



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 05:55 PM UTC

PDB ID : 1SZE / pdb_00001sze
Title : L230A mutant flavocytochrome b2 with benzoylformate
Authors : Mowat, C.G.; Wehenkel, A.; Green, A.J.; Walkinshaw, M.D.; Reid, G.A.; Chapman, S.K.
Deposited on : 2004-04-05
Resolution : 3.00 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 ⓘ](#)) 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

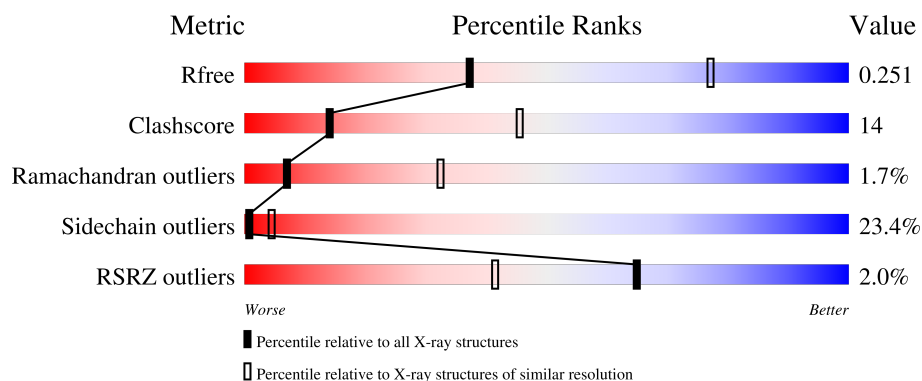
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	511	
1	B	511	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6291 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.

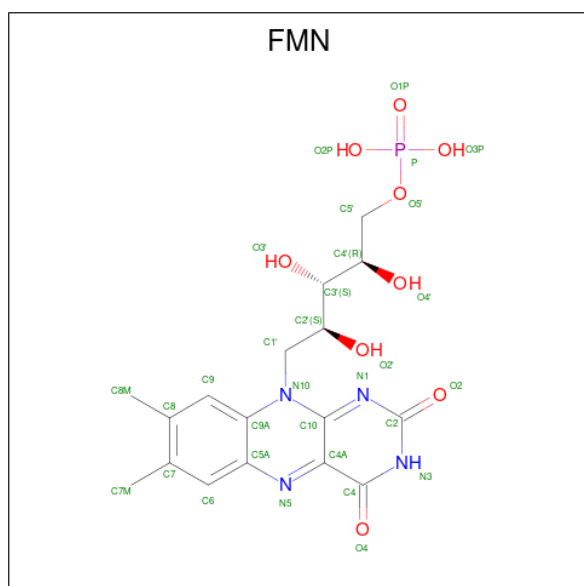
- Molecule 1 is a protein called Cytochrome b2, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	392	Total	C	N	O	S	0	0	0
			3053	1936	521	585	11			
1	B	389	Total	C	N	O	S	0	0	0
			3030	1924	514	581	11			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	230	ALA	LEU	engineered mutation	UNP P00175
B	230	ALA	LEU	engineered mutation	UNP P00175

- Molecule 2 is FLAVIN MONONUCLEOTIDE (CCD ID: FMN) (formula: C₁₇H₂₁N₄O₉P).



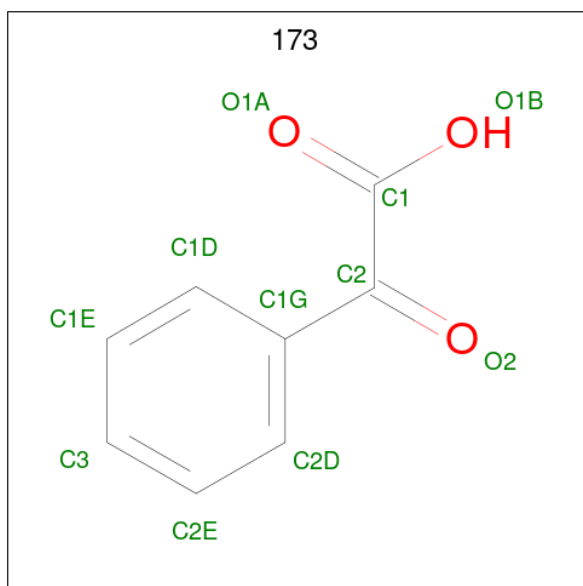
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	P	0	0
			31	17	4	9	1		

- Molecule 3 is BENZOYL-FORMIC ACID (CCD ID: 173) (formula: $C_8H_6O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			11	8	3		
3	B	1	Total	C	O	0	0
			11	8	3		

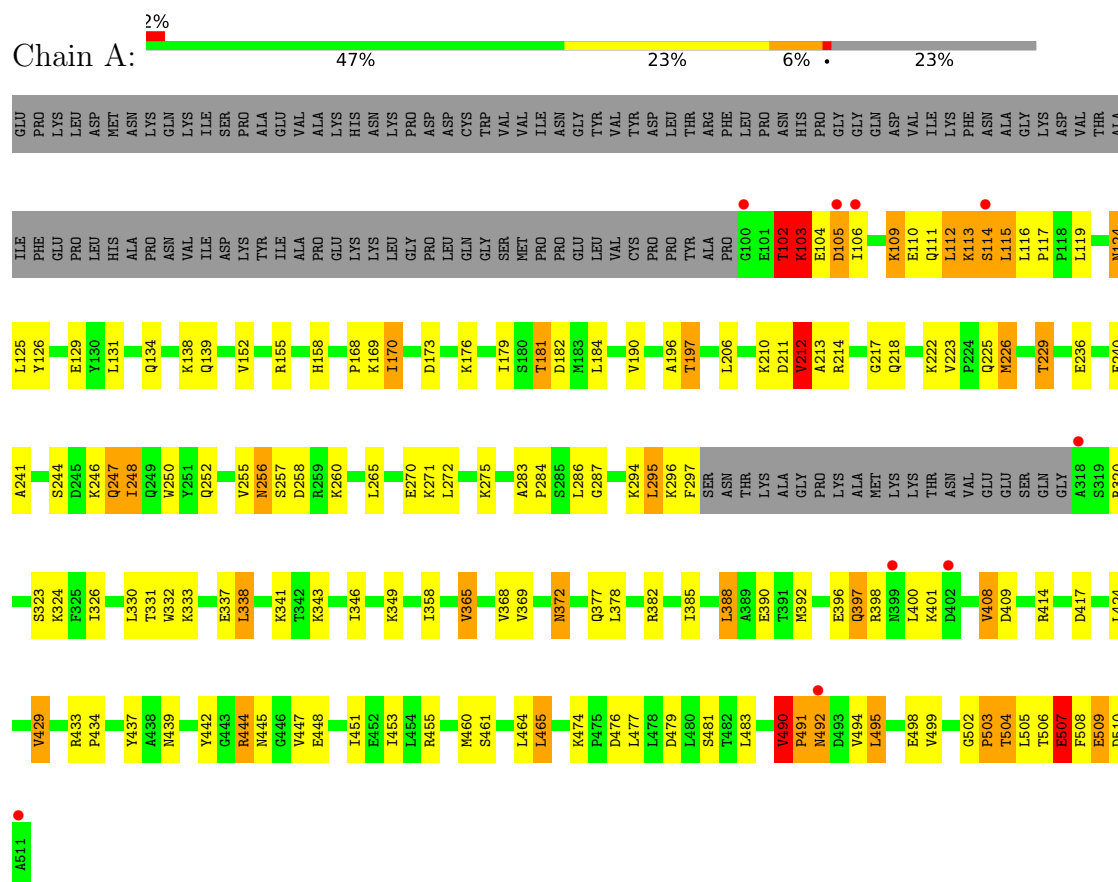
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	69	Total	O	0	0
			69	69		
4	B	55	Total	O	0	0
			55	55		

