



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 6, 2020 – 11:50 pm BST

PDB ID : 3L9W
Title : KefC C-terminal domain in complex with KefF and GSH
Authors : Roosild, T.P.
Deposited on : 2010-01-05
Resolution : 1.75 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 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

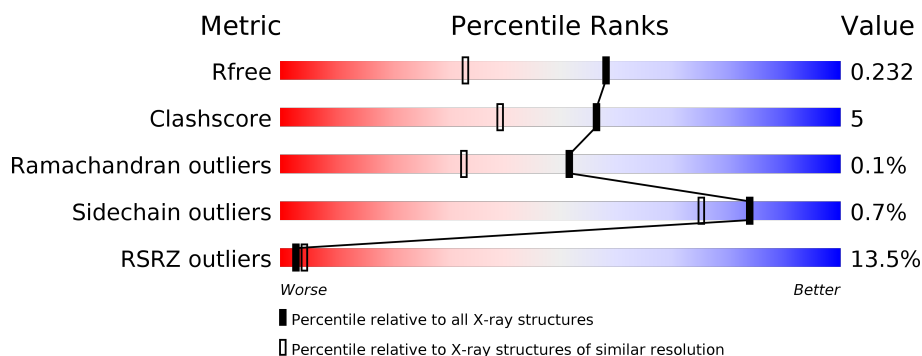
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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	2340 (1.76-1.76)
Clashscore	141614	2466 (1.76-1.76)
Ramachandran outliers	138981	2437 (1.76-1.76)
Sidechain outliers	138945	2437 (1.76-1.76)
RSRZ outliers	127900	2298 (1.76-1.76)

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	413	<div> <div>12%</div> <div> <div></div> <div>73%</div> <div>9%</div> <div>18%</div> </div> </div>
1	B	413	<div> <div>11%</div> <div> <div></div> <div>75%</div> <div>11%</div> <div>14%</div> </div> </div>

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 5981 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 Glutathione-regulated potassium-efflux system protein kefC, linker, ancillary protein kefF.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	338	Total	C	N	O	S	0	0	0
			2707	1732	480	480	15			
1	B	357	Total	C	N	O	S	0	0	0
			2853	1820	508	509	16			

There are 34 discrepancies between the modelled and reference sequences:

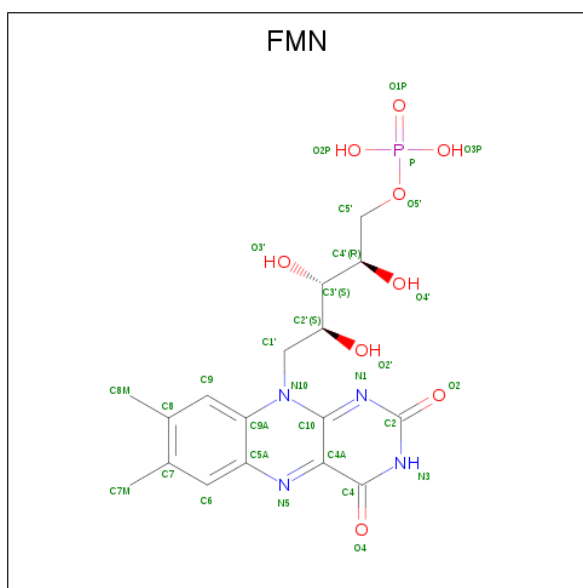
Chain	Residue	Modelled	Actual	Comment	Reference
A	396	GLY	-	EXPRESSION TAG	UNP P03819
A	397	SER	-	EXPRESSION TAG	UNP P03819
A	398	HIS	-	EXPRESSION TAG	UNP P03819
A	399	GLY	-	EXPRESSION TAG	UNP P03819
A	400	MET	-	EXPRESSION TAG	UNP P03819
A	989	THR	-	linker	UNP P03819
A	990	SER	-	linker	UNP P03819
A	991	GLY	-	linker	UNP P03819
A	992	GLY	-	linker	UNP P03819
A	993	LEU	-	linker	UNP P03819
A	994	VAL	-	linker	UNP P03819
A	995	PRO	-	linker	UNP P03819
A	996	ARG	-	linker	UNP P03819
A	997	GLY	-	linker	UNP P03819
A	998	SER	-	linker	UNP P03819
A	999	SER	-	linker	UNP P03819
A	1000	GLY	-	linker	UNP P03819
B	396	GLY	-	EXPRESSION TAG	UNP P03819
B	397	SER	-	EXPRESSION TAG	UNP P03819
B	398	HIS	-	EXPRESSION TAG	UNP P03819
B	399	GLY	-	EXPRESSION TAG	UNP P03819
B	400	MET	-	EXPRESSION TAG	UNP P03819
B	989	THR	-	linker	UNP P03819
B	990	SER	-	linker	UNP P03819

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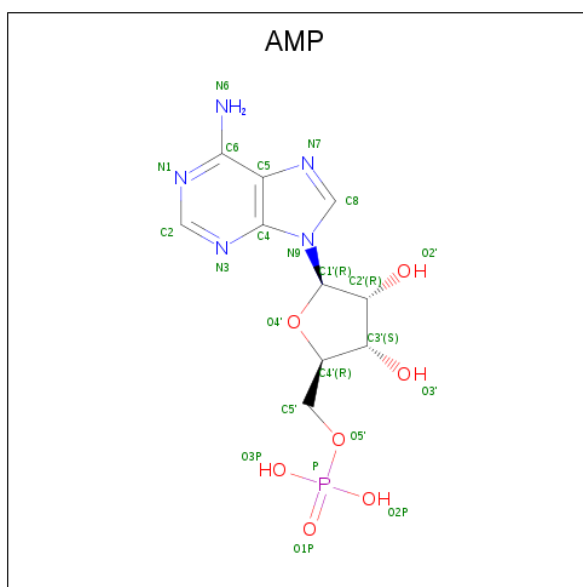
Chain	Residue	Modelled	Actual	Comment	Reference
B	991	GLY	-	linker	UNP P03819
B	992	GLY	-	linker	UNP P03819
B	993	LEU	-	linker	UNP P03819
B	994	VAL	-	linker	UNP P03819
B	995	PRO	-	linker	UNP P03819
B	996	ARG	-	linker	UNP P03819
B	997	GLY	-	linker	UNP P03819
B	998	SER	-	linker	UNP P03819
B	999	SER	-	linker	UNP P03819
B	1000	GLY	-	linker	UNP P03819

- Molecule 2 is FLAVIN MONONUCLEOTIDE (three-letter code: FMN) (formula: $C_{17}H_{21}N_4O_9P$).



