



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 5, 2026 – 02:24 AM JST

PDB ID : 4YTP / pdb_00004ytp
Title : CRYSTAL STRUCTURE OF PORCINE HEART MITOCHONDRIAL COMPLEX II BOUND WITH N-[(4-tert-butylphenyl)methyl]-2-(trifluoromethyl)benzamide
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Deposited on : 2015-03-18
Resolution : 3.10 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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](#) ①) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	1.8.5 (274361), CSD as541be (2020)
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	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

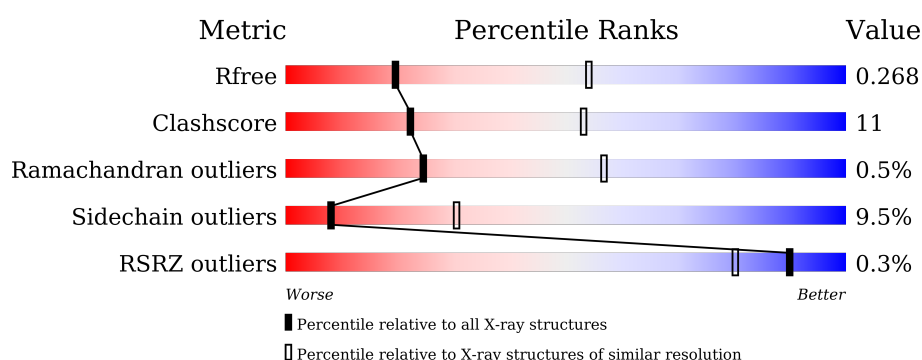
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	664	
2	B	280	
3	C	169	
4	D	159	

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
8	F3S	B	303	-	-	X	-

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 8641 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 Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	613	Total	C	N	O	S	0	0	0
			4729	2954	848	895	32			

- Molecule 2 is a protein called Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	239	Total	C	N	O	S	0	0	0
			1922	1214	326	360	22			

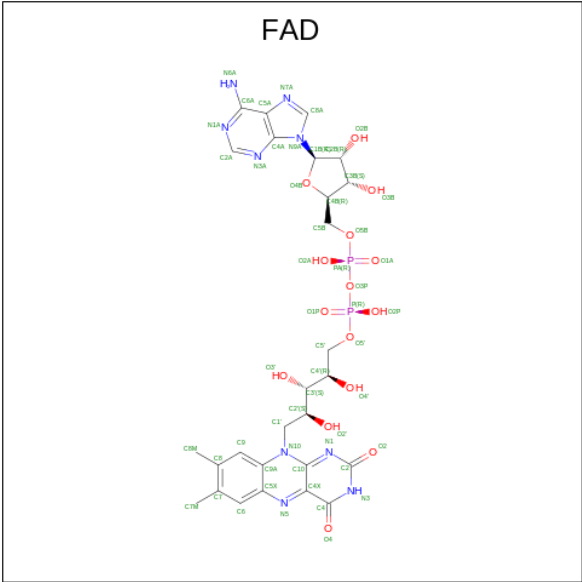
- Molecule 3 is a protein called Succinate dehydrogenase cytochrome b560 subunit, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	138	Total	C	N	O	S	0	0	0
			1064	695	179	183	7			

- Molecule 4 is a protein called Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial.

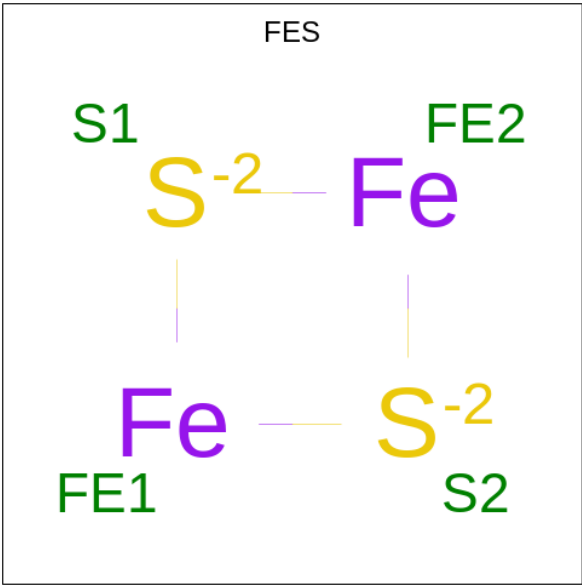
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	102	Total	C	N	O	S	0	0	0
			765	499	128	133	5			

- Molecule 5 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula: C₂₇H₃₃N₉O₁₅P₂).



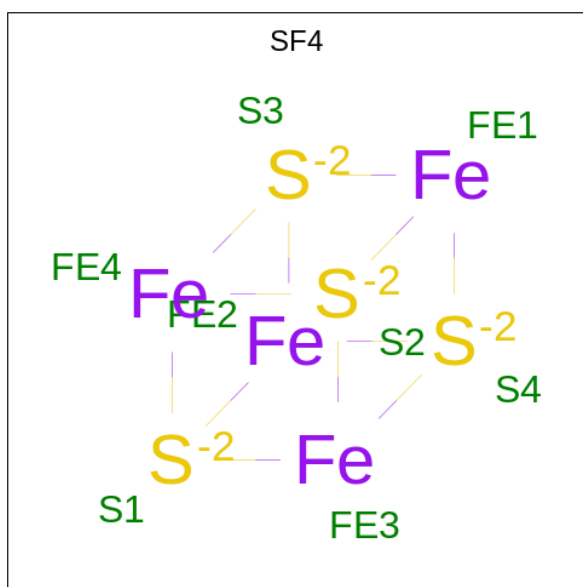
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0
			53	27	9	15	2	

- Molecule 6 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe₂S₂).



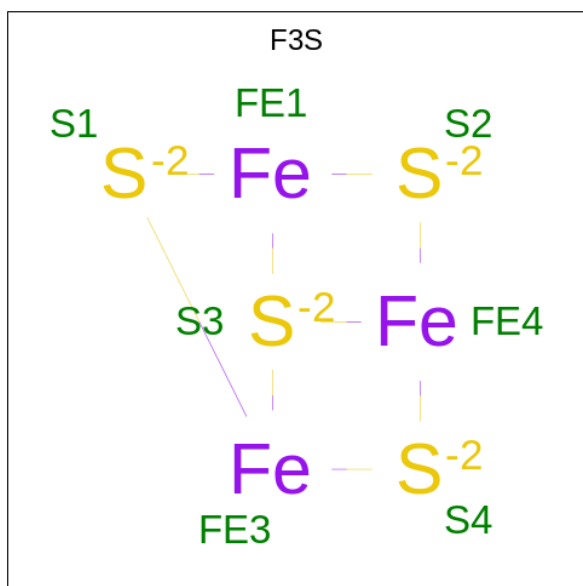
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	1	Total	Fe	S	0
			4	2	2	

- Molecule 7 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄).