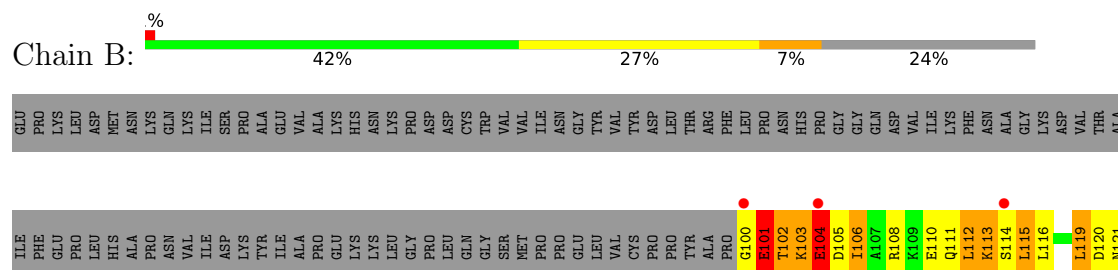
3 Residue-property plots

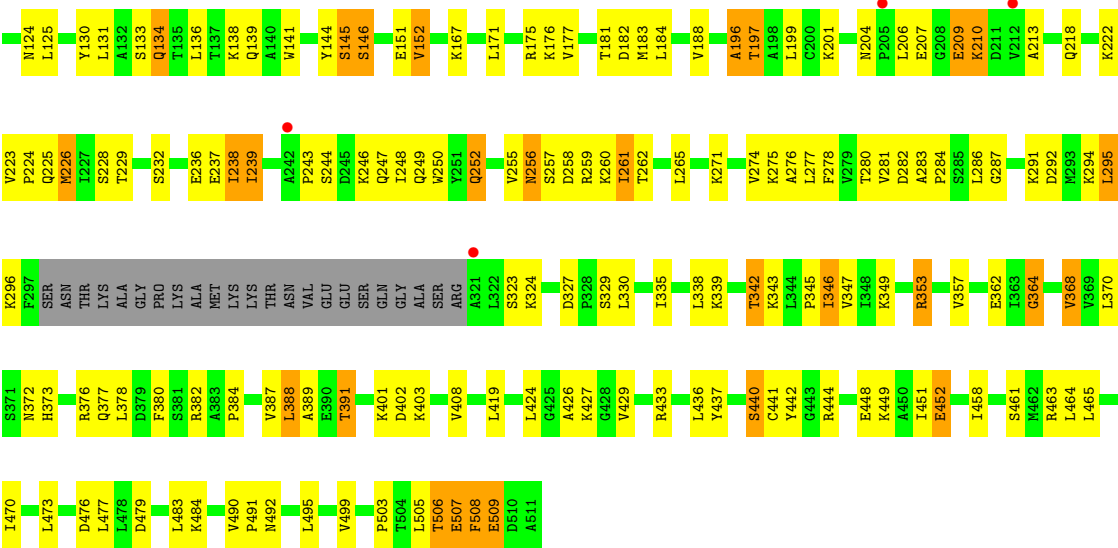
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Cytochrome b2, mitochondrial



• Molecule 1: Cytochrome b2, mitochondrial





4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	163.03Å 163.03Å 112.47Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	24.00 – 3.00 24.00 – 3.00	Depositor EDS
% Data completeness (in resolution range)	90.6 (24.00-3.00) 90.4 (24.00-3.00)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.47 (at 2.99Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.200 , 0.249 0.206 , 0.251	Depositor DCC
R_{free} test set	1577 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	57.5	Xtriage
Anisotropy	0.010	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 42.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.024 for -h,-k,l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	6291	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.77% 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: 173, FMN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.99	3/3102 (0.1%)	1.19	14/4191 (0.3%)
1	B	0.96	2/3079 (0.1%)	1.18	8/4161 (0.2%)
All	All	0.98	5/6181 (0.1%)	1.19	22/8352 (0.3%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	2
All	All	0	4

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	460	MET	SD-CE	6.78	1.96	1.79
1	B	183	MET	SD-CE	-6.30	1.63	1.79
1	B	101	GLU	CA-C	6.26	1.61	1.52
1	A	226	MET	SD-CE	-6.04	1.64	1.79
1	A	490	VAL	CA-CB	5.10	1.60	1.54

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	507	GLU	N-CA-C	10.47	126.74	113.55
1	A	507	GLU	N-CA-C	8.56	124.21	113.43
1	B	509	GLU	N-CA-C	7.60	126.99	110.80
1	A	491	PRO	CA-C-N	-6.79	109.70	122.73

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	491	PRO	C-N-CA	-6.79	109.70	122.73
1	B	357	VAL	N-CA-C	-6.75	104.08	110.42
1	A	115	LEU	N-CA-C	-6.73	104.08	112.90
1	A	492	ASN	N-CA-C	6.52	120.18	109.94
1	B	104	GLU	N-CA-C	-6.41	104.16	114.09
1	A	444	ARG	N-CA-C	6.39	118.33	111.36
1	B	115	LEU	N-CA-C	-6.32	104.26	112.23
1	B	102	THR	N-CA-C	6.22	124.05	110.80
1	A	491	PRO	CA-C-O	-6.13	114.35	121.34
1	A	102	THR	N-CA-C	6.06	120.72	109.56
1	B	106	ILE	N-CA-C	-5.90	106.07	111.67
1	A	509	GLU	N-CA-C	5.80	120.04	111.04
1	A	112	LEU	N-CA-C	-5.74	101.90	111.37
1	A	365	VAL	CB-CA-C	5.58	117.72	111.59
1	B	342	THR	N-CA-C	5.51	117.47	108.76
1	A	212	VAL	N-CA-CB	5.38	117.46	110.57
1	A	212	VAL	N-CA-C	-5.22	105.62	110.53
1	A	116	LEU	N-CA-C	-5.11	103.28	109.57

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	492	ASN	Peptide
1	A	506	THR	Peptide
1	B	104	GLU	Peptide
1	B	506	THR	Peptide

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	3053	0	3113	87	0
1	B	3030	0	3088	99	0
2	A	31	0	19	2	0
2	B	31	0	18	2	0
3	A	11	0	5	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	11	0	5	0	0
4	A	69	0	0	3	0
4	B	55	0	0	4	0
All	All	6291	0	6248	177	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 14.