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

- Molecule 3 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula: $C_{10}H_{14}N_5O_7P$).

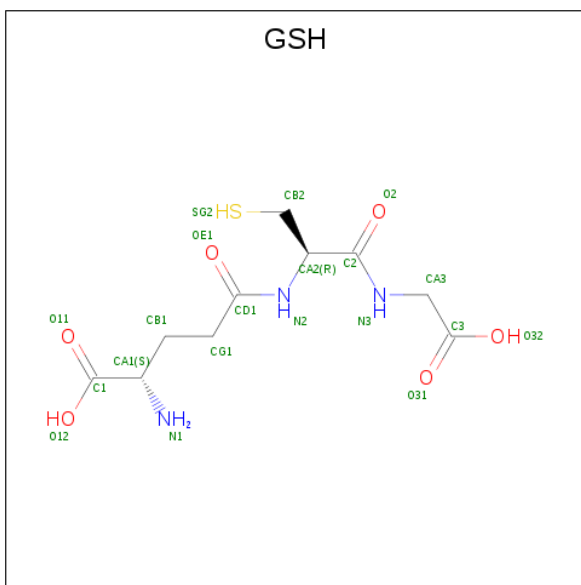


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
3	B	1	Total	C	N	O	P	0	0
			23	10	5	7	1		

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

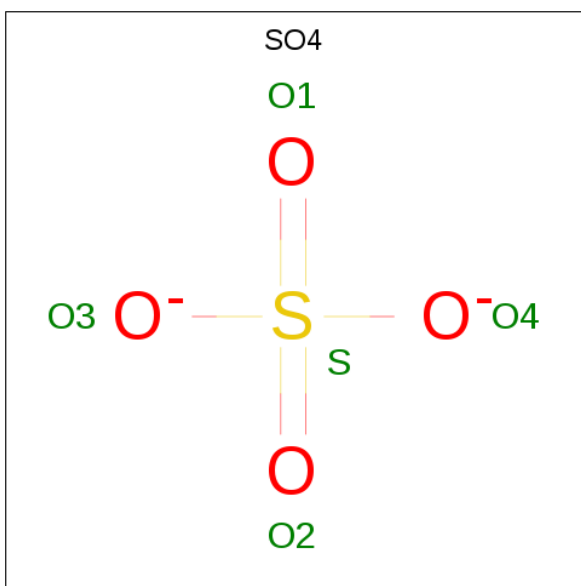
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Zn	0	0
			1	1		
4	A	1	Total	Zn	0	0
			1	1		

- Molecule 5 is GLUTATHIONE (three-letter code: GSH) (formula: C₁₀H₁₇N₃O₆S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	B	1	Total	C	N	O	S	0	0
			20	10	3	6	1		

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	142	Total 142	O 142	0	0
7	B	144	Total 144	O 144	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	64.76 Å 85.85 Å 189.23 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.46 – 1.75 33.47 – 1.75	Depositor EDS
% Data completeness (in resolution range)	90.2 (33.46-1.75) 90.2 (33.47-1.75)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.83 (at 1.75 Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.209 , 0.234 0.206 , 0.232	Depositor DCC
R_{free} test set	4764 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	27.3	Xtriage
Anisotropy	0.372	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 50.7	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	0.95	EDS
Total number of atoms	5981	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.58% 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: FMN, AMP, ZN, SO4, GSH

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	0.87	1/2778 (0.0%)	0.83	2/3761 (0.1%)
1	B	0.84	0/2925	0.80	0/3958
All	All	0.85	1/5703 (0.0%)	0.81	2/7719 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1031	GLU	CB-CG	5.18	1.61	1.52

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	499	ASP	CB-CG-OD1	5.92	123.63	118.30
1	A	1079	ASP	CB-CG-OD1	5.47	123.23	118.30

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	2707	0	2659	26	0
1	B	2853	0	2809	35	0
2	A	31	0	19	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	31	0	19	0	0
3	A	23	0	12	0	0
3	B	23	0	12	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	B	20	0	14	0	0
6	B	5	0	0	0	0
7	A	142	0	0	0	0
7	B	144	0	0	1	0
All	All	5981	0	5544	56	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 5.

