Full wwPDB X-ray Structure Validation Report ⓘ

Jan 14, 2024 – 03:53 am GMT

PDB ID	:	6RKB
Title	:	Crystal structure of human monoamine oxidase B in complex with styrylpiperidine analogue 1
Authors	:	Iacovino, L.G.; Knez, D.; Colettis, N.; Sova, M.; Pislar, A.; Higgs, J.; Kamecki, F.; Mangialavori, I.; Dolsak, A.; Zakelj, S.; Trontelj, J.; Kos, J.; Marder, N.M.; Gobec, S.; Binda, C.
Deposited on	:	2019-04-30
Resolution	:	2.30 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:

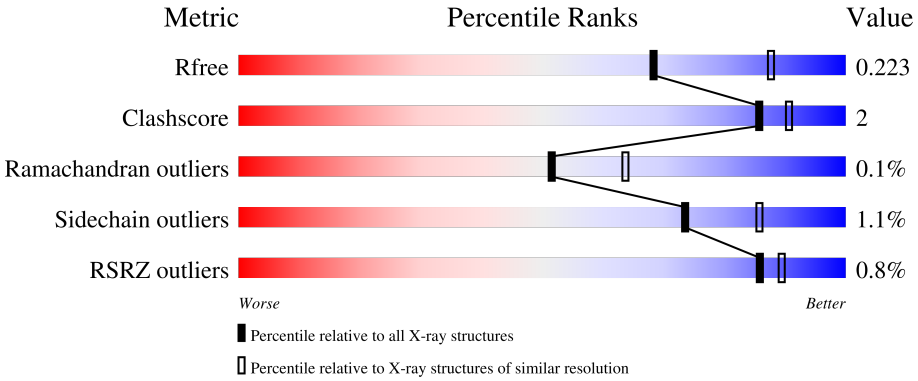
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

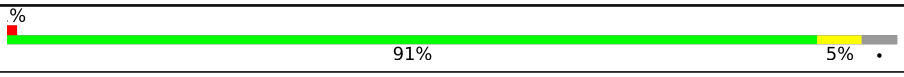
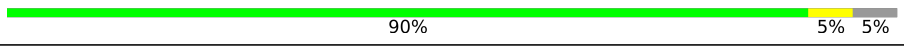
The reported resolution of this entry is 2.30 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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 <=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	520	
1	B	520	

2 Entry composition

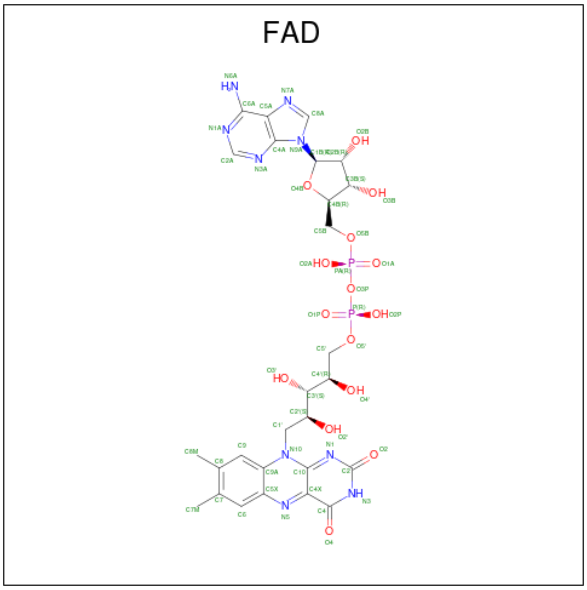
There are 5 unique types of molecules in this entry. The entry contains 8514 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Amine oxidase [flavin-containing] B.

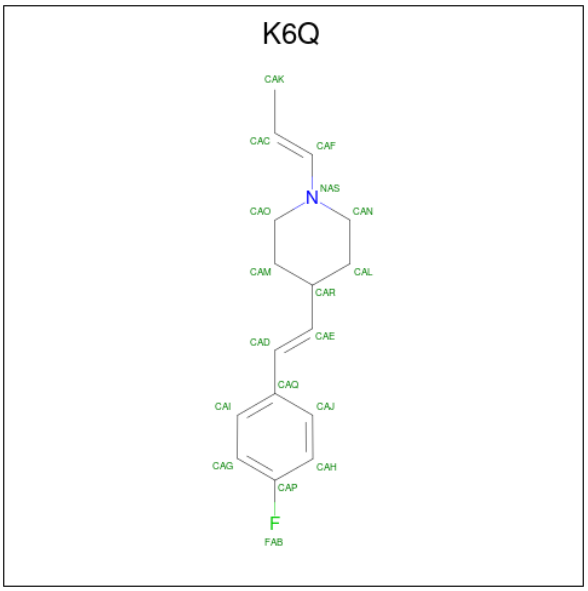
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	499	Total	C	N	O	S	0	0	0
			3974	2541	681	728	24			
1	B	494	Total	C	N	O	S	0	0	0
			3940	2519	676	721	24			

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$) (labeled as "Ligand of Interest" by depositor).