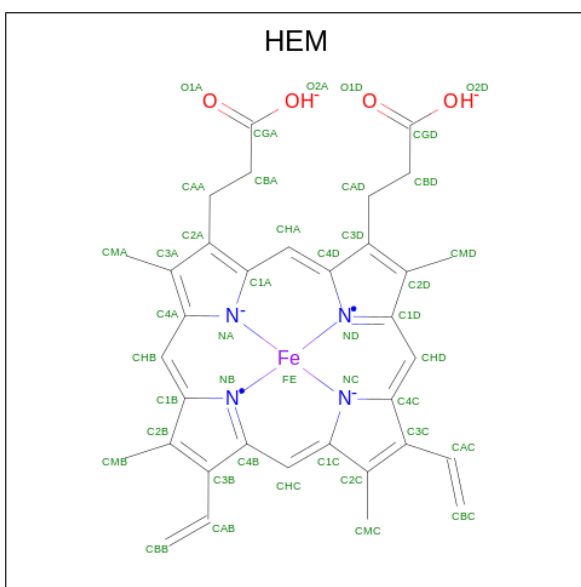
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 8 is FE3-S4 CLUSTER (CCD ID: F3S) (formula: Fe_3S_4).



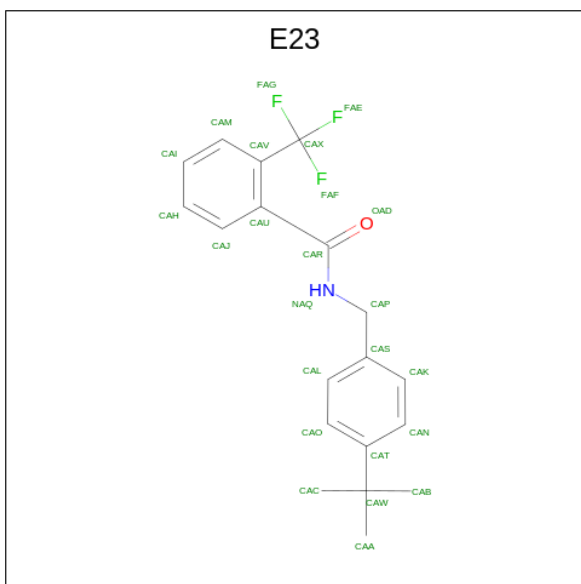
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	B	1	Total	Fe	S	0	0
			7	3	4		

- Molecule 9 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $\text{C}_{34}\text{H}_{32}\text{FeN}_4\text{O}_4$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
9	C	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 10 is N-(4-tert-butylbenzyl)-2-(trifluoromethyl)benzamide (CCD ID: E23) (formula: C₁₉H₂₀F₃NO).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
10	C	1	Total	C	F	N	O	0	0
			24	19	3	1	1		

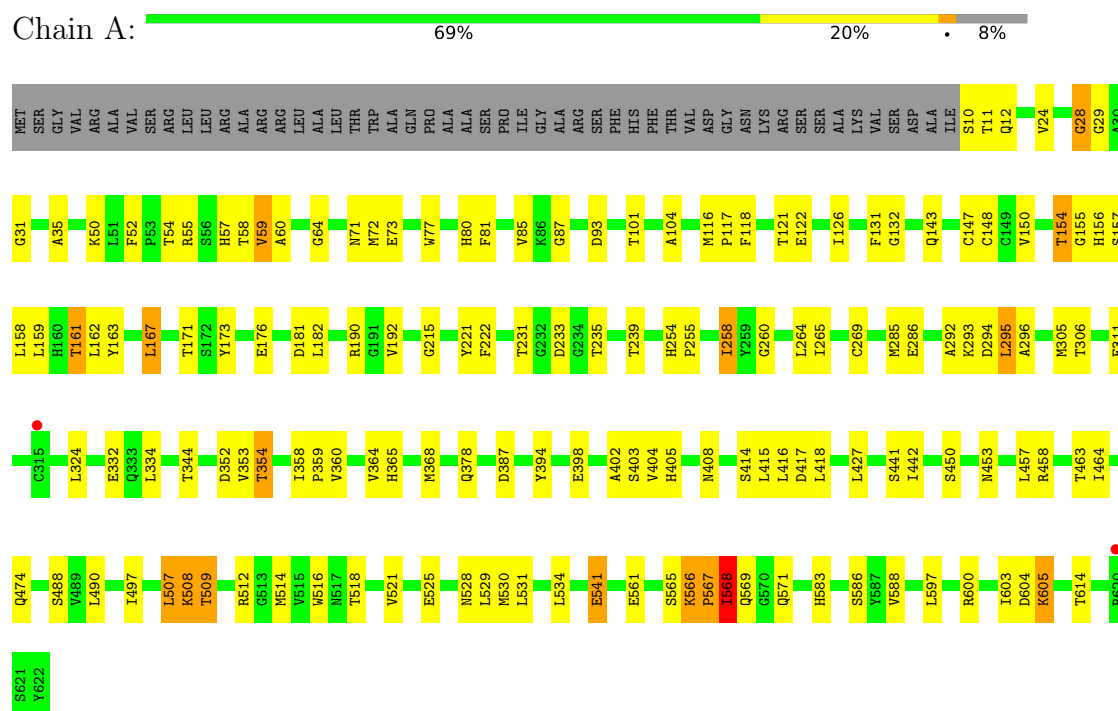
- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	9	Total 9	O 9	0	0
11	B	6	Total 6	O 6	0	0
11	C	5	Total 5	O 5	0	0
11	D	2	Total 2	O 2	0	0

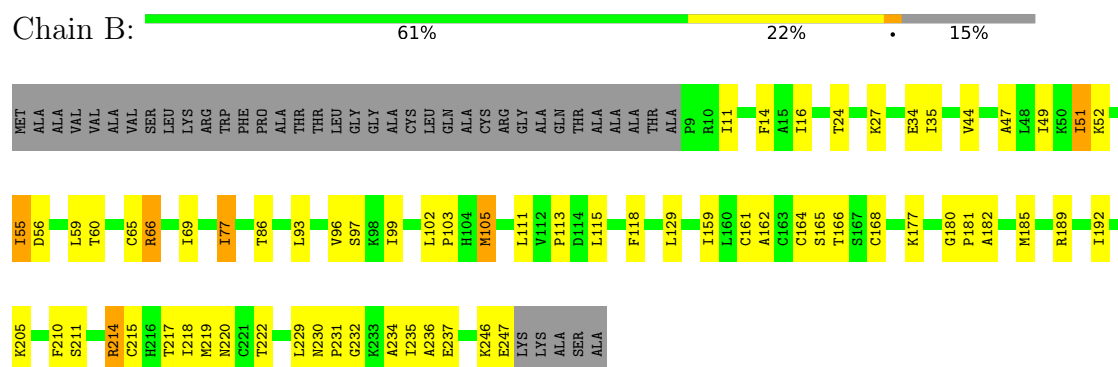
3 Residue-property plots

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.