All (177) 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:256:ASN:HD22	1:A:258:ASP:H	1.07	0.94
1:A:113:LYS:O	1:A:115:LEU:N	2.02	0.91
1:A:218:GLN:HE22	1:A:444:ARG:HD2	1.39	0.88
1:A:331:THR:HB	4:A:5623:HOH:O	1.80	0.80
1:A:211:ASP:HB3	1:A:439:ASN:HD21	1.47	0.79
1:B:197:THR:HG21	1:B:436:LEU:CD1	2.11	0.79
1:A:129:GLU:HG3	1:A:437:TYR:CE2	2.19	0.78
1:B:197:THR:HG21	1:B:436:LEU:HD11	1.64	0.78
1:A:124:ASN:C	1:A:124:ASN:HD22	1.95	0.75
1:A:256:ASN:ND2	1:A:258:ASP:H	1.84	0.75
1:B:105:ASP:HA	1:B:108:ARG:HB2	1.66	0.75
1:B:102:THR:O	1:B:102:THR:HG22	1.87	0.74
1:B:113:LYS:O	1:B:115:LEU:N	2.22	0.73
1:B:339:LYS:NZ	1:B:364:GLY:O	2.22	0.73
1:A:113:LYS:O	1:A:113:LYS:HG3	1.93	0.68
1:A:113:LYS:C	1:A:115:LEU:H	2.00	0.68
1:A:479:ASP:OD2	1:B:382:ARG:HD3	1.94	0.67
1:B:104:GLU:C	1:B:106:ILE:H	2.02	0.66
1:B:507:GLU:O	1:B:508:PHE:HB2	1.96	0.66
1:A:119:LEU:HD21	1:A:445:ASN:O	1.96	0.65
1:A:499:VAL:HG13	1:B:505:LEU:HD11	1.80	0.64
1:B:113:LYS:C	1:B:115:LEU:H	2.06	0.64
1:A:223:VAL:HG21	1:A:451:ILE:HG12	1.79	0.64
1:B:136:LEU:HD21	1:B:440:SER:HB3	1.81	0.63
1:A:495:LEU:HD13	1:B:503:PRO:HB2	1.81	0.62
1:B:108:ARG:O	1:B:112:LEU:HD23	1.99	0.62
1:B:111:GLN:O	1:B:115:LEU:HB2	1.99	0.62
1:A:155:ARG:NH2	1:B:492:ASN:O	2.32	0.61
1:B:256:ASN:HD22	1:B:258:ASP:H	1.49	0.61
1:B:243:PRO:HD2	1:B:247:GLN:HE22	1.65	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:120:ASP:C	1:B:121:ASN:HD22	2.10	0.60
1:B:213:ALA:CA	1:B:225:GLN:HE22	2.15	0.60
1:B:124:ASN:ND2	4:B:9623:HOH:O	2.32	0.60
1:B:119:LEU:HD23	1:B:442:TYR:CD1	2.38	0.59
1:B:349:LYS:NZ	2:B:9570:FMN:O2'	2.35	0.59
1:A:213:ALA:HB2	1:A:225:GLN:HE22	1.67	0.59
1:A:408:VAL:HG12	1:A:429:VAL:HB	1.84	0.58
1:B:197:THR:CG2	1:B:436:LEU:HD11	2.32	0.58
1:A:382:ARG:HD2	4:A:5583:HOH:O	2.03	0.58
1:B:389:ALA:HB2	1:B:424:LEU:HD13	1.86	0.57
1:B:144:TYR:CD2	1:B:436:LEU:HD13	2.40	0.57
1:B:278:PHE:CE2	1:B:347:VAL:HG11	2.40	0.56
1:B:119:LEU:HD23	1:B:442:TYR:CG	2.41	0.56
1:A:113:LYS:C	1:A:115:LEU:N	2.62	0.56
1:A:210:LYS:O	1:A:214:ARG:HG3	2.06	0.56
1:A:331:THR:HG22	1:A:332:TRP:N	2.21	0.55
1:A:129:GLU:HG3	1:A:437:TYR:CD2	2.42	0.55
1:A:173:ASP:OD1	1:B:329:SER:HA	2.05	0.55
1:B:218:GLN:HE22	1:B:444:ARG:HG3	1.72	0.55
1:B:275:LYS:O	1:B:345:PRO:HD2	2.07	0.55
1:A:385:ILE:HD11	1:A:424:LEU:HD12	1.89	0.54
1:B:388:LEU:HD11	1:B:426:ALA:HB2	1.89	0.53
1:B:448:GLU:O	1:B:452:GLU:HG2	2.09	0.53
1:B:223:VAL:HG21	1:B:451:ILE:HG12	1.91	0.53
1:B:213:ALA:HB2	1:B:225:GLN:HE22	1.74	0.52
1:B:327:ASP:OD1	1:B:329:SER:OG	2.27	0.52
1:A:155:ARG:CZ	1:B:491:PRO:HB2	2.39	0.52
1:A:226:MET:HE1	1:A:349:LYS:HE3	1.91	0.52
1:B:144:TYR:CG	1:B:436:LEU:HD13	2.45	0.52
1:A:102:THR:C	1:A:104:GLU:N	2.67	0.52
1:B:209:GLU:HG3	1:B:238:ILE:HD11	1.92	0.52
1:B:389:ALA:HB2	1:B:424:LEU:CD1	2.39	0.52
1:B:207:GLU:O	1:B:210:LYS:HB2	2.10	0.52
1:A:102:THR:C	1:A:104:GLU:H	2.16	0.52
1:A:119:LEU:HD13	1:A:442:TYR:CD1	2.45	0.51
1:A:349:LYS:NZ	2:A:5570:FMN:N1	2.58	0.51
1:B:287:GLY:H	1:B:377:GLN:HE22	1.58	0.51
1:A:499:VAL:HG13	1:B:505:LEU:CD1	2.40	0.51
1:A:372:ASN:C	1:A:372:ASN:HD22	2.18	0.51
1:B:104:GLU:C	1:B:106:ILE:N	2.68	0.51
1:B:196:ALA:HB2	1:B:226:MET:HG2	1.93	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:213:ALA:HA	1:B:225:GLN:HE22	1.76	0.50
1:A:124:ASN:C	1:A:124:ASN:ND2	2.63	0.50
1:B:152:VAL:HG21	1:B:380:PHE:CE1	2.47	0.50
1:B:197:THR:HG21	1:B:436:LEU:CG	2.42	0.50
1:A:181:THR:OG1	1:A:182:ASP:N	2.45	0.49
1:A:283:ALA:N	1:A:284:PRO:CD	2.76	0.49
1:A:490:VAL:HG23	1:A:491:PRO:HD2	1.95	0.49
1:A:196:ALA:H	1:A:226:MET:HE2	1.77	0.49
1:A:256:ASN:HD22	1:A:257:SER:N	2.11	0.48
1:A:117:PRO:HD2	1:A:442:TYR:OH	2.13	0.48
1:A:326:ILE:HD11	3:A:5580:173:H1E	1.95	0.48
1:A:349:LYS:HG3	1:A:369:VAL:HG21	1.94	0.48
1:B:113:LYS:C	1:B:115:LEU:N	2.71	0.48
1:A:504:THR:CG2	4:A:5581:HOH:O	2.61	0.48
1:B:347:VAL:HG13	1:B:368:VAL:N	2.29	0.48
1:A:170:ILE:HG12	1:B:281:VAL:HG23	1.94	0.48