All (56) 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:1031:GLU:OE1	1:A:1055:ARG:NH2	2.07	0.88
1:B:485:LYS:HE2	1:B:493:ILE:HD12	1.69	0.73
1:B:501:ASP:OD1	1:B:568:ARG:NH1	2.22	0.73
1:A:1148:THR:HA	1:A:1151:CYS:SG	2.32	0.69
1:B:451:THR:O	1:B:483:MET:SD	2.52	0.67
1:B:1019:ARG:HH11	1:B:1157:GLU:HG2	1.59	0.67
1:A:1056:ALA:O	1:A:1098:LYS:NZ	2.26	0.62
1:A:451:THR:O	1:A:483:MET:HE1	1.99	0.62
1:A:1051:GLU:OE1	1:A:1055:ARG:NH1	2.32	0.62
1:B:466:VAL:CG1	1:B:494:ILE:HD12	2.29	0.61
1:B:1019:ARG:HD2	1:B:1156:LEU:CD2	2.32	0.60
1:B:466:VAL:HG13	1:B:494:ILE:HD12	1.87	0.56
1:A:503:TYR:CE1	1:A:555:VAL:HG12	2.40	0.56
1:B:428:LEU:HD23	1:B:446:PHE:HB2	1.87	0.55
1:B:1157:GLU:O	1:B:1161:ARG:HG3	2.07	0.54
1:A:529:ALA:HA	1:B:494:ILE:CD1	2.38	0.54
1:B:431:ASP:HB3	1:B:434:HIS:CD2	2.44	0.53
1:B:1019:ARG:HD2	1:B:1156:LEU:HD23	1.91	0.52
1:A:440:LYS:HD3	1:B:565:THR:HG21	1.92	0.52
1:B:400:MET:H	1:B:424:LYS:HB3	1.74	0.52
1:A:494:ILE:HG22	1:B:525:THR:HG23	1.92	0.52
1:A:529:ALA:HA	1:B:494:ILE:HD13	1.90	0.51
1:A:1145:MET:HA	1:A:1159:GLN:HE21	1.77	0.50
1:A:443:MET:HG3	1:A:445:VAL:HG23	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:448:GLY:HA3	1:B:455:LEU:HD11	1.94	0.49
1:B:561:VAL:HG12	1:B:562:GLU:H	1.76	0.49
1:B:1051:GLU:OE2	1:B:1055:ARG:HD3	2.12	0.49
1:B:1019:ARG:NH1	1:B:1157:GLU:HG2	2.27	0.49
1:A:1151:CYS:SG	1:A:1156:LEU:HD13	2.53	0.49
1:B:434:HIS:HE1	7:B:346:HOH:O	1.96	0.49
1:B:1062:GLN:HA	1:B:1103:ALA:O	2.13	0.48
1:B:554:MET:HG3	1:B:571:VAL:HG12	1.97	0.46
1:A:426:VAL:HG21	1:A:459:ALA:HB1	1.98	0.46
1:B:400:MET:H	1:B:424:LYS:CB	2.29	0.46
1:B:429:ASP:OD1	1:B:434:HIS:HD2	1.98	0.46
1:A:1150:ILE:HD12	1:A:1150:ILE:O	2.16	0.46
1:A:1145:MET:HG3	1:A:1159:GLN:HB3	1.97	0.46
1:A:435:ILE:HD13	1:A:445:VAL:HG12	1.98	0.45
1:B:1147:CYS:O	1:B:1151:CYS:HB3	2.16	0.45
1:B:1021:LEU:HD22	1:B:1032:ILE:HD13	1.99	0.45
1:A:1145:MET:CG	1:A:1159:GLN:HB3	2.46	0.45
1:B:407:PHE:CE1	1:B:412:GLN:HG2	2.52	0.45
1:B:449:ASP:O	1:B:455:LEU:HD12	2.18	0.44
1:A:1007:ALA:O	1:A:1071:PRO:HG2	2.17	0.44
1:A:466:VAL:CG1	1:A:494:ILE:HD12	2.48	0.43
1:A:1109:GLY:HA2	1:A:1146:HIS:HB3	2.01	0.43
1:A:1009:PRO:HA	1:A:1036:TYR:CG	2.53	0.43
1:A:437:THR:HA	1:A:440:LYS:HD2	2.00	0.43
1:B:1145:MET:HG3	1:B:1159:GLN:HG3	2.01	0.42
1:B:561:VAL:HG11	1:B:567:ALA:HB1	2.01	0.42
1:B:554:MET:HB2	1:B:575:THR:HG21	2.00	0.42
1:A:466:VAL:HG13	1:A:494:ILE:HD12	2.02	0.41
1:A:523:LEU:HD21	1:A:547:PHE:HD2	1.84	0.41
1:B:449:ASP:HB3	1:B:452:ARG:HG3	2.03	0.41
1:B:504:ILE:HG23	1:B:559:ALA:HA	2.02	0.40
1:A:529:ALA:CA	1:B:494:ILE:HD13	2.52	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	334/413 (81%)	326 (98%)	7 (2%)	1 (0%)	41	22
1	B	353/413 (86%)	345 (98%)	8 (2%)	0	100	100
All	All	687/826 (83%)	671 (98%)	15 (2%)	1 (0%)	51	33

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1110	GLU

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	279/340 (82%)	277 (99%)	2 (1%)	84	75
1	B	294/340 (86%)	292 (99%)	2 (1%)	84	75
All	All	573/680 (84%)	569 (99%)	4 (1%)	84	75

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	430	HIS
1	A	1096	HIS
1	B	1096	HIS
1	B	1157	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 ⓘ

Of 8 ligands modelled in this entry, 2 are monoatomic - leaving 6 for Mogul analysis.

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	$\# Z > 2$
2	FMN	A	2400	-	31,33,33	1.56	5 (16%)	40,50,50	1.74	10 (25%)
6	SO4	B	1177	-	4,4,4	0.18	0	6,6,6	0.82	0
3	AMP	B	2401	-	22,25,25	1.16	2 (9%)	25,38,38	1.39	4 (16%)
3	AMP	A	2401	-	22,25,25	1.37	2 (9%)	25,38,38	2.04	7 (28%)
2	FMN	B	2400	-	31,33,33	1.91	7 (22%)	40,50,50	1.70	6 (15%)
5	GSH	B	1	-	12,19,19	3.23	3 (25%)	15,24,24	2.32	3 (20%)

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
2	FMN	B	2400	-	-	0/18/18/18	0/3/3/3
2	FMN	A	2400	-	-	0/18/18/18	0/3/3/3
3	AMP	A	2401	-	-	1/6/26/26	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	AMP	B	2401	-	-	1/6/26/26	0/3/3/3
5	GSH	B	1	-	-	1/18/24/24	-

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	1	GSH	OE1-CD1	8.49	1.40	1.23
5	B	1	GSH	O2-C2	6.60	1.36	1.23
2	B	2400	FMN	C10-N1	5.54	1.40	1.33
2	B	2400	FMN	C4A-N5	5.33	1.40	1.33
2	A	2400	FMN	C4A-N5	4.26	1.39	1.33
2	A	2400	FMN	C1'-N10	3.97	1.52	1.48
3	A	2401	AMP	O4'-C1'	3.54	1.46	1.41
2	A	2400	FMN	C10-N1	3.52	1.37	1.33
3	A	2401	AMP	C2-N3	3.49	1.37	1.32
2	B	2400	FMN	C5A-N5	3.21	1.40	1.35
3	B	2401	AMP	C5-C4	3.14	1.49	1.40
2	B	2400	FMN	C4-N3	2.92	1.38	1.33
2	A	2400	FMN	C4-N3	2.91	1.38	1.33
2	B	2400	FMN	C4A-C10	2.80	1.41	1.38
2	A	2400	FMN	C5A-N5	2.71	1.39	1.35
3	B	2401	AMP	C2-N3	2.59	1.36	1.32
2	B	2400	FMN	C9A-N10	2.41	1.41	1.38
2	B	2400	FMN	C1'-N10	2.18	1.50	1.48
5	B	1	GSH	CA1-N1	2.01	1.51	1.47