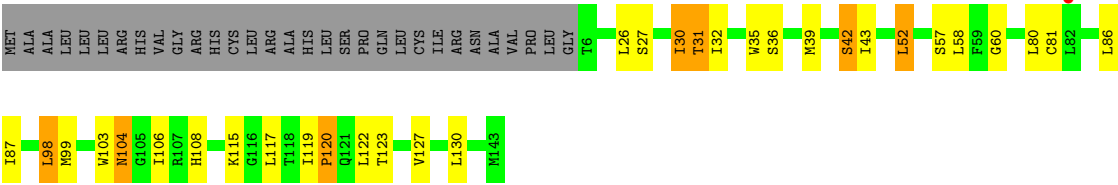
- Molecule 1: Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial



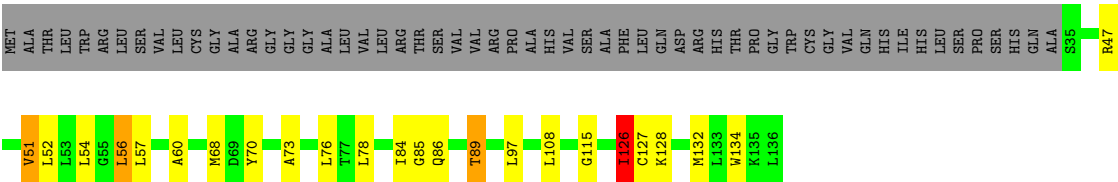
- Molecule 2: Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial



- Molecule 3: Succinate dehydrogenase cytochrome b560 subunit, mitochondrial



• Molecule 4: Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	71.43Å 84.01Å 294.82Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.10 20.00 – 3.10	Depositor EDS
% Data completeness (in resolution range)	80.7 (20.00-3.10) 80.5 (20.00-3.10)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.36 (at 3.09Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.206 , 0.269 0.206 , 0.268	Depositor DCC
R_{free} test set	1346 reflections (4.08%)	wwPDB-VP
Wilson B-factor (Å ²)	69.4	Xtriage
Anisotropy	0.011	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 35.3	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	0.92	EDS
Total number of atoms	8641	wwPDB-VP
Average B, all atoms (Å ²)	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.49% 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: HEM, E23, SF4, FAD, FES, F3S

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	0.56	0/4828	0.87	4/6531 (0.1%)
2	B	0.50	0/1964	0.83	2/2648 (0.1%)
3	C	0.53	0/1091	0.84	0/1483
4	D	0.54	0/784	0.92	1/1066 (0.1%)
All	All	0.54	0/8667	0.86	7/11728 (0.1%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	28	GLY	N-CA-C	-9.71	96.92	111.10
2	B	180	GLY	CA-C-N	9.07	128.67	119.24
2	B	180	GLY	C-N-CA	9.07	128.67	119.24
1	A	402	ALA	N-CA-C	-6.94	104.79	113.18
1	A	295	LEU	N-CA-C	-6.33	105.51	112.72
4	D	126	ILE	N-CA-CB	5.32	116.42	110.62
1	A	567	PRO	N-CA-C	-5.21	102.93	111.21

There are no chirality outliers.

There are no planarity outliers.

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	4729	0	4618	116	0
2	B	1922	0	1901	38	0
3	C	1064	0	1104	15	0
4	D	765	0	770	12	0
5	A	53	0	31	7	0
6	B	4	0	0	0	0
7	B	8	0	0	0	0
8	B	7	0	0	3	0
9	C	43	0	30	7	0
10	C	24	0	20	0	0
11	A	9	0	0	0	0
11	B	6	0	0	0	0
11	C	5	0	0	0	0
11	D	2	0	0	0	0
All	All	8641	0	8474	180	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.