1:B:283:ALA:N	1:B:284:PRO:CD	2.77	0.48
1:B:102:THR:O	1:B:102:THR:CG2	2.57	0.48
1:B:138:LYS:HB3	1:B:295:LEU:CD1	2.44	0.48
1:A:236:GLU:HG3	1:A:272:LEU:HD21	1.96	0.48
1:B:479:ASP:C	1:B:479:ASP:OD1	2.56	0.48
1:A:505:LEU:HD22	1:B:130:TYR:HB2	1.96	0.47
1:B:213:ALA:CB	1:B:225:GLN:HE22	2.26	0.47
1:A:217:GLY:HA3	1:A:247:GLN:OE1	2.15	0.47
1:A:287:GLY:H	1:A:377:GLN:HE22	1.62	0.47
1:A:179:ILE:HD11	1:A:455:ARG:HG3	1.95	0.47
1:B:121:ASN:HD22	1:B:121:ASN:N	2.11	0.47
1:B:141:TRP:O	1:B:145:SER:OG	2.31	0.47
1:B:465:LEU:HD13	1:B:477:LEU:HD23	1.97	0.47
1:A:507:GLU:O	1:A:508:PHE:HB2	2.15	0.47
1:B:226:MET:CE	1:B:349:LYS:HD2	2.44	0.47
1:B:282:ASP:O	1:B:377:GLN:HG3	2.15	0.47
1:B:209:GLU:OE2	1:B:232:SER:HB2	2.15	0.47
1:B:295:LEU:HD23	1:B:296:LYS:N	2.30	0.47
1:B:470:ILE:HA	1:B:473:LEU:HD12	1.97	0.47
1:A:109:LYS:HA	1:A:112:LEU:HD13	1.96	0.46
1:A:168:PRO:O	1:B:353:ARG:HD2	2.15	0.46
1:A:248:ILE:HD11	1:A:250:TRP:CE2	2.50	0.46
1:A:409:ASP:OD1	1:A:409:ASP:C	2.58	0.46
1:B:507:GLU:O	1:B:508:PHE:CB	2.62	0.46
1:A:126:TYR:OH	1:A:158:HIS:CE1	2.69	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:335:ILE:O	1:B:338:LEU:N	2.49	0.46
1:A:213:ALA:CB	1:A:225:GLN:HE22	2.28	0.45
1:A:287:GLY:H	1:A:377:GLN:NE2	2.15	0.45
1:B:252:GLN:HA	1:B:278:PHE:O	2.16	0.45
1:B:258:ASP:HB3	1:B:261:ILE:HG13	1.99	0.45
1:A:211:ASP:HB3	1:A:439:ASN:ND2	2.24	0.45
1:A:337:GLU:OE1	1:A:341:LYS:NZ	2.49	0.45
1:A:433:ARG:N	1:A:434:PRO:CD	2.79	0.45
1:A:388:LEU:HD22	1:A:392:MET:HG2	1.98	0.45
1:A:502:GLY:C	1:A:503:PRO:O	2.58	0.44
1:A:102:THR:O	1:A:103:LYS:C	2.60	0.44
1:A:461:SER:O	1:A:465:LEU:HB2	2.18	0.44
1:B:171:LEU:HD23	1:B:171:LEU:HA	1.92	0.44
1:A:229:THR:H	1:A:252:GLN:NE2	2.16	0.44
1:A:414:ARG:O	1:A:417:ASP:HB2	2.18	0.44
1:B:338:LEU:HG	1:B:346:ILE:HD11	2.00	0.44
1:A:105:ASP:O	1:A:109:LYS:HB2	2.18	0.44
1:B:100:GLY:O	1:B:138:LYS:HD2	2.18	0.44
1:B:213:ALA:HA	1:B:225:GLN:NE2	2.33	0.44
1:B:495:LEU:O	1:B:499:VAL:HG22	2.18	0.44
1:A:124:ASN:HD22	1:A:126:TYR:N	2.17	0.43
1:B:108:ARG:HH22	1:B:138:LYS:N	2.16	0.43
1:B:372:ASN:ND2	1:B:384:PRO:HD3	2.34	0.43
1:A:256:ASN:HD22	1:A:258:ASP:N	1.92	0.43
1:A:197:THR:O	1:A:197:THR:CG2	2.67	0.43
1:A:196:ALA:CB	1:A:226:MET:HE2	2.49	0.43
1:A:210:LYS:HG2	1:A:241:ALA:HB2	2.01	0.43
1:B:209:GLU:CG	1:B:238:ILE:HD11	2.49	0.43
1:B:387:VAL:O	1:B:391:THR:HG23	2.19	0.43
2:B:9570:FMN:H9	2:B:9570:FMN:H1'2	1.82	0.43
1:B:250:TRP:CD1	1:B:276:ALA:HB3	2.54	0.42
1:A:170:ILE:HD12	1:A:170:ILE:HA	1.86	0.42
1:A:244:SER:HB2	1:A:247:GLN:HB3	2.01	0.42
1:B:133:SER:OG	1:B:134:GLN:NE2	2.52	0.42
1:A:252:GLN:NE2	2:A:5570:FMN:HN3	2.16	0.42
1:B:226:MET:HE1	1:B:349:LYS:HD2	2.02	0.42
1:B:101:GLU:H	1:B:101:GLU:HG2	1.60	0.42
1:B:238:ILE:HG22	1:B:239:ILE:N	2.35	0.42
1:B:181:THR:HG21	4:B:9606:HOH:O	2.18	0.42
1:B:151:GLU:OE2	1:B:291:LYS:NZ	2.53	0.42
1:B:201:LYS:HA	1:B:204:ASN:O	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:252:GLN:NE2	1:B:280:THR:OG1	2.53	0.41
1:B:449:LYS:HA	1:B:452:GLU:CG	2.50	0.41
1:A:170:ILE:HB	4:B:9594:HOH:O	2.20	0.41
1:B:419:LEU:HD21	1:B:458:ILE:HG23	2.02	0.41
1:B:387:VAL:O	1:B:388:LEU:C	2.63	0.41
1:B:373:HIS:O	1:B:376:ARG:HB2	2.20	0.41
1:A:111:GLN:O	1:A:112:LEU:C	2.62	0.41
1:A:448:GLU:HA	1:A:451:ILE:HD12	2.03	0.41
1:B:108:ARG:NH1	4:B:9589:HOH:O	2.46	0.41
1:B:188:VAL:HG11	1:B:224:PRO:HG3	2.03	0.41
1:B:433:ARG:HB3	1:B:437:TYR:CE2	2.56	0.41
1:A:212:VAL:HA	1:A:447:VAL:HG21	2.02	0.41
1:B:449:LYS:HA	1:B:452:GLU:HG3	2.03	0.41
1:A:102:THR:O	1:A:104:GLU:N	2.54	0.40
1:A:111:GLN:C	1:A:113:LYS:N	2.76	0.40
1:A:331:THR:CG2	1:A:332:TRP:N	2.84	0.40
1:A:214:ARG:O	1:A:218:GLN:HB3	2.20	0.40
1:A:337:GLU:O	1:A:341:LYS:HD3	2.21	0.40
1:B:197:THR:HG21	1:B:436:LEU:HG	2.02	0.40
1:A:338:LEU:HD13	1:A:346:ILE:HD13	2.04	0.40
1:B:102:THR:O	1:B:103:LYS:C	2.63	0.40
1:B:461:SER:O	1:B:465:LEU:HB2	2.22	0.40
1:A:295:LEU:O	1:A:296:LYS:C	2.64	0.40
1:A:338:LEU:HD13	1:A:346:ILE:CD1	2.52	0.40