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2400	FMN	C4-N3-C2	7.67	121.62	115.14
5	B	1	GSH	CA2-CB2-SG2	-6.62	106.75	114.19
2	A	2400	FMN	C4-N3-C2	5.62	119.89	115.14
3	A	2401	AMP	N3-C2-N1	-5.49	120.11	128.68
2	A	2400	FMN	C1'-N10-C9A	4.17	121.57	118.29
5	B	1	GSH	CB1-CG1-CD1	-4.06	103.97	113.04
3	A	2401	AMP	O2P-P-O5'	-3.53	97.34	106.73
3	A	2401	AMP	O4'-C1'-C2'	-3.42	101.92	106.93
3	B	2401	AMP	N3-C2-N1	-3.40	123.37	128.68
2	A	2400	FMN	C4A-N5-C5A	3.22	119.99	116.77
2	B	2400	FMN	C4A-C4-N3	-3.19	119.07	123.43
5	B	1	GSH	CA3-N3-C2	-3.15	117.81	122.34
2	A	2400	FMN	O2'-C2'-C1'	3.13	117.13	109.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2400	FMN	C1'-N10-C9A	3.11	120.74	118.29
3	A	2401	AMP	C2-N1-C6	3.07	124.01	118.75
2	B	2400	FMN	C4A-N5-C5A	2.81	119.58	116.77
2	A	2400	FMN	C5A-C9A-N10	2.67	119.65	117.72
2	B	2400	FMN	C10-C4A-N5	-2.60	119.46	121.26
2	A	2400	FMN	C10-C4A-N5	-2.60	119.46	121.26
3	A	2401	AMP	C1'-N9-C4	-2.54	122.18	126.64
2	A	2400	FMN	C4A-C4-N3	-2.34	120.22	123.43
3	B	2401	AMP	C4-C5-N7	-2.31	106.99	109.40
2	A	2400	FMN	C4-C4A-N5	2.27	121.19	118.60
2	A	2400	FMN	C9A-N10-C10	-2.24	118.98	121.91
3	A	2401	AMP	N6-C6-N1	2.21	123.17	118.57
3	B	2401	AMP	C2-N1-C6	2.16	122.44	118.75
3	A	2401	AMP	O3P-P-O2P	2.13	115.78	107.64
2	B	2400	FMN	C4-C4A-N5	2.13	121.03	118.60
2	A	2400	FMN	O2P-P-O1P	2.08	118.82	110.68
3	B	2401	AMP	O4'-C1'-C2'	-2.04	103.95	106.93

There are no chirality outliers.

All (3) torsion outliers are listed below:

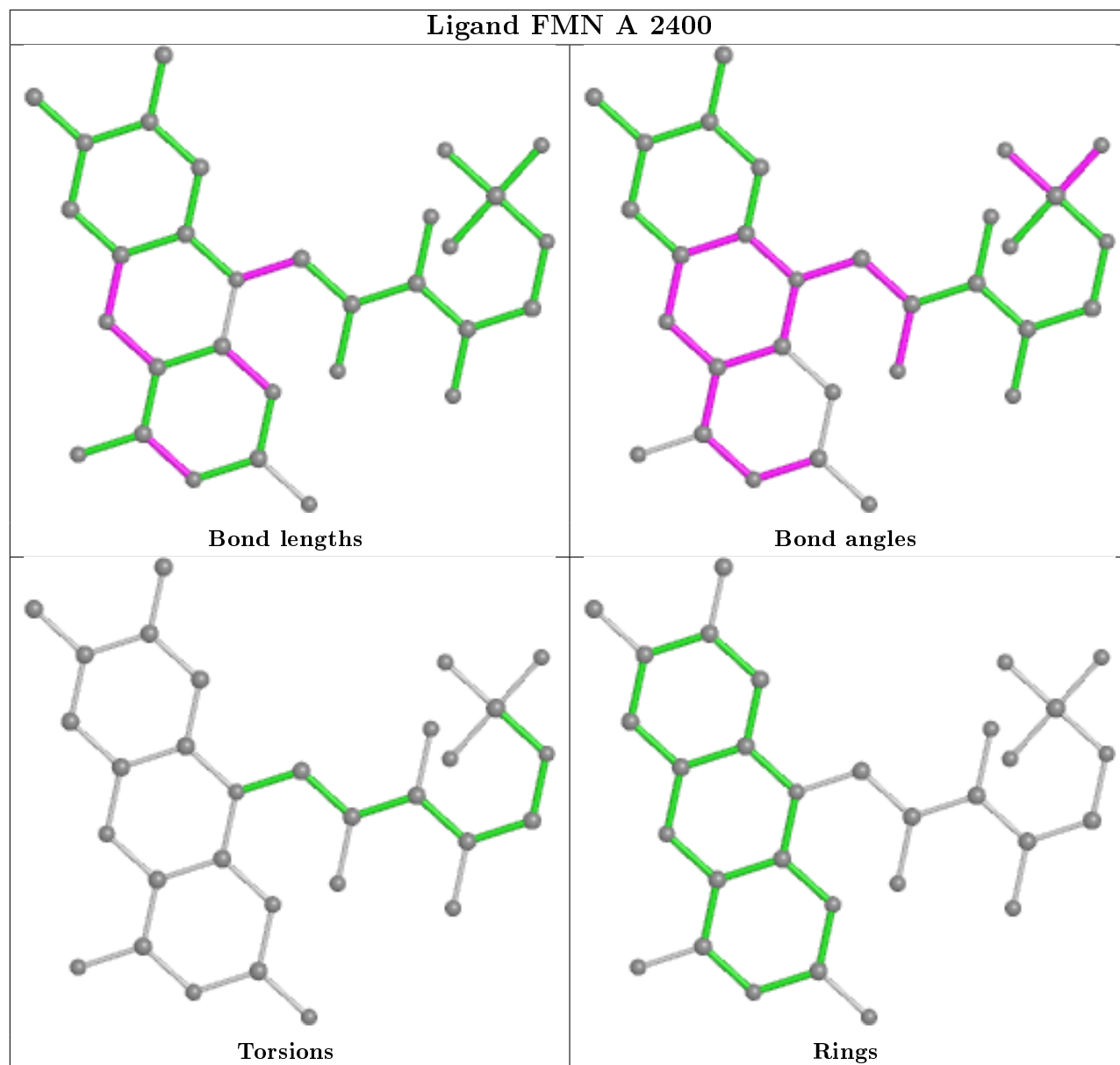
Mol	Chain	Res	Type	Atoms
5	B	1	GSH	N1-CA1-CB1-CG1
3	B	2401	AMP	O4'-C4'-C5'-O5'
3	A	2401	AMP	O4'-C4'-C5'-O5'

There are no ring outliers.