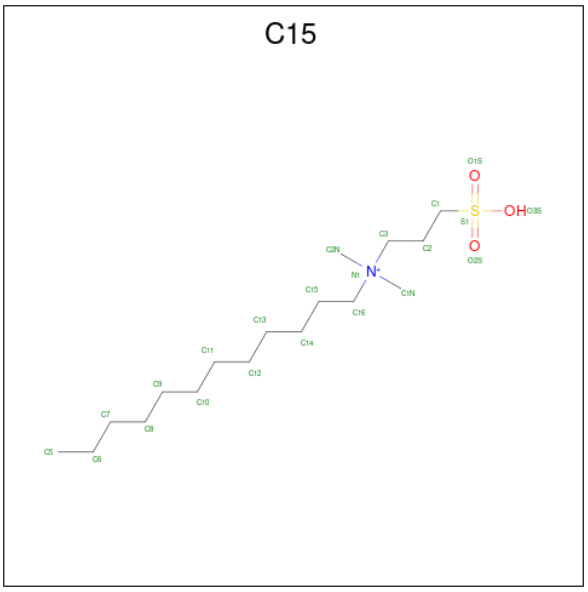
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 3 is 4-[({E})-2-(4-fluorophenyl)ethenyl]-1-[({E})-prop-1-enyl]piperidine (three-letter code: K6Q) (formula: $C_{16}H_{20}FN$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	F	N	0	0
			18	16	1	1		
3	B	1	Total	C	F	N	0	0
			18	16	1	1		

- Molecule 4 is N-DODECYL-N,N-DIMETHYL-3-AMMONIO-1-PROPANESULFONATE (three-letter code: C15) (formula: $C_{17}H_{38}NO_3S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			15	10	1	3	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	N	O	S	0	0
			11	6	1	3	1		

- Molecule 5 is water.

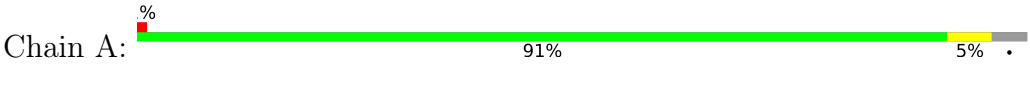
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	186	Total	O	0	0
			186	186		
5	B	246	Total	O	0	0
			246	246		

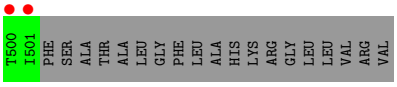
3 Residue-property plots (i)

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: Amine oxidase [flavin-containing] B

Chain A:





• Molecule 1: Amine oxidase [flavin-containing] B

Chain B:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 2	Depositor
Cell constants a, b, c, α, β, γ	132.34Å 222.40Å 86.39Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	68.89 – 2.30 68.79 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.2 (68.89-2.30) 99.2 (68.79-2.30)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.46 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.8.0230	Depositor
R, R_{free}	0.173 , 0.214 0.181 , 0.223	Depositor DCC
R_{free} test set	1456 reflections (2.58%)	wwPDB-VP
Wilson B-factor (Å^2)	22.9	Xtriage
Anisotropy	0.095	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 30.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.013 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.013 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	8514	wwPDB-VP
Average B, all atoms (Å^2)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.61% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: K6Q, FAD, C15

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	0.43	0/4071	0.59	0/5526
1	B	0.44	0/4037	0.59	0/5479
All	All	0.44	0/8108	0.59	0/11005

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	1
1	B	0	3
All	All	0	4

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	415	ARG	Sidechain
1	B	127	ARG	Sidechain
1	B	350	ARG	Sidechain
1	B	415	ARG	Sidechain

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	3974	0	3976	25	1
1	B	3940	0	3937	19	0
2	A	53	0	29	1	0
2	B	53	0	29	1	0
3	A	18	0	0	0	0
3	B	18	0	0	0	0
4	A	15	0	21	0	0
4	B	11	0	12	0	0
5	A	186	0	0	4	1
5	B	246	0	0	2	3
All	All	8514	0	8004	35	5

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 2.