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	388/511 (76%)	355 (92%)	26 (7%)	7 (2%)	6 31

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	385/511 (75%)	334 (87%)	45 (12%)	6 (2%)	7	34
All	All	773/1022 (76%)	689 (89%)	71 (9%)	13 (2%)	7	32

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	103	LYS
1	A	114	SER
1	A	397	GLN
1	B	114	SER
1	B	146	SER
1	A	105	ASP
1	A	138	LYS
1	B	362	GLU
1	B	364	GLY
1	B	508	PHE
1	A	510	ASP
1	B	196	ALA
1	A	503	PRO

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	336/439 (76%)	261 (78%)	75 (22%)	1	5
1	B	334/439 (76%)	252 (75%)	82 (25%)	1	4
All	All	670/878 (76%)	513 (77%)	157 (23%)	1	4

All (157) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	102	THR
1	A	103	LYS
1	A	106	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	109	LYS
1	A	110	GLU
1	A	113	LYS
1	A	114	SER
1	A	124	ASN
1	A	125	LEU
1	A	131	LEU
1	A	134	GLN
1	A	139	GLN
1	A	152	VAL
1	A	169	LYS
1	A	170	ILE
1	A	176	LYS
1	A	181	THR
1	A	184	LEU
1	A	190	VAL
1	A	197	THR
1	A	206	LEU
1	A	212	VAL
1	A	222	LYS
1	A	229	THR
1	A	240	GLU
1	A	246	LYS
1	A	247	GLN
1	A	248	ILE
1	A	255	VAL
1	A	256	ASN
1	A	260	LYS
1	A	265	LEU
1	A	270	GLU
1	A	271	LYS
1	A	275	LYS
1	A	286	LEU
1	A	294	LYS
1	A	295	LEU
1	A	297	PHE
1	A	320	ARG
1	A	323	SER
1	A	324	LYS
1	A	330	LEU
1	A	333	LYS
1	A	338	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	343	LYS
1	A	358	ILE
1	A	365	VAL
1	A	368	VAL
1	A	372	ASN
1	A	378	LEU
1	A	388	LEU
1	A	390	GLU
1	A	396	GLU
1	A	397	GLN
1	A	398	ARG
1	A	400	LEU
1	A	401	LYS
1	A	408	VAL
1	A	429	VAL
1	A	453	ILE
1	A	464	LEU
1	A	465	LEU
1	A	474	LYS
1	A	476	ASP
1	A	477	LEU
1	A	481	SER
1	A	483	LEU
1	A	490	VAL
1	A	494	VAL
1	A	495	LEU
1	A	498	GLU
1	A	504	THR
1	A	507	GLU
1	A	509	GLU
1	B	101	GLU
1	B	103	LYS
1	B	110	GLU
1	B	112	LEU
1	B	113	LYS
1	B	116	LEU
1	B	119	LEU
1	B	125	LEU
1	B	131	LEU
1	B	134	GLN
1	B	139	GLN
1	B	145	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	146	SER
1	B	152	VAL
1	B	167	LYS
1	B	175	ARG
1	B	176	LYS
1	B	177	VAL
1	B	182	ASP
1	B	184	LEU
1	B	197	THR
1	B	199	LEU
1	B	206	LEU
1	B	209	GLU
1	B	210	LYS
1	B	222	LYS
1	B	226	MET
1	B	228	SER
1	B	229	THR
1	B	236	GLU
1	B	237	GLU
1	B	238	ILE
1	B	239	ILE
1	B	244	SER
1	B	246	LYS
1	B	248	ILE
1	B	249	GLN
1	B	252	GLN
1	B	255	VAL
1	B	256	ASN
1	B	257	SER
1	B	259	ARG
1	B	260	LYS
1	B	261	ILE
1	B	262	THR
1	B	265	LEU
1	B	271	LYS
1	B	274	VAL
1	B	277	LEU
1	B	286	LEU
1	B	292	ASP
1	B	294	LYS
1	B	295	LEU
1	B	323	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	324	LYS
1	B	330	LEU
1	B	342	THR
1	B	343	LYS
1	B	346	ILE
1	B	353	ARG
1	B	368	VAL
1	B	370	LEU
1	B	378	LEU
1	B	388	LEU
1	B	391	THR
1	B	401	LYS
1	B	402	ASP
1	B	403	LYS
1	B	408	VAL
1	B	427	LYS
1	B	429	VAL
1	B	440	SER
1	B	441	CYS
1	B	452	GLU
1	B	463	ARG
1	B	464	LEU
1	B	476	ASP
1	B	483	LEU
1	B	484	LYS
1	B	490	VAL
1	B	506	THR
1	B	509	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	121	ASN
1	A	124	ASN
1	A	134	GLN
1	A	139	GLN
1	A	157	ASN
1	A	158	HIS
1	A	159	ASN
1	A	218	GLN
1	A	225	GLN
1	A	252	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	256	ASN
1	A	372	ASN
1	A	377	GLN
1	A	439	ASN
1	B	121	ASN
1	B	124	ASN
1	B	134	GLN
1	B	139	GLN
1	B	154	HIS
1	B	162	HIS
1	B	204	ASN
1	B	218	GLN
1	B	225	GLN
1	B	247	GLN
1	B	249	GLN
1	B	252	GLN
1	B	256	ASN
1	B	268	ASN
1	B	377	GLN
1	B	439	ASN
1	B	497	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The

Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	173	B	9580	-	11,11,11	1.48	2 (18%)	14,14,14	2.24	6 (42%)
2	FMN	B	9570	-	33,33,33	1.24	2 (6%)	48,50,50	2.30	19 (39%)
2	FMN	A	5570	-	33,33,33	1.16	2 (6%)	48,50,50	1.84	16 (33%)
3	173	A	5580	-	11,11,11	1.71	3 (27%)	14,14,14	2.04	6 (42%)

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	173	B	9580	-	-	1/8/8/8	0/1/1/1
2	FMN	B	9570	-	-	5/18/18/18	0/3/3/3
2	FMN	A	5570	-	-	4/18/18/18	0/3/3/3
3	173	A	5580	-	-	1/8/8/8	0/1/1/1

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	5580	173	C1G-C2	-4.03	1.41	1.49
2	A	5570	FMN	C1'-C2'	-3.32	1.48	1.52
2	B	9570	FMN	C9A-N10	-3.09	1.35	1.41
3	B	9580	173	C1G-C2	-2.61	1.43	1.49
2	A	5570	FMN	C6-C7	-2.41	1.36	1.39
3	A	5580	173	C1-C2	-2.39	1.52	1.54
2	B	9570	FMN	C4-N3	-2.31	1.34	1.38
3	A	5580	173	O1B-C1	-2.09	1.24	1.30
3	B	9580	173	O1A-C1	2.02	1.27	1.22

All (47) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	9580	173	C1G-C2-C1	4.72	126.45	118.91
2	B	9570	FMN	O3'-C3'-C2'	-4.53	98.63	108.93
2	B	9570	FMN	O3'-C3'-C4'	4.22	118.51	108.93
2	B	9570	FMN	O2'-C2'-C3'	4.17	119.01	109.25

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	5580	173	C1G-C2-C1	4.08	125.43	118.91
2	B	9570	FMN	C4-C4A-N5	3.98	123.71	118.21
2	B	9570	FMN	C6-C5A-N5	3.73	124.63	118.44
2	B	9570	FMN	C4'-C3'-C2'	3.72	119.75	113.57
2	B	9570	FMN	O2-C2-N1	3.59	127.76	121.80
2	A	5570	FMN	C5'-C4'-C3'	-3.55	105.51	112.22
2	B	9570	FMN	O2P-P-O5'	-3.52	97.50	106.67
2	A	5570	FMN	C4'-C3'-C2'	3.48	119.36	113.57
2	B	9570	FMN	O4'-C4'-C5'	3.47	117.65	109.99
2	B	9570	FMN	C7M-C7-C6	3.43	125.62	119.57
2	A	5570	FMN	O2'-C2'-C3'	3.42	117.25	109.25
2	B	9570	FMN	C10-N1-C2	3.42	124.25	116.85
3	B	9580	173	O1B-C1-C2	3.32	122.25	112.94
2	B	9570	FMN	C9A-C5A-N5	-3.30	118.95	122.45
3	B	9580	173	C1E-C1D-C1G	3.23	123.54	120.36
2	A	5570	FMN	C8M-C8-C9	-3.10	114.11	119.57
2	A	5570	FMN	O3'-C3'-C4'	3.08	115.92	108.93
2	A	5570	FMN	O2-C2-N1	3.06	126.88	121.80
2	B	9570	FMN	C5'-C4'-C3'	-3.05	106.46	112.22
2	A	5570	FMN	C1'-C2'-C3'	2.87	117.45	109.66
2	A	5570	FMN	C6-C7-C8	-2.87	115.48	119.69
2	A	5570	FMN	C9A-C5A-N5	-2.86	119.42	122.45
3	B	9580	173	C1D-C1G-C2D	-2.83	114.97	118.57
2	A	5570	FMN	C9-C9A-N10	2.82	125.65	121.85
2	B	9570	FMN	O2'-C2'-C1'	2.75	121.52	110.20
3	A	5580	173	C1E-C1D-C1G	2.64	122.96	120.36
2	B	9570	FMN	C7M-C7-C8	-2.63	115.39	120.76
3	A	5580	173	O1B-C1-C2	2.58	120.18	112.94
2	A	5570	FMN	C10-N1-C2	2.58	122.43	116.85
3	A	5580	173	C1D-C1G-C2D	-2.53	115.35	118.57
2	A	5570	FMN	O4'-C4'-C5'	2.40	115.29	109.99
2	B	9570	FMN	C6-C7-C8	-2.36	116.22	119.69
2	B	9570	FMN	C9A-N10-C10	2.34	124.32	120.75
3	A	5580	173	C2D-C1G-C2	2.33	125.64	120.42
3	B	9580	173	C2D-C1G-C2	2.32	125.61	120.42
2	B	9570	FMN	N3-C2-N1	-2.29	114.64	119.50
2	A	5570	FMN	O3'-C3'-C2'	-2.16	104.03	108.93
3	B	9580	173	C2E-C2D-C1G	2.15	122.48	120.36
2	B	9570	FMN	C5A-C6-C7	2.12	124.74	120.83
2	A	5570	FMN	O3P-P-O1P	2.09	118.99	110.83
2	A	5570	FMN	C5A-C6-C7	2.07	124.65	120.83
2	A	5570	FMN	C9-C9A-C5A	-2.06	116.39	120.03

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	5580	173	C2E-C2D-C1G	2.06	122.39	120.36

There are no chirality outliers.

