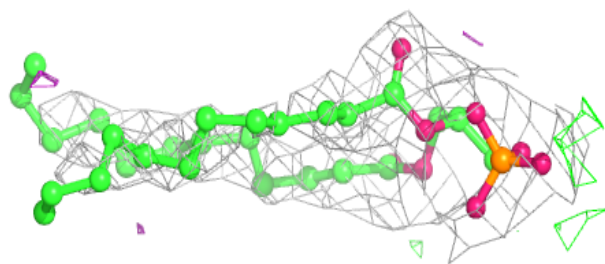
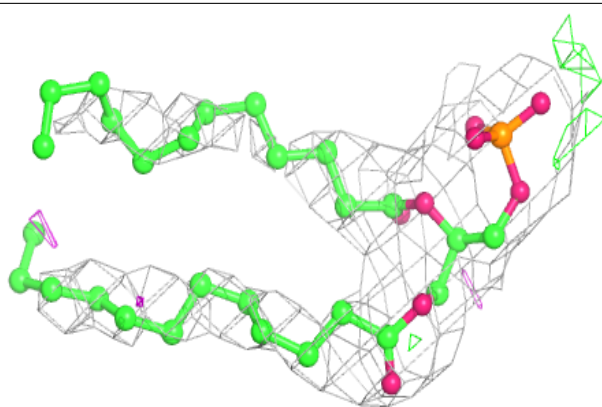
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	PX2	F	201	36/36	0.85	0.50	54,63,76,78	0
3	PX2	B	201	36/36	0.92	0.38	44,55,62,63	0

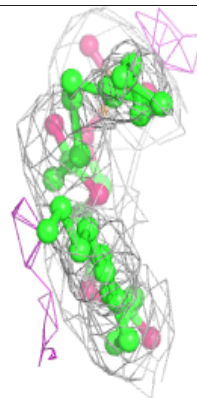
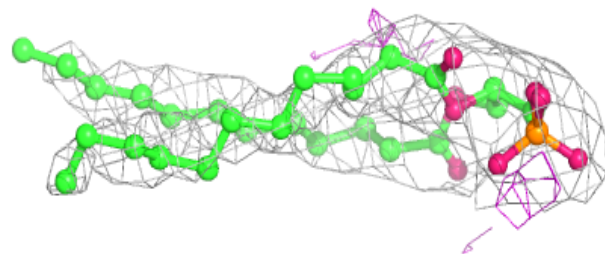
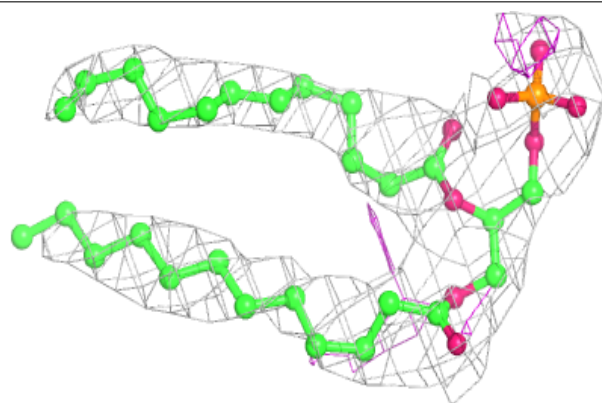
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around PX2 F 201:

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

**Electron density around PX2 B 201:**

$2mF_o-DF_c$ (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.