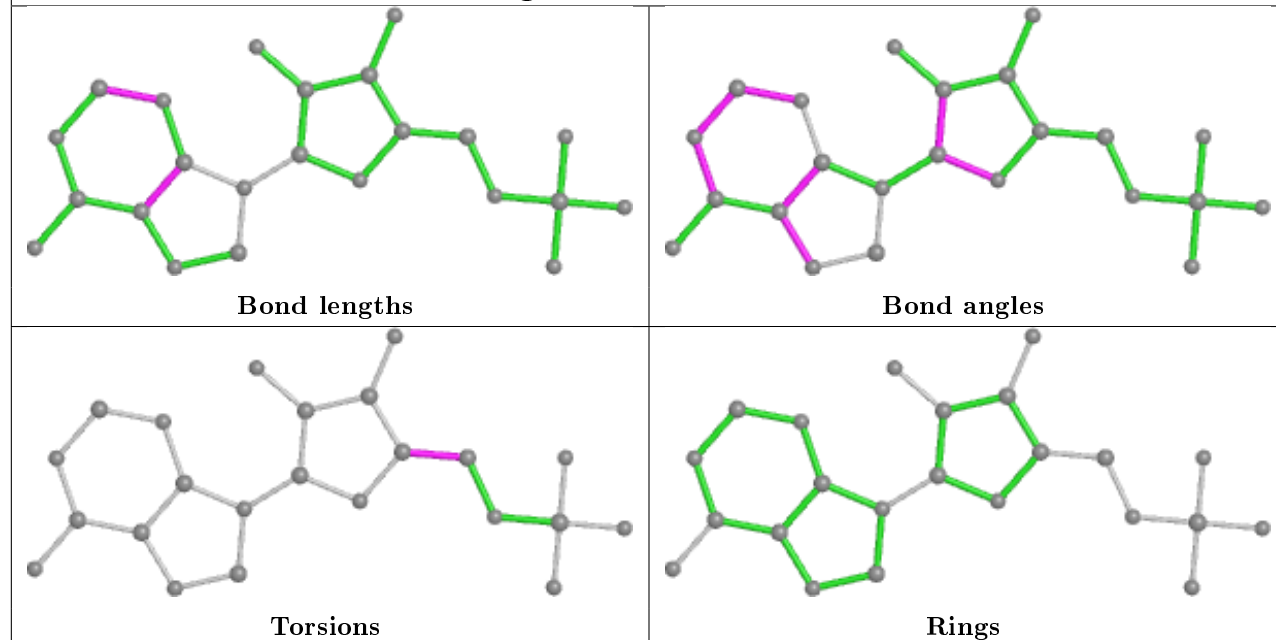
No monomer is involved in short contacts.

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.