All (11) torsion outliers are listed below:

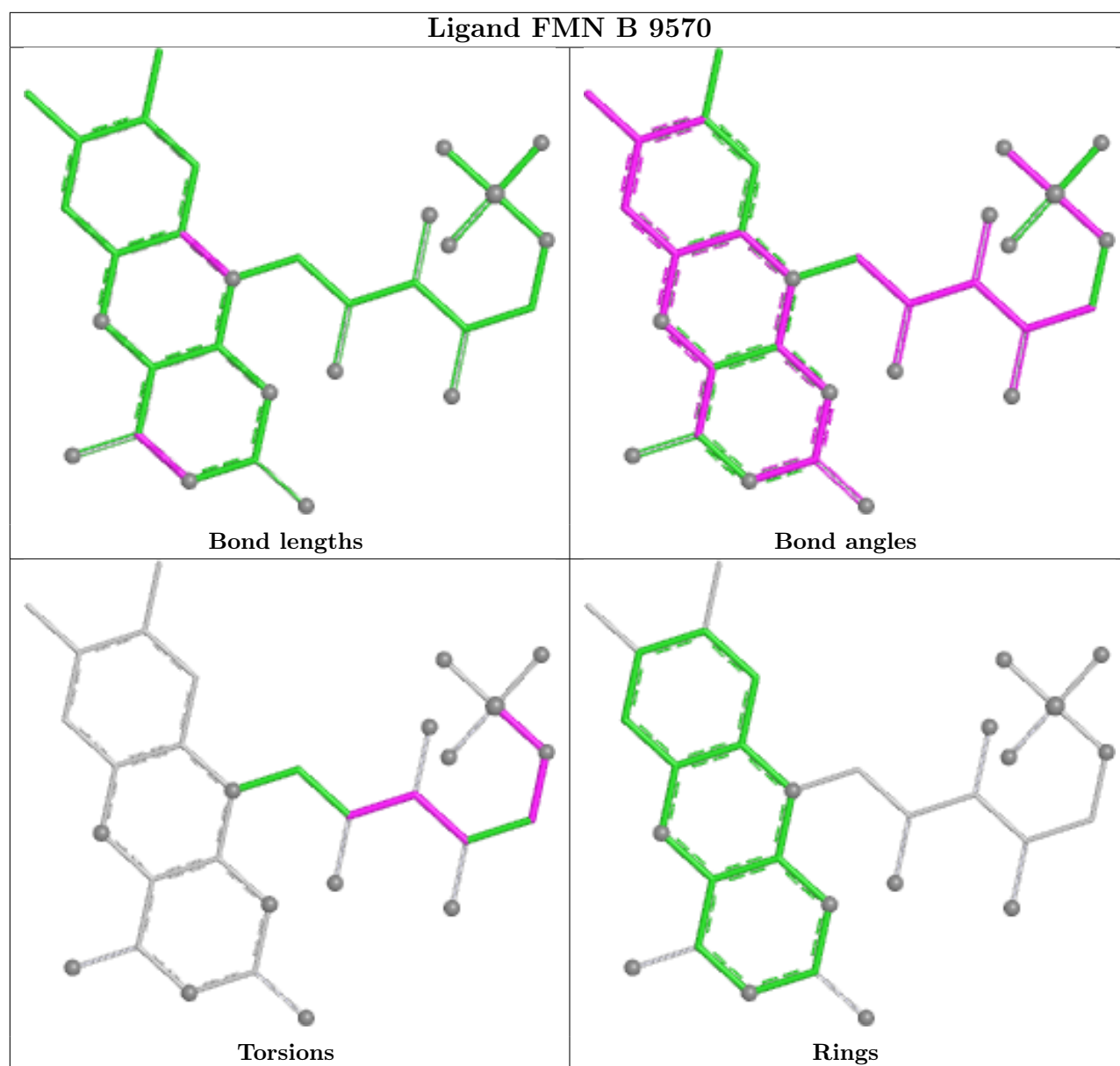
Mol	Chain	Res	Type	Atoms
2	A	5570	FMN	C5'-O5'-P-O1P
2	A	5570	FMN	C5'-O5'-P-O3P
2	A	5570	FMN	O2'-C2'-C3'-C4'
2	A	5570	FMN	C4'-C5'-O5'-P
2	B	9570	FMN	C4'-C5'-O5'-P
2	B	9570	FMN	O2'-C2'-C3'-C4'
3	A	5580	173	O1A-C1-C2-O2
3	B	9580	173	O1A-C1-C2-O2
2	B	9570	FMN	C5'-O5'-P-O3P
2	B	9570	FMN	C2'-C3'-C4'-O4'
2	B	9570	FMN	O3'-C3'-C4'-O4'