All (180) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:568:ILE:HG12	1:A:569:GLN:H	1.06	1.17
1:A:566:LYS:CG	1:A:567:PRO:HD2	1.82	1.09
1:A:566:LYS:HG3	1:A:567:PRO:O	1.55	1.06
1:A:566:LYS:HG3	1:A:567:PRO:HD2	1.39	0.98
1:A:566:LYS:CD	1:A:567:PRO:HD2	1.95	0.96
1:A:568:ILE:HG12	1:A:569:GLN:N	1.78	0.94
1:A:566:LYS:HG3	1:A:567:PRO:CD	2.00	0.92
1:A:568:ILE:CG1	1:A:569:GLN:N	2.30	0.91
1:A:566:LYS:HD2	1:A:567:PRO:HD2	1.51	0.91
1:A:568:ILE:CG1	1:A:569:GLN:H	1.79	0.91
1:A:258:ILE:HD12	1:A:265:ILE:HD11	1.54	0.88
2:B:168:CYS:HG	8:B:303:F3S:FE3	0.65	0.88
1:A:285:MET:HB3	1:A:294:ASP:HB3	1.61	0.81
2:B:219:MET:HE3	3:C:117:LEU:HD22	1.62	0.80
1:A:72:MET:HE1	1:A:121:THR:HG21	1.64	0.79
1:A:414:SER:O	1:A:418:LEU:HD13	1.84	0.77
1:A:566:LYS:CG	1:A:567:PRO:CD	2.59	0.77
1:A:285:MET:HE2	1:A:294:ASP:HA	1.68	0.76
1:A:566:LYS:CG	1:A:567:PRO:O	2.34	0.74
1:A:293:LYS:O	1:A:294:ASP:CG	2.30	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:132:GLY:HA2	1:A:295:LEU:O	1.89	0.72
1:A:285:MET:CB	1:A:294:ASP:HB3	2.20	0.71
2:B:185:MET:HE1	2:B:229:LEU:HB3	1.73	0.71
1:A:568:ILE:HA	1:A:571:GLN:OE1	1.92	0.69
3:C:98:LEU:HD13	3:C:99:MET:HE3	1.74	0.69
2:B:219:MET:HE1	2:B:232:GLY:HA3	1.75	0.68
1:A:72:MET:HE1	1:A:121:THR:CG2	2.27	0.64
1:A:29:GLY:H	1:A:58:THR:HG21	1.62	0.64
3:C:52:LEU:HB3	9:C:301:HEM:CBC	2.28	0.64
9:C:301:HEM:HBB2	9:C:301:HEM:HMB2	1.80	0.64
1:A:190:ARG:NH1	1:A:441:SER:O	2.31	0.64
2:B:51:ILE:HD11	2:B:59:LEU:HD22	1.81	0.63
1:A:233:ASP:OD2	1:A:528:ASN:ND2	2.26	0.63
2:B:44:VAL:HG11	2:B:77:ILE:HD12	1.83	0.60
9:C:301:HEM:HMC2	9:C:301:HEM:HBC2	1.83	0.60
1:A:64:GLY:HA2	1:A:154:THR:HG21	1.81	0.60
1:A:518:THR:HA	1:A:521:VAL:HG22	1.83	0.59
2:B:222:THR:OG1	2:B:230:ASN:ND2	2.36	0.58
2:B:69:ILE:C	2:B:69:ILE:HD12	2.28	0.58
1:A:57:HIS:NE2	5:A:701:FAD:C8M	2.67	0.58
1:A:221:TYR:CG	1:A:364:VAL:HG21	2.39	0.58
2:B:246:LYS:O	2:B:247:GLU:HB2	2.03	0.58
2:B:218:ILE:HD12	8:B:303:F3S:S1	2.44	0.57
1:A:28:GLY:O	1:A:29:GLY:C	2.48	0.57
3:C:52:LEU:HB3	9:C:301:HEM:CAC	2.35	0.57
2:B:214:ARG:NH2	4:D:86:GLN:OE1	2.37	0.57
2:B:35:ILE:HD11	2:B:51:ILE:HG22	1.86	0.56
1:A:57:HIS:NE2	5:A:701:FAD:HM83	2.20	0.56
1:A:87:GLY:O	1:A:408:ASN:HB3	2.05	0.56
1:A:352:ASP:OD1	1:A:354:THR:HG22	2.05	0.56
1:A:565:SER:OG	1:A:566:LYS:N	2.38	0.56
1:A:286:GLU:CD	1:A:293:LYS:HD3	2.31	0.55
2:B:164:CYS:SG	2:B:165:SER:N	2.79	0.55
1:A:181:ASP:OD2	1:A:450:SER:HB3	2.08	0.54
1:A:568:ILE:O	1:A:569:GLN:HB3	2.07	0.54
1:A:378:GLN:HG2	1:A:394:TYR:CE2	2.43	0.54
9:C:301:HEM:CBB	4:D:54:LEU:HA	2.38	0.54
1:A:57:HIS:CD2	5:A:701:FAD:HM83	2.43	0.53
2:B:231:PRO:O	2:B:234:ALA:N	2.42	0.53
1:A:28:GLY:O	1:A:31:GLY:N	2.41	0.53
1:A:58:THR:O	1:A:155:GLY:HA3	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:219:MET:CE	2:B:232:GLY:HA3	2.38	0.52
1:A:294:ASP:C	1:A:294:ASP:OD1	2.52	0.52
3:C:104:ASN:HD22	3:C:104:ASN:C	2.17	0.52
2:B:162:ALA:O	2:B:166:THR:HG22	2.10	0.52
3:C:99:MET:HA	3:C:99:MET:HE2	1.92	0.51
4:D:85:GLY:O	4:D:89:THR:HG22	2.11	0.51
1:A:81:PHE:O	1:A:85:VAL:HG12	2.10	0.51
1:A:415:LEU:HG	5:A:701:FAD:C2	2.40	0.51
1:A:59:VAL:HG12	1:A:60:ALA:N	2.25	0.51
2:B:105:MET:HA	2:B:105:MET:HE2	1.92	0.51
1:A:143:GLN:NE2	1:A:295:LEU:HD23	2.26	0.51
1:A:254:HIS:NE2	1:A:264:LEU:HD11	2.27	0.50
1:A:353:VAL:HG12	1:A:358:ILE:HD11	1.93	0.50
2:B:210:PHE:O	2:B:211:SER:C	2.55	0.50
4:D:84:ILE:O	4:D:85:GLY:C	2.55	0.50
1:A:57:HIS:O	1:A:60:ALA:N	2.41	0.49
1:A:126:ILE:HG21	1:A:148:CYS:HB3	1.93	0.49
1:A:292:ALA:CB	1:A:296:ALA:HB2	2.42	0.49
2:B:231:PRO:O	2:B:232:GLY:C	2.55	0.49
1:A:567:PRO:O	1:A:567:PRO:CD	2.57	0.49
2:B:55:ILE:HG22	2:B:56:ASP:N	2.26	0.49
1:A:569:GLN:O	1:A:571:GLN:N	2.46	0.49
1:A:293:LYS:O	1:A:294:ASP:OD1	2.30	0.48
2:B:52:LYS:HA	2:B:56:ASP:O	2.13	0.48
1:A:265:ILE:HD12	1:A:360:VAL:HG12	1.94	0.48
2:B:65:CYS:O	2:B:66:ARG:HG3	2.14	0.48
1:A:358:ILE:HG22	1:A:359:PRO:HD2	1.95	0.48
3:C:103:TRP:HA	3:C:106:ILE:HD12	1.95	0.48
1:A:162:LEU:O	1:A:163:TYR:C	2.55	0.48
1:A:414:SER:O	1:A:417:ASP:HB3	2.14	0.47
1:A:116:MET:N	1:A:161:THR:HG21	2.29	0.47
4:D:86:GLN:HA	4:D:89:THR:HG23	1.97	0.47
1:A:258:ILE:CD1	1:A:265:ILE:HD11	2.37	0.47
1:A:568:ILE:O	1:A:569:GLN:CB	2.61	0.47
3:C:35:TRP:CZ3	3:C:39:MET:HE3	2.50	0.47
3:C:60:GLY:O	4:D:115:GLY:HA3	2.15	0.47
1:A:567:PRO:HD2	1:A:567:PRO:O	2.15	0.47
1:A:81:PHE:HA	1:A:101:THR:HG21	1.97	0.47
1:A:150:VAL:HG11	1:A:157:SER:OG	2.15	0.47
4:D:128:LYS:O	4:D:132:MET:HG3	2.14	0.47
2:B:168:CYS:SG	8:B:303:F3S:S1	3.13	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:C:301:HEM:HBB2	9:C:301:HEM:CMB	2.44	0.46
2:B:115:LEU:O	2:B:118:PHE:HB3	2.15	0.46
1:A:117:PRO:O	1:A:150:VAL:HG13	2.16	0.46
1:A:404:VAL:HG12	1:A:405:HIS:CD2	2.50	0.46
1:A:215:GLY:HA2	1:A:398:GLU:HB3	1.98	0.46
1:A:603:ILE:HG23	1:A:605:LYS:CE	2.46	0.46
4:D:126:ILE:O	4:D:127:CYS:C	2.57	0.46
1:A:285:MET:HE2	1:A:294:ASP:CA	2.43	0.46
1:A:254:HIS:HB2	1:A:365:HIS:CB	2.46	0.46
1:A:222:PHE:HA	1:A:474:GLN:HE21	1.81	0.46
1:A:293:LYS:O	1:A:294:ASP:CB	2.64	0.46
2:B:215:CYS:SG	2:B:235:ILE:HG21	2.56	0.45
4:D:47:ARG:O	4:D:51:VAL:HG13	2.17	0.45
2:B:105:MET:H	3:C:27:SER:HG	1.62	0.45
4:D:60:ALA:HA	4:D:68:MET:HG2	1.99	0.45
1:A:52:PHE:HB3	1:A:55:ARG:HG2	1.98	0.45
1:A:11:THR:HG22	1:A:11:THR:O	2.17	0.45
2:B:47:ALA:O	2:B:51:ILE:HG23	2.16	0.45
1:A:490:LEU:HD13	1:A:541:GLU:HA	1.98	0.45
1:A:57:HIS:NE2	5:A:701:FAD:HM81	2.31	0.45
1:A:58:THR:HG23	5:A:701:FAD:O1A	2.17	0.45
1:A:59:VAL:HG23	1:A:159:LEU:HD23	1.98	0.45
1:A:464:ILE:O	1:A:508:LYS:N	2.42	0.45
1:A:50:LYS:O	1:A:176:GLU:HA	2.17	0.44
1:A:464:ILE:O	1:A:507:LEU:HA	2.17	0.44
9:C:301:HEM:HBC2	9:C:301:HEM:CMC	2.45	0.44
3:C:80:LEU:O	3:C:81:CYS:C	2.60	0.44
1:A:334:LEU:HD13	1:A:353:VAL:HG23	1.99	0.44
4:D:70:TYR:O	4:D:73:ALA:HB3	2.17	0.44
1:A:58:THR:HG22	5:A:701:FAD:O4'	2.17	0.44
1:A:530:MET:O	1:A:531:LEU:C	2.59	0.44
4:D:56:LEU:O	4:D:57:LEU:C	2.61	0.44
1:A:77:TRP:O	1:A:80:HIS:HB3	2.18	0.44
2:B:55:ILE:N	2:B:55:ILE:HD12	2.33	0.44
1:A:93:ASP:OD1	1:A:583:HIS:NE2	2.45	0.44
2:B:181:PRO:O	2:B:182:ALA:C	2.61	0.44
3:C:30:ILE:HD12	3:C:31:THR:H	1.83	0.44
1:A:10:SER:C	1:A:12:GLN:H	2.25	0.43
1:A:457:LEU:O	1:A:509:THR:HG21	2.18	0.43
2:B:102:LEU:HA	2:B:103:PRO:HD3	1.88	0.43
1:A:231:THR:HG21	1:A:525:GLU:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:516:TRP:HB3	2:B:60:THR:HG21	2.01	0.43
2:B:14:PHE:HB3	2:B:16:ILE:HD11	2.00	0.43
1:A:118:PHE:HA	1:A:150:VAL:HG22	2.01	0.43
1:A:171:THR:HB	1:A:173:TYR:CE1	2.54	0.43
1:A:231:THR:OG1	1:A:233:ASP:OD1	2.29	0.43
1:A:231:THR:HG22	1:A:529:LEU:HD11	2.01	0.43
1:A:255:PRO:HB3	1:A:305:MET:SD	2.59	0.43
1:A:453:ASN:O	1:A:457:LEU:HD13	2.19	0.43
1:A:387:ASP:OD2	1:A:600:ARG:NH1	2.52	0.42
1:A:566:LYS:CB	1:A:567:PRO:CD	2.95	0.42
1:A:264:LEU:HD22	1:A:365:HIS:CE1	2.54	0.42
3:C:98:LEU:HD13	3:C:99:MET:CE	2.47	0.42
1:A:24:VAL:HG21	1:A:35:ALA:HA	2.01	0.42
1:A:566:LYS:HD2	1:A:567:PRO:CD	2.34	0.42
2:B:11:ILE:O	2:B:93:LEU:HD22	2.20	0.42
1:A:157:SER:O	1:A:158:LEU:C	2.62	0.42
1:A:603:ILE:HG23	1:A:605:LYS:HE2	2.01	0.41
2:B:161:CYS:O	2:B:162:ALA:HB3	2.20	0.41
1:A:64:GLY:HA3	1:A:147:CYS:SG	2.60	0.41
1:A:254:HIS:CE1	1:A:264:LEU:HD11	2.55	0.41
2:B:111:LEU:O	2:B:113:PRO:HD3	2.20	0.41
2:B:235:ILE:O	2:B:236:ALA:C	2.63	0.41
3:C:119:ILE:N	3:C:120:PRO:HD2	2.36	0.41
2:B:118:PHE:CZ	2:B:162:ALA:HB2	2.55	0.41
3:C:42:SER:O	3:C:43:ILE:C	2.62	0.41
1:A:71:ASN:C	1:A:72:MET:HE2	2.46	0.41
1:A:143:GLN:CD	1:A:295:LEU:CD2	2.94	0.41
1:A:442:ILE:O	1:A:442:ILE:HG23	2.20	0.41
1:A:163:TYR:O	1:A:167:LEU:HD22	2.20	0.41
1:A:59:VAL:HA	1:A:156:HIS:HA	2.03	0.41
1:A:286:GLU:OE1	1:A:293:LYS:HD3	2.20	0.41
1:A:497:ILE:HG22	1:A:534:LEU:HD12	2.01	0.41
1:A:597:LEU:HD23	1:A:597:LEU:N	2.36	0.40
1:A:104:ALA:HA	1:A:416:LEU:HD11	2.02	0.40
2:B:34:GLU:CD	2:B:34:GLU:N	2.80	0.40
1:A:265:ILE:HG22	1:A:269:CYS:SG	2.61	0.40
1:A:604:ASP:O	1:A:614:THR:HG23	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	611/664 (92%)	540 (88%)	69 (11%)	2 (0%)	36	67
2	B	237/280 (85%)	214 (90%)	21 (9%)	2 (1%)	16	47
3	C	136/169 (80%)	123 (90%)	12 (9%)	1 (1%)	18	49
4	D	100/159 (63%)	91 (91%)	9 (9%)	0	100	100
All	All	1084/1272 (85%)	968 (89%)	111 (10%)	5 (0%)	24	57