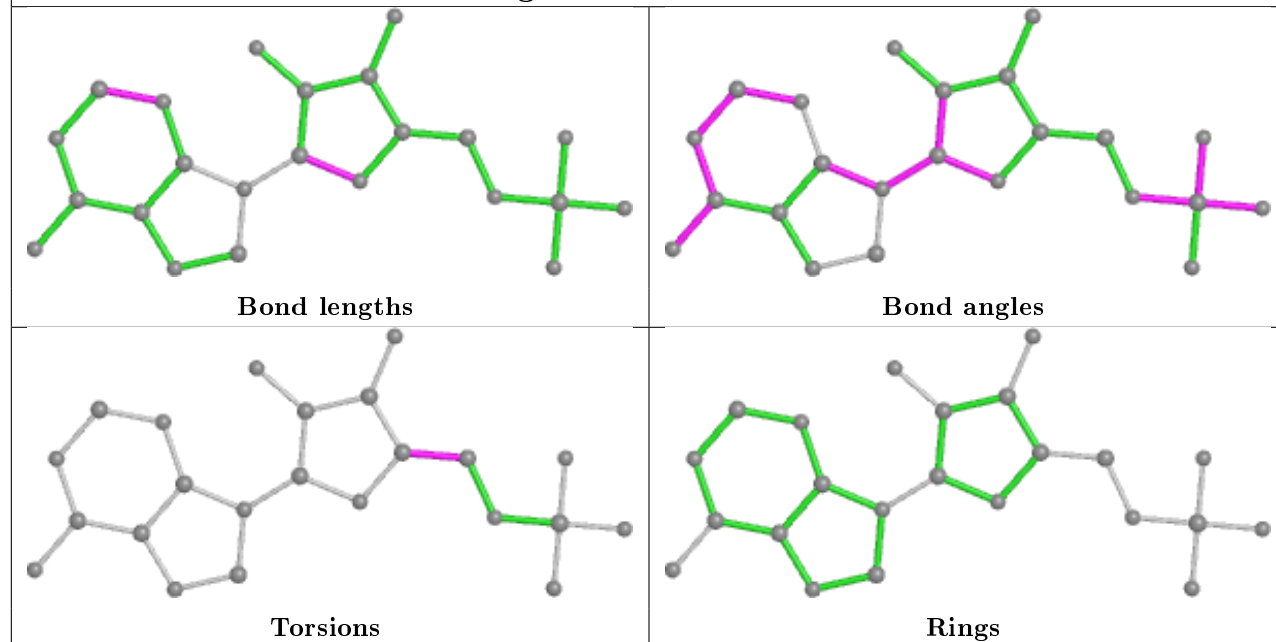
Ligand FMN A 2400



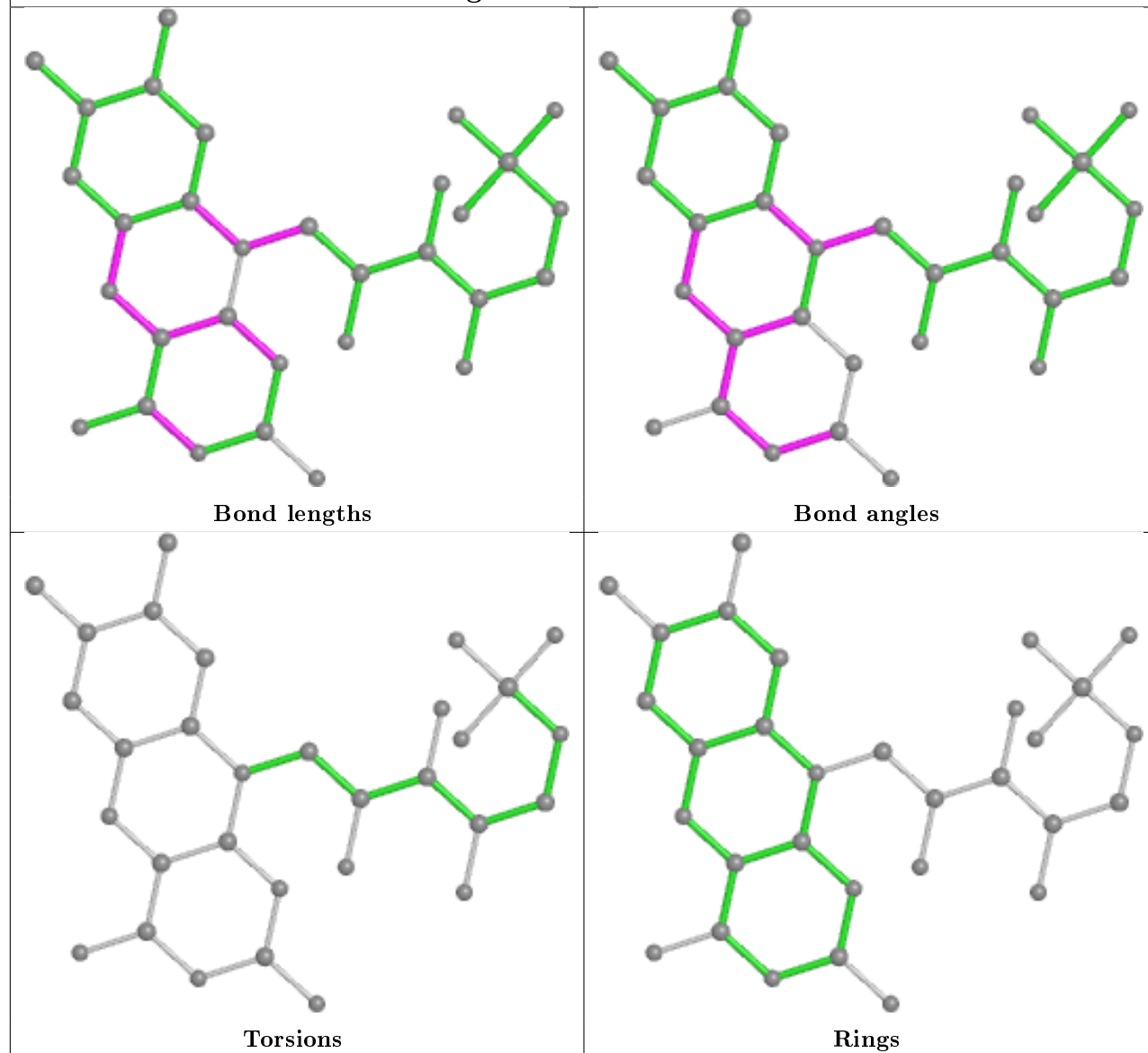
Ligand AMP B 2401



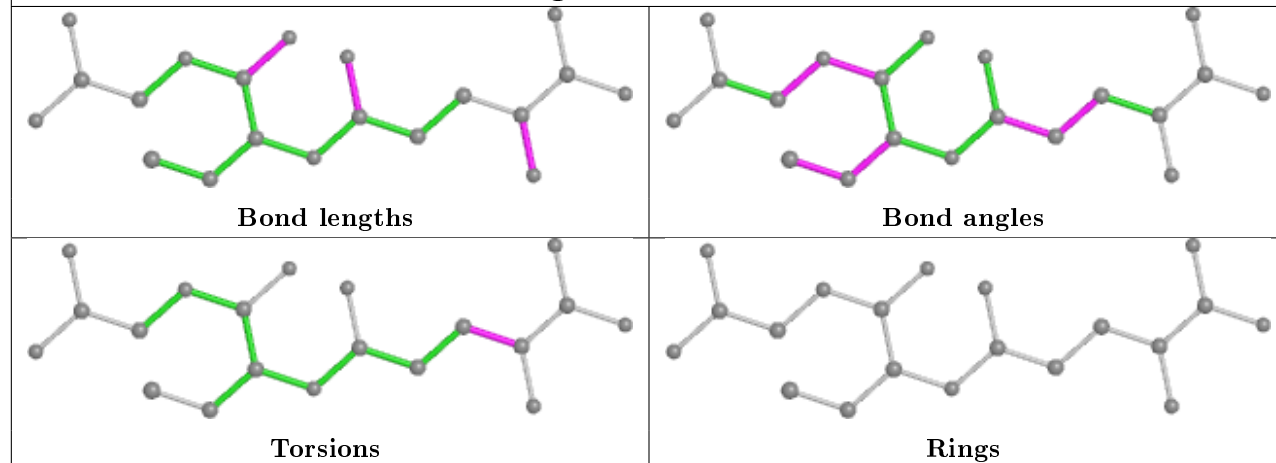
Ligand AMP A 2401



Ligand FMN B 2400



Ligand GSH B 1



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	338/413 (81%)	0.90	48 (14%) 2 3	18, 30, 61, 84	0
1	B	357/413 (86%)	0.73	46 (12%) 3 5	18, 30, 59, 83	0
All	All	695/826 (84%)	0.81	94 (13%) 3 4	18, 30, 61, 84	0

All (94) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1150	ILE	18.6
1	A	1149	PHE	14.0
1	A	1147	CYS	12.9
1	A	1148	THR	11.8
1	A	1151	CYS	10.1
1	A	1111	SER	8.6
1	B	1149	PHE	7.6
1	B	399	GLY	7.6
1	B	1151	CYS	7.4
1	B	1150	ILE	6.5
1	B	563	ASN	6.1
1	B	1147	CYS	6.1
1	A	561	VAL	6.0
1	A	1108	GLY	5.5
1	A	439	ARG	5.4
1	B	561	VAL	5.3
1	A	1110	GLU	5.2
1	B	1152	ASP	5.2
1	A	560	MET	4.9
1	A	1152	ASP	4.8
1	A	399	GLY	4.6
1	A	1109	GLY	4.4
1	B	564	ASP	4.4
1	B	1156	LEU	4.4

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Mol	Chain	Res	Type	RSRZ
1	A	1173	ALA	4.3
1	B	577	ALA	4.3
1	B	578	MET	4.2
1	B	565	THR	4.2
1	B	1155	THR	3.9
1	B	400	MET	3.9
1	A	444	LYS	3.9
1	A	400	MET	3.8
1	B	576	SER	3.8
1	A	1159	GLN	3.8
1	A	1162	HIS	3.7
1	A	1112	HIS	3.7
1	B	1090	HIS	3.6
1	A	1074	LEU	3.6
1	A	410	PHE	3.5
1	B	580	SER	3.5
1	A	1155	THR	3.4
1	B	566	LYS	3.4
1	B	1174	HIS	3.4
1	B	562	GLU	3.4
1	B	1061	TRP	3.4
1	B	447	TYR	3.3
1	A	1090	HIS	3.3
1	A	1001	MET	3.3
1	A	1027	LEU	3.3
1	B	570	ALA	3.2
1	A	1146	HIS	3.2
1	A	1028	GLU	3.2
1	B	1154	GLU	3.2
1	B	1122	ASP	3.0
1	B	573	LYS	3.0
1	A	1161	ARG	3.0
1	A	1128	LEU	2.9
1	A	1070	ILE	2.9
1	A	1114	GLU	2.9
1	B	1070	ILE	2.9
1	A	1156	LEU	2.8
1	A	1174	HIS	2.7
1	B	1102	TRP	2.7
1	A	1168	LEU	2.7
1	B	1128	LEU	2.7
1	B	1093	THR	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	1153	ASP	2.7
1	B	1028	GLU	2.6
1	A	1157	GLU	2.6
1	A	1172	GLU	2.5
1	B	567	ALA	2.5
1	B	430	HIS	2.5
1	B	574	ARG	2.4
1	A	1025	ARG	2.4
1	B	1124	LEU	2.4
1	A	1102	TRP	2.4
1	A	1153	ASP	2.4
1	A	1026	THR	2.4
1	B	560	MET	2.3
1	A	1000	GLY	2.2
1	B	1123	VAL	2.2
1	B	494	ILE	2.2
1	B	1078	ILE	2.2
1	A	1154	GLU	2.2
1	B	1173	ALA	2.2
1	A	440	LYS	2.1
1	A	443	MET	2.1
1	B	1104	VAL	2.1
1	A	1169	GLU	2.1
1	B	1073	LEU	2.1
1	A	413	ILE	2.1
1	A	1103	ALA	2.0
1	B	1165	GLN	2.0
1	B	1085	GLY	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 carbohydrates in this entry.