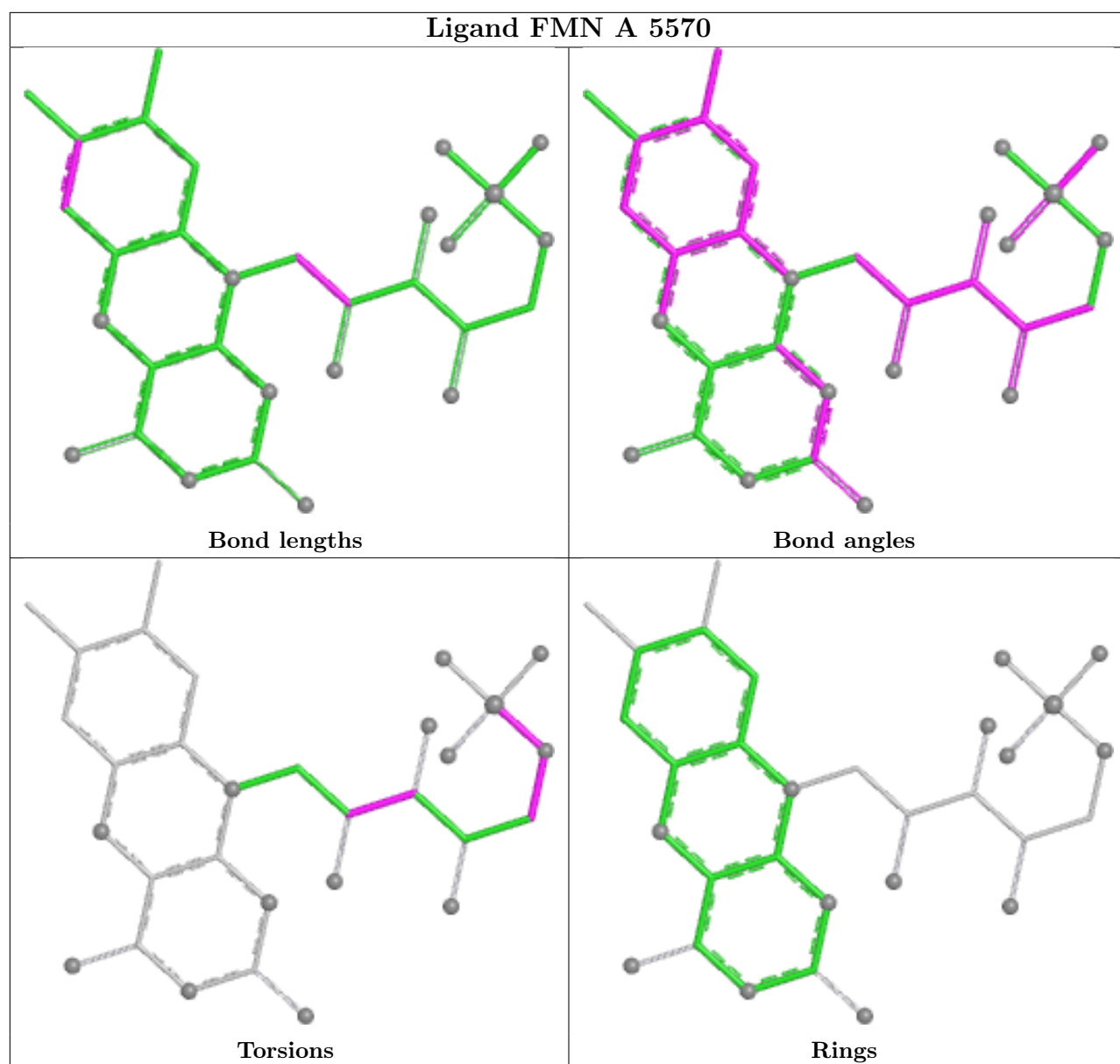
There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	9570	FMN	2	0
2	A	5570	FMN	2	0
3	A	5580	173	1	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	392/511 (76%)	-0.42	9 (2%) 61 38	24, 43, 75, 88	0
1	B	389/511 (76%)	-0.09	7 (1%) 67 44	30, 54, 85, 89	0
All	All	781/1022 (76%)	-0.25	16 (2%) 65 41	24, 47, 83, 89	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	114	SER	5.5
1	A	114	SER	4.6
1	A	492	ASN	3.4
1	B	100	GLY	3.2
1	B	205	PRO	2.9
1	A	318	ALA	2.8
1	A	105	ASP	2.8
1	A	100	GLY	2.6
1	B	212	VAL	2.5
1	A	511	ALA	2.4
1	B	242	ALA	2.4
1	A	106	ILE	2.2
1	A	399	ASN	2.2
1	B	321	ALA	2.2
1	B	104	GLU	2.1
1	A	402	ASP	2.0

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](#)

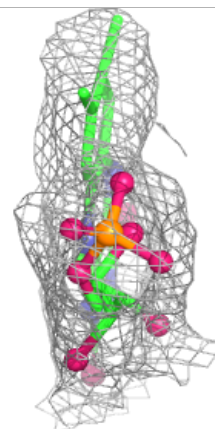
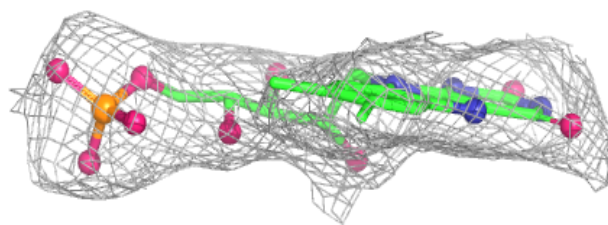
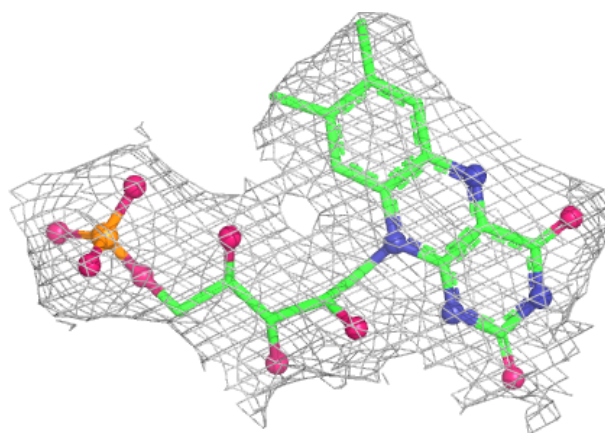
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
3	173	B	9580	11/11	0.91	0.12	56,64,71,72	0
3	173	A	5580	11/11	0.92	0.13	57,62,64,65	0
2	FMN	A	5570	31/31	0.98	0.05	18,27,32,33	0
2	FMN	B	9570	31/31	0.98	0.06	34,40,43,45	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.

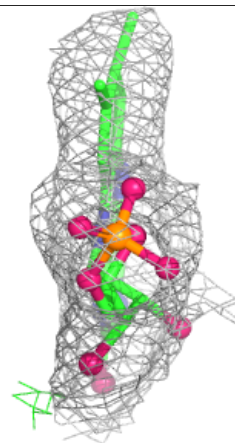
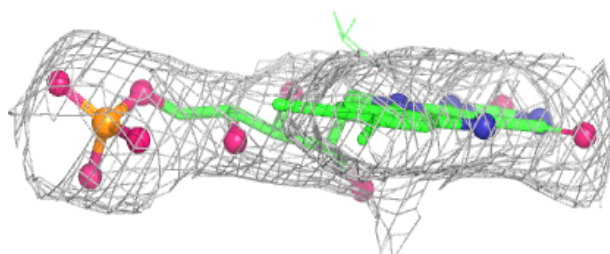
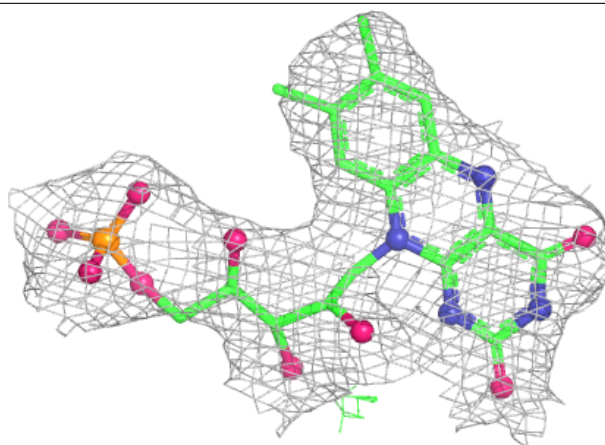
Electron density around FMN A 5570:

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 B 9570:

$2mF_o-DF_c$ (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.