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	568	ILE
2	B	66	ARG
2	B	55	ILE
3	C	120	PRO
1	A	260	GLY

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	499/538 (93%)	462 (93%)	37 (7%)	13	40
2	B	214/239 (90%)	194 (91%)	20 (9%)	8	31
3	C	117/142 (82%)	98 (84%)	19 (16%)	2	11
4	D	76/122 (62%)	66 (87%)	10 (13%)	4	17
All	All	906/1041 (87%)	820 (90%)	86 (10%)	8	30

All (86) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	54	THR
1	A	59	VAL
1	A	73	GLU
1	A	122	GLU
1	A	131	PHE
1	A	154	THR
1	A	161	THR
1	A	167	LEU
1	A	182	LEU
1	A	192	VAL
1	A	235	THR
1	A	239	THR
1	A	258	ILE
1	A	306	THR
1	A	311	GLU
1	A	324	LEU
1	A	332	GLU
1	A	344	THR
1	A	354	THR
1	A	368	MET
1	A	403	SER
1	A	427	LEU
1	A	458	ARG
1	A	463	THR
1	A	488	SER
1	A	507	LEU
1	A	508	LYS
1	A	509	THR
1	A	512	ARG
1	A	514	MET
1	A	541	GLU
1	A	561	GLU
1	A	566	LYS
1	A	568	ILE
1	A	586	SER
1	A	588	VAL
1	A	605	LYS
2	B	24	THR
2	B	27	LYS
2	B	49	ILE
2	B	51	ILE
2	B	77	ILE

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Mol	Chain	Res	Type
2	B	86	THR
2	B	96	VAL
2	B	97	SER
2	B	99	ILE
2	B	105	MET
2	B	129	LEU
2	B	159	ILE
2	B	177	LYS
2	B	189	ARG
2	B	192	ILE
2	B	205	LYS
2	B	214	ARG
2	B	217	THR
2	B	220	ASN
2	B	237	GLU
3	C	26	LEU
3	C	30	ILE
3	C	31	THR
3	C	32	ILE
3	C	36	SER
3	C	42	SER
3	C	52	LEU
3	C	57	SER
3	C	58	LEU
3	C	86	LEU
3	C	87	ILE
3	C	98	LEU
3	C	104	ASN
3	C	108	HIS
3	C	115	LYS
3	C	122	LEU
3	C	123	THR
3	C	127	VAL
3	C	130	LEU
4	D	51	VAL
4	D	52	LEU
4	D	56	LEU
4	D	76	LEU
4	D	78	LEU
4	D	89	THR
4	D	97	LEU
4	D	108	LEU

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Mol	Chain	Res	Type
4	D	126	ILE
4	D	134	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	62	GLN
1	A	94	GLN
1	A	98	HIS
1	A	143	GLN
1	A	228	HIS
1	A	325	GLN
1	A	378	GLN
1	A	384	ASN
1	A	453	ASN
1	A	461	ASN
1	A	474	GLN
1	A	527	GLN
1	A	550	HIS
2	B	31	GLN
2	B	121	GLN
2	B	136	GLN
2	B	144	GLN
2	B	174	ASN
2	B	220	ASN
2	B	230	ASN
3	C	17	ASN
3	C	29	HIS
3	C	104	ASN
4	D	63	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