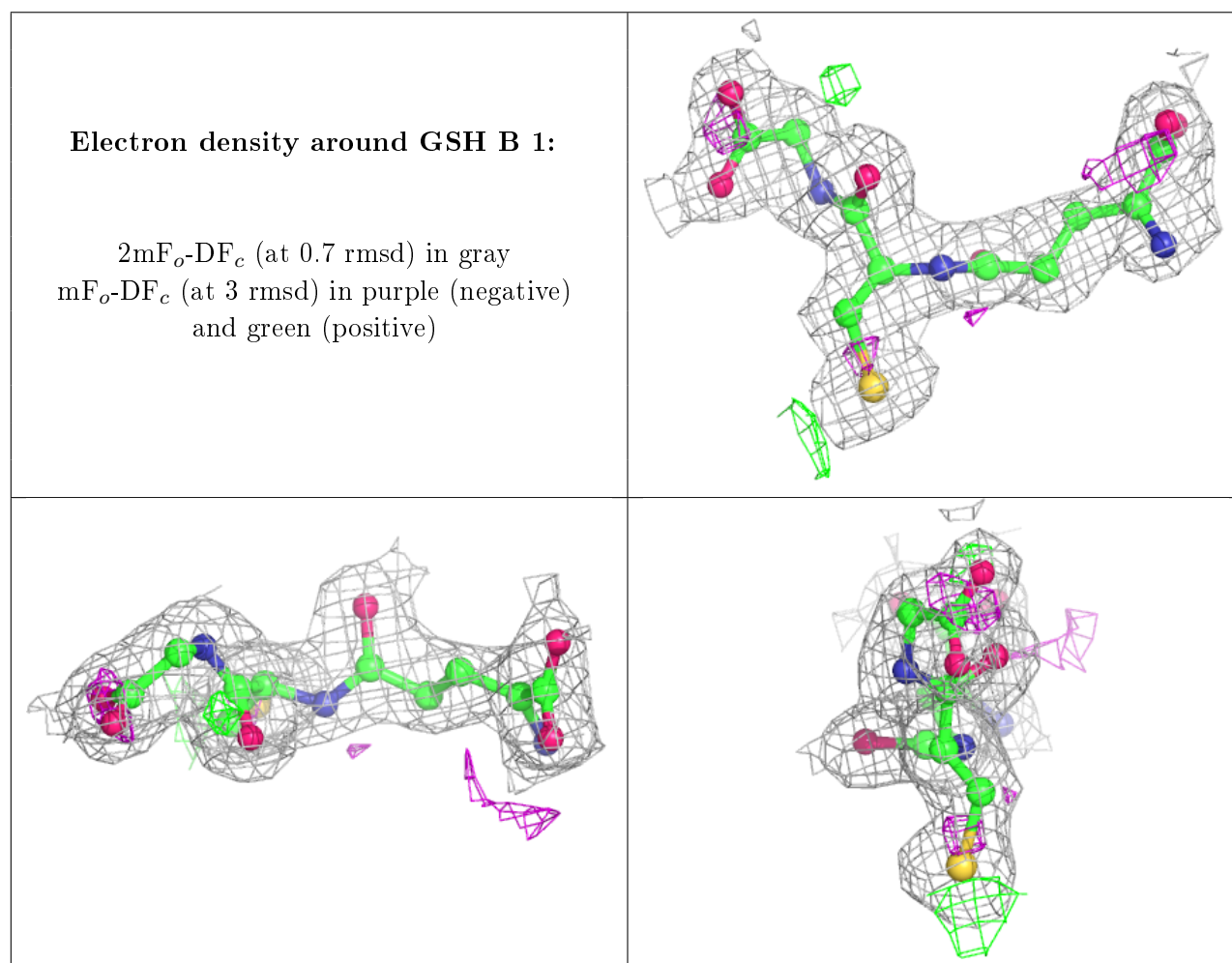
6.4 Ligands [i](#)

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.

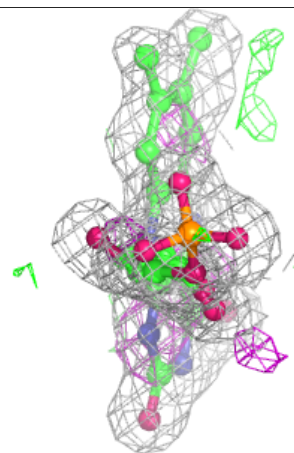
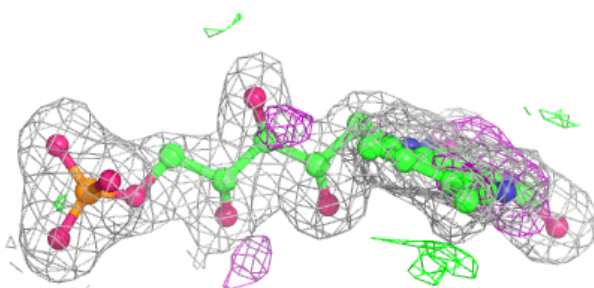
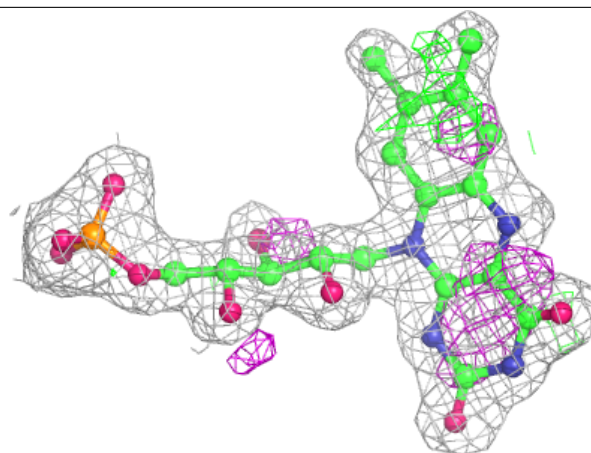
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
6	SO4	B	1177	5/5	0.77	0.20	67,68,71,72	0
5	GSH	B	1	20/20	0.89	0.12	25,38,48,49	0
2	FMN	B	2400	31/31	0.95	0.13	24,32,34,35	0
2	FMN	A	2400	31/31	0.95	0.09	25,34,37,39	0
3	AMP	B	2401	23/23	0.96	0.15	23,41,44,45	0
4	ZN	B	2402	1/1	0.98	0.12	44,44,44,44	0
4	ZN	A	2402	1/1	0.98	0.11	45,45,45,45	0
3	AMP	A	2401	23/23	0.98	0.08	19,25,28,31	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.