6 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	FES	B	301	2	0,4,4	-	-	-		
10	E23	C	302	-	25,25,25	0.47	0	37,37,37	0.91	2 (5%)
8	F3S	B	303	2	0,9,9	-	-	-		
5	FAD	A	701	-	56,58,58	1.43	9 (16%)	81,89,89	1.74	21 (25%)
9	HEM	C	301	3,4	50,50,50	1.57	6 (12%)	66,82,82	1.76	10 (15%)
7	SF4	B	302	2	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	E23	C	302	-	-	0/21/21/21	0/2/2/2
6	FES	B	301	2	-	-	0/1/1/1
8	F3S	B	303	2	-	-	0/3/3/3
9	HEM	C	301	3,4	-	3/14/54/54	-
5	FAD	A	701	-	-	2/34/50/50	0/6/6/6
7	SF4	B	302	2	-	-	0/6/5/5

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	701	FAD	C9A-C5X	4.76	1.49	1.41
9	C	301	HEM	C1B-NB	-4.45	1.32	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	701	FAD	C5A-C4A	4.29	1.47	1.39
9	C	301	HEM	FE-NB	4.18	2.07	1.94
9	C	301	HEM	FE-NC	3.87	2.08	1.95
9	C	301	HEM	C4D-ND	-3.75	1.33	1.40
5	A	701	FAD	C8-C7	3.20	1.48	1.40
5	A	701	FAD	C5A-C6A	2.86	1.49	1.41
9	C	301	HEM	C4B-NB	-2.63	1.33	1.38
5	A	701	FAD	C8A-N7A	2.54	1.36	1.31
5	A	701	FAD	C5A-N7A	-2.20	1.34	1.39
5	A	701	FAD	C4-N3	-2.20	1.34	1.38
5	A	701	FAD	C5X-N5	-2.08	1.35	1.39
5	A	701	FAD	C4X-N5	2.07	1.34	1.30
9	C	301	HEM	C4C-NC	-2.07	1.35	1.39

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	C	301	HEM	CHC-C4B-NB	5.58	130.48	124.42
9	C	301	HEM	C1B-NB-C4B	5.52	110.78	105.07
5	A	701	FAD	C5A-C4A-N3A	-5.41	119.69	126.75
9	C	301	HEM	CHD-C1D-ND	5.12	129.99	124.42
5	A	701	FAD	N3A-C2A-N1A	-4.28	121.90	128.60
5	A	701	FAD	C2A-N3A-C4A	4.22	121.71	111.75
9	C	301	HEM	CHD-C1D-C2D	-4.19	118.43	124.98
9	C	301	HEM	CHA-C4D-ND	3.97	129.27	124.37
5	A	701	FAD	N3A-C4A-N9A	3.83	133.39	127.08
5	A	701	FAD	O4B-C1B-N9A	3.60	115.15	108.06
5	A	701	FAD	C4A-C5A-N7A	-3.58	106.26	110.62
9	C	301	HEM	C4C-NC-C1C	3.22	108.50	105.35
5	A	701	FAD	C6A-C5A-N7A	3.18	137.94	132.02
5	A	701	FAD	C5A-N7A-C8A	3.04	107.83	103.51
9	C	301	HEM	CHA-C4D-C3D	-2.97	119.75	125.33
5	A	701	FAD	C4-C4X-N5	2.90	122.37	118.23
5	A	701	FAD	C4X-C10-N1	-2.83	118.17	124.73
5	A	701	FAD	C10-N1-C2	2.75	122.39	116.90
10	C	302	E23	FAG-CAX-CAV	-2.70	108.00	112.70
5	A	701	FAD	O2-C2-N1	-2.68	117.39	121.83
10	C	302	E23	CAP-NAQ-CAR	2.57	127.89	121.81
9	C	301	HEM	C1A-CHA-C4D	-2.56	120.27	126.34
5	A	701	FAD	C4'-C3'-C2'	-2.52	108.12	113.36
5	A	701	FAD	P-O3P-PA	-2.50	124.25	132.83
5	A	701	FAD	C2A-N1A-C6A	2.49	123.04	118.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	701	FAD	C4A-N9A-C8A	2.46	108.39	105.73
5	A	701	FAD	N9A-C8A-N7A	-2.42	110.61	113.91
5	A	701	FAD	O4-C4-C4X	-2.33	120.42	126.60
5	A	701	FAD	C4X-C10-N10	2.29	119.83	116.48
9	C	301	HEM	CBD-CAD-C3D	-2.09	106.83	112.63
5	A	701	FAD	C4X-C4-N3	2.05	118.39	113.19
5	A	701	FAD	C10-C4X-N5	-2.05	120.51	124.86
9	C	301	HEM	O2A-CGA-CBA	2.01	120.48	114.03

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	C	301	HEM	C3D-CAD-CBD-CGD
5	A	701	FAD	N10-C1'-C2'-O2'
9	C	301	HEM	CAA-CBA-CGA-O1A
9	C	301	HEM	CAA-CBA-CGA-O2A
5	A	701	FAD	O4B-C4B-C5B-O5B

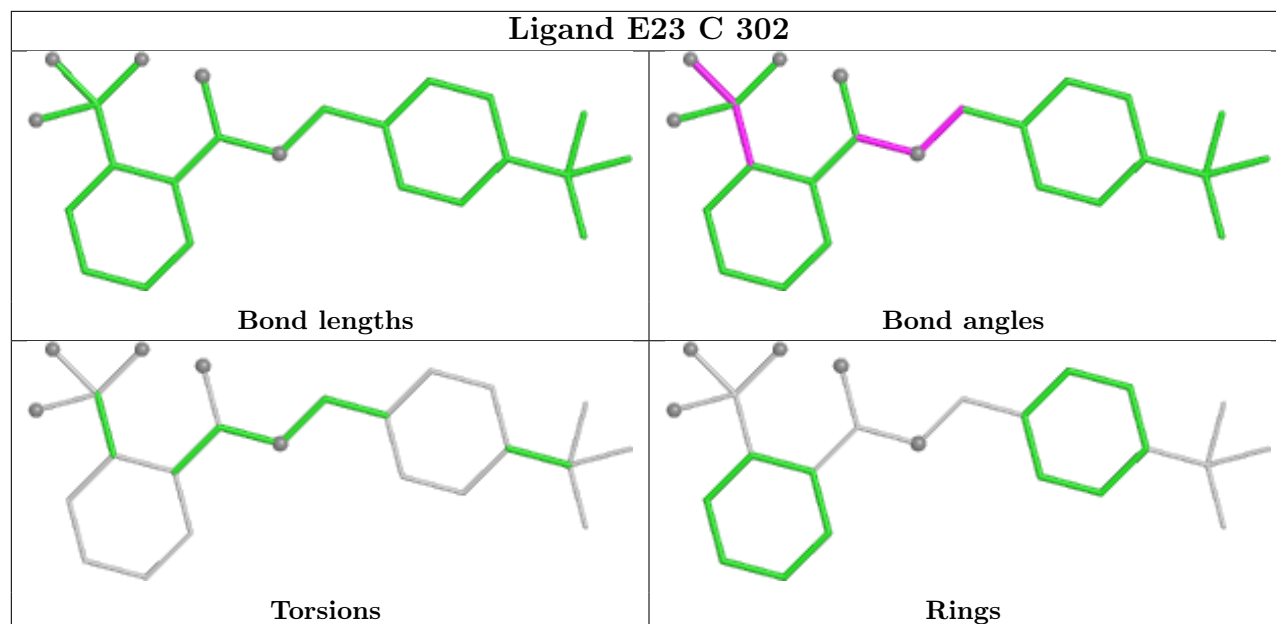
There are no ring outliers.

3 monomers are involved in 17 short contacts:

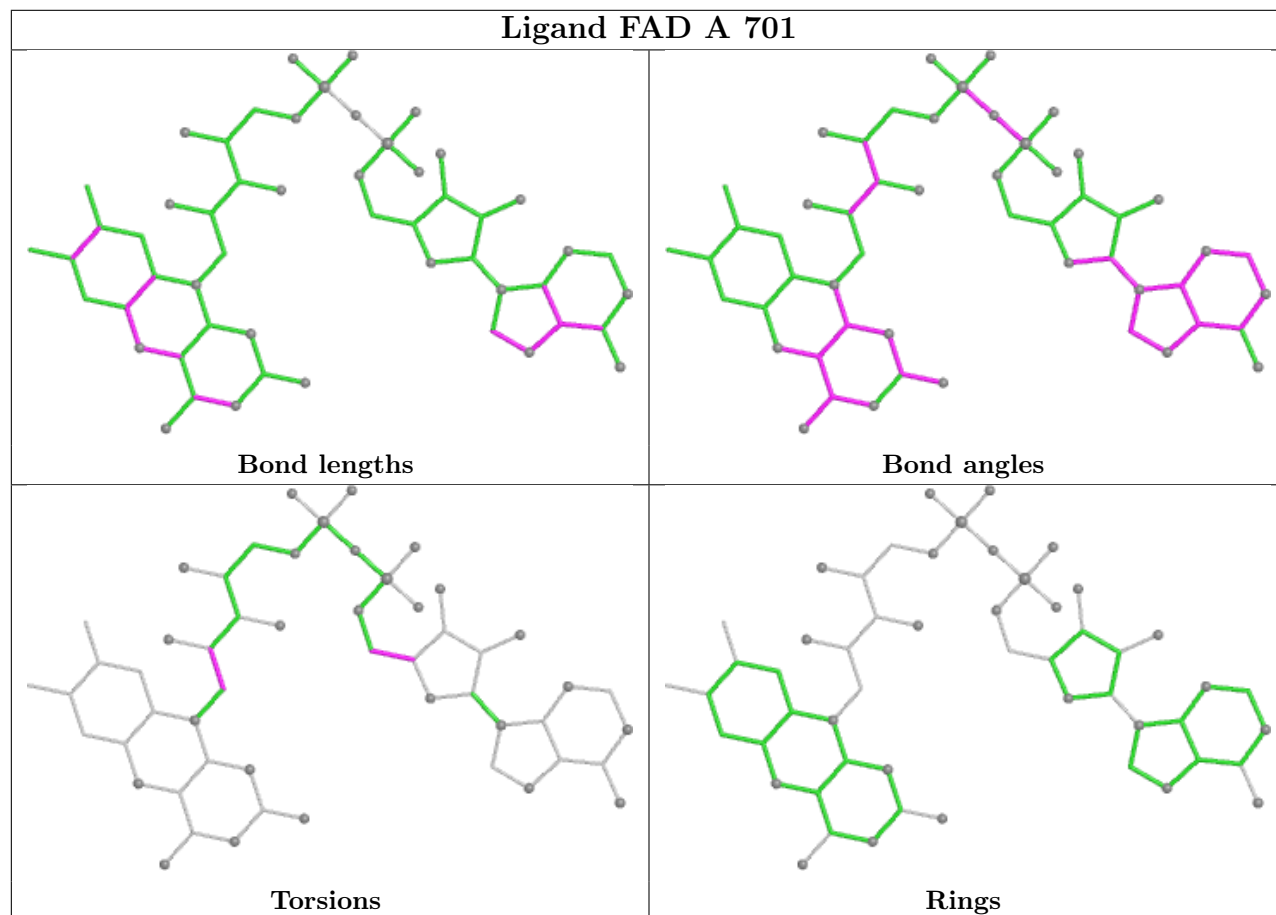
Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	B	303	F3S	3	0
5	A	701	FAD	7	0
9	C	301	HEM	7	0

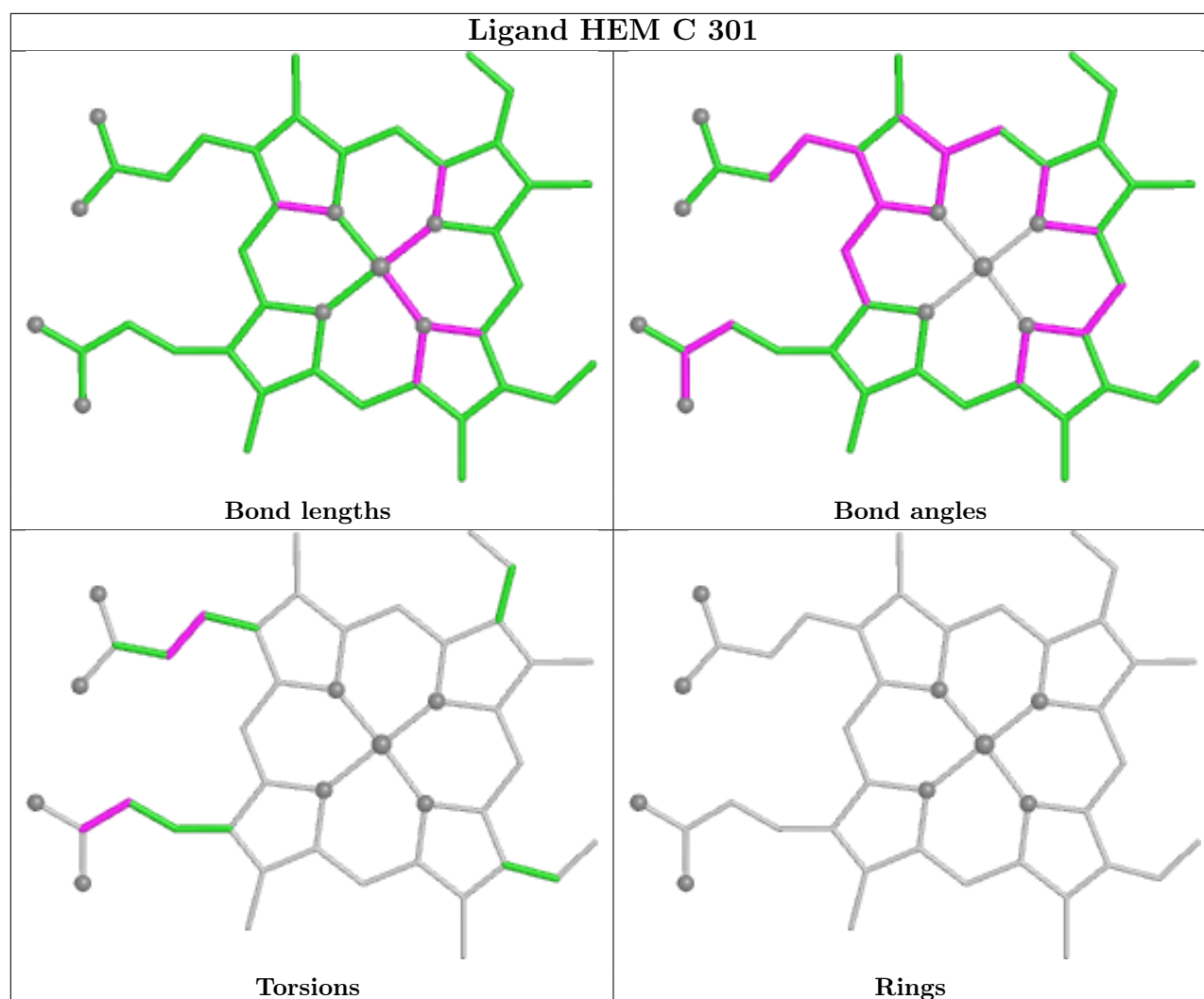
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