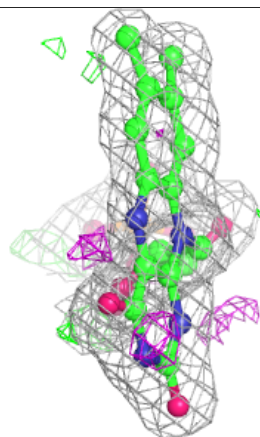
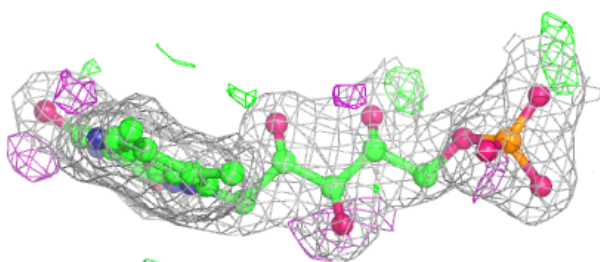
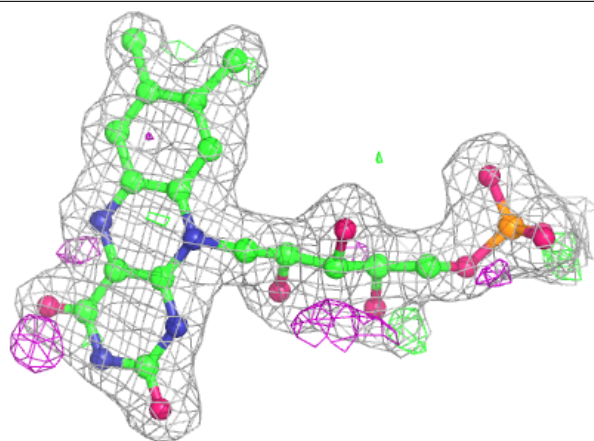
Electron density around FMN B 2400:

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

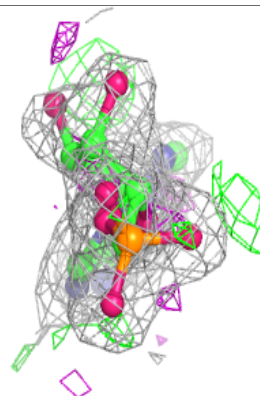
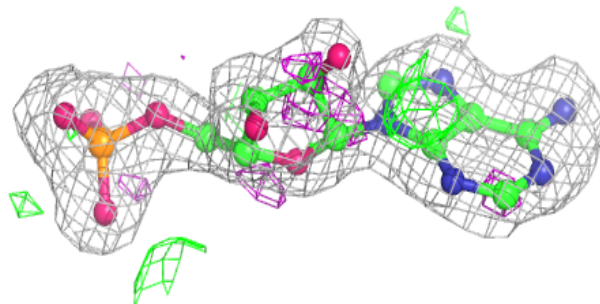
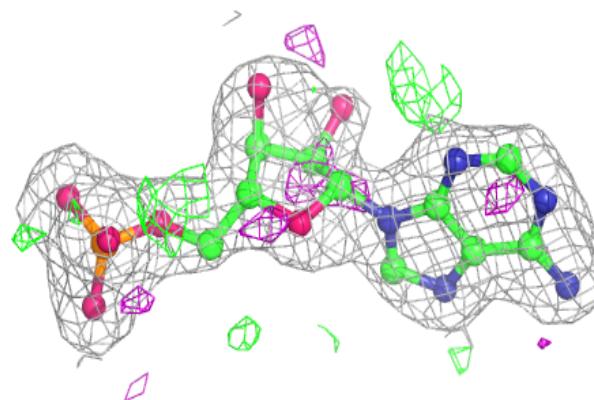


Electron density around FMN A 2400:

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

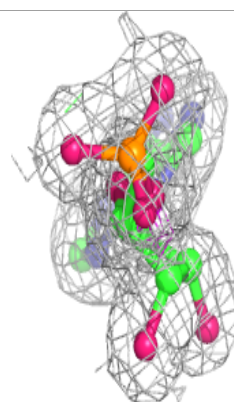
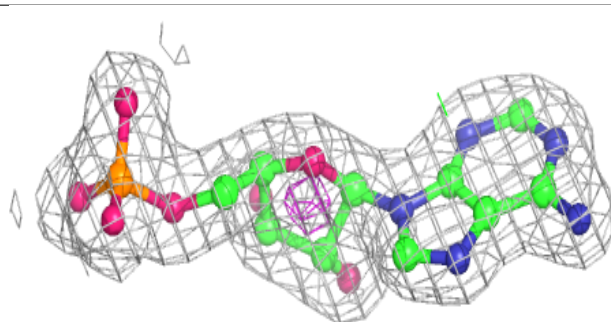
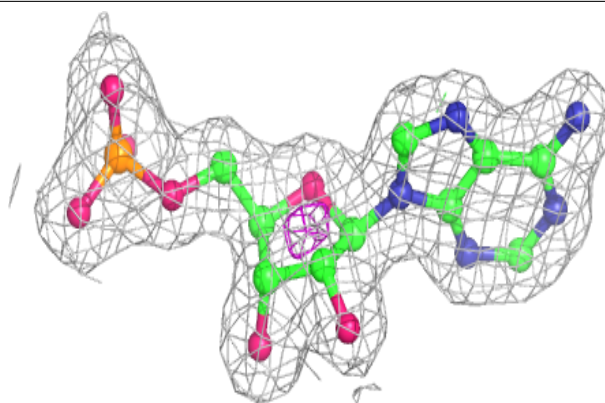
**Electron density around AMP B 2401:**

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



Electron density around AMP A 2401:

$2mF_o-DF_c$ (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.