Ligand E23 C 302



Ligand FAD A 701





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	613/664 (92%)	-0.25	2 (0%) 90 80	42, 71, 112, 147	0
2	B	239/280 (85%)	-0.38	0 100 100	41, 63, 92, 102	0
3	C	138/169 (81%)	-0.31	1 (0%) 84 68	43, 64, 93, 144	0
4	D	102/159 (64%)	-0.45	0 100 100	45, 61, 86, 93	0
All	All	1092/1272 (85%)	-0.30	3 (0%) 90 80	41, 67, 105, 147	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	82	LEU	2.8
1	A	315	CYS	2.4
1	A	620	ARG	2.2

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](#)

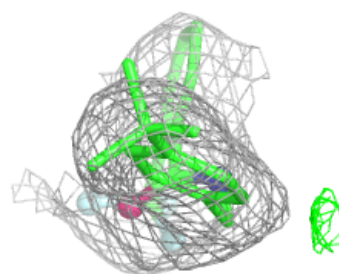
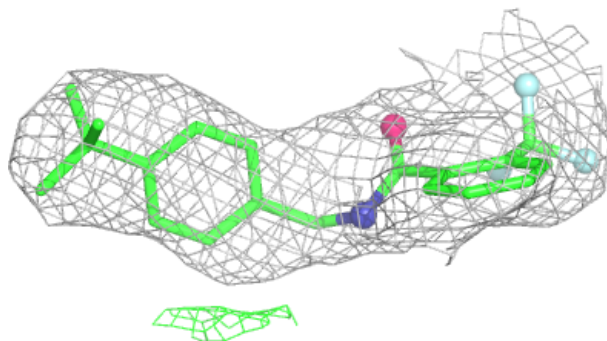
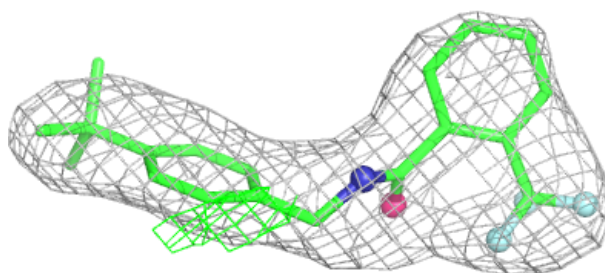
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
10	E23	C	302	24/24	0.95	0.08	55,61,68,70	0
5	FAD	A	701	53/53	0.96	0.07	46,56,75,76	0
9	HEM	C	301	43/43	0.97	0.10	53,60,64,66	0
8	F3S	B	303	7/7	0.98	0.05	42,49,53,54	0
7	SF4	B	302	8/8	0.99	0.03	50,55,57,58	0
6	FES	B	301	4/4	0.99	0.04	58,58,66,66	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.

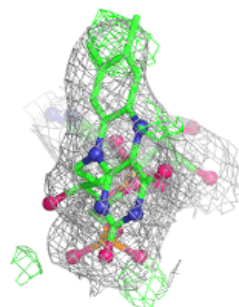
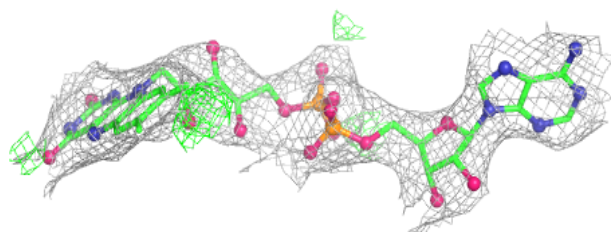
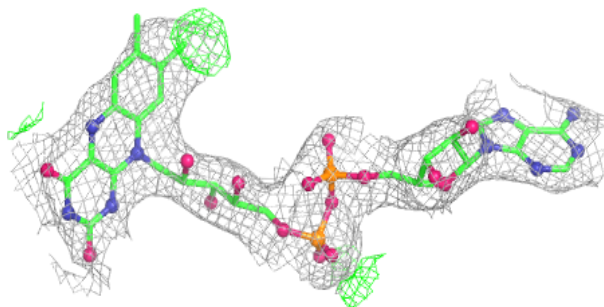
Electron density around E23 C 302:

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



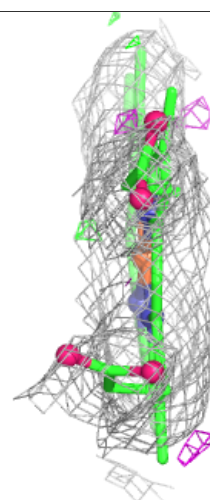
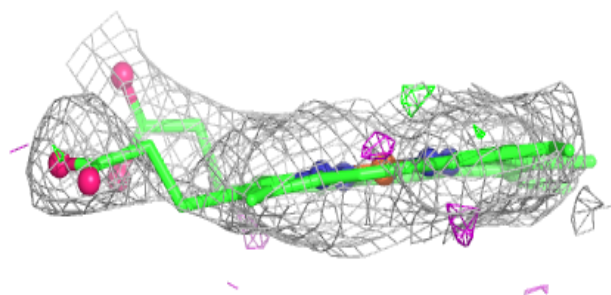
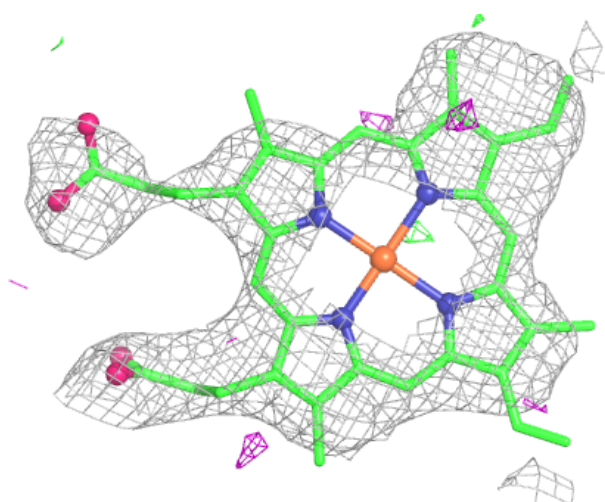
Electron density around FAD A 701:

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



Electron density around HEM C 301:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.