All (35) 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:117:ASN:HD22	1:A:120:ARG:HH21	1.25	0.85
1:A:280:MET:HE1	1:B:353:ALA:HB1	1.69	0.73
1:B:117:ASN:HD22	1:B:120:ARG:HH21	1.39	0.70
1:A:353:ALA:HB1	1:B:280:MET:HE1	1.73	0.69
1:A:28:LEU:HD11	1:A:454:MET:HE1	1.78	0.66
1:A:280:MET:HE1	1:B:353:ALA:CB	2.26	0.65
1:A:251:ASN:HD22	1:A:251:ASN:H	1.46	0.62
1:A:117:ASN:HD22	1:A:120:ARG:NH2	1.96	0.60
1:A:117:ASN:ND2	1:A:120:ARG:HH21	1.99	0.58
1:B:468:GLU:OE1	5:B:701:HOH:O	2.18	0.57
1:A:387:ASN:ND2	1:B:280:MET:CE	2.67	0.57
1:A:100:ARG:NH2	5:A:702:HOH:O	2.33	0.56
1:A:280:MET:HG3	1:B:389:CYS:HB2	1.88	0.55
1:B:233:ARG:HG3	1:B:251:ASN:HD21	1.72	0.54
1:A:251:ASN:H	1:A:251:ASN:ND2	2.09	0.50
1:B:281:MET:HB3	1:B:413:VAL:HG11	1.94	0.49
1:A:106:VAL:HG11	1:A:111:THR:HG22	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:88:LEU:HD12	1:A:88:LEU:N	2.30	0.47
1:A:280:MET:HG3	1:B:389:CYS:CB	2.45	0.47
1:B:454:MET:HB2	1:B:454:MET:HE2	1.70	0.46
1:B:58:GLY:HA2	2:B:601:FAD:C4X	2.46	0.46
1:A:387:ASN:HD21	1:B:280:MET:CE	2.29	0.46
1:A:58:GLY:HA2	2:A:601:FAD:C4X	2.46	0.45
1:A:60:TYR:HB3	1:A:206:GLN:HA	2.00	0.44
1:A:243:GLU:O	1:A:420:ARG:NH1	2.50	0.44
1:A:387:ASN:ND2	1:B:280:MET:HE1	2.32	0.43
1:A:271:LYS:HE2	5:A:707:HOH:O	2.18	0.43
1:B:71:LEU:O	1:B:75:LEU:HG	2.19	0.43
1:B:451:LEU:HD23	1:B:454:MET:HE1	2.01	0.43
1:B:237:TYR:HB3	1:B:248:GLU:HB3	2.01	0.42
1:B:323:PRO:HD2	1:B:367:LEU:HD22	2.02	0.42
1:A:271:LYS:CE	5:A:707:HOH:O	2.68	0.41
1:A:149:LYS:HD3	5:B:798:HOH:O	2.21	0.40
1:A:387:ASN:ND2	1:B:280:MET:HE2	2.37	0.40
1:A:448:ARG:NH2	5:A:703:HOH:O	2.37	0.40

All (5) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:881:HOH:O	5:B:881:HOH:O[4_565]	0.70	1.50
5:A:884:HOH:O	5:A:884:HOH:O[3_655]	1.11	1.09
5:B:757:HOH:O	5:B:757:HOH:O[2_565]	1.60	0.60
1:A:475:GLN:NE2	1:A:475:GLN:NE2[3_656]	1.89	0.31
5:B:924:HOH:O	5:B:924:HOH:O[2_565]	2.09	0.11

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	497/520 (96%)	484 (97%)	12 (2%)	1 (0%)	47 58
1	B	492/520 (95%)	483 (98%)	9 (2%)	0	100 100
All	All	989/1040 (95%)	967 (98%)	21 (2%)	1 (0%)	51 64

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	52	LYS

5.3.2 Protein sidechains (i)

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	428/444 (96%)	424 (99%)	4 (1%)	78 89
1	B	424/444 (96%)	419 (99%)	5 (1%)	71 84
All	All	852/888 (96%)	843 (99%)	9 (1%)	73 86

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	ASN
1	A	251	ASN
1	A	350	ARG
1	A	397	CYS
1	B	92	VAL
1	B	106	VAL
1	B	190	LYS
1	B	350	ARG
1	B	397	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	3	ASN

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Mol	Chain	Res	Type
1	A	117	ASN
1	A	170	ASN
1	A	251	ASN
1	A	387	ASN
1	A	475	GLN
1	B	116	ASN
1	B	117	ASN
1	B	251	ASN
1	B	464	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides 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	$\#\|Z\| > 2$
3	K6Q	A	602	2	19,19,19	1.72	4 (21%)	20,24,24	1.69	3 (15%)
2	FAD	B	601	3,1	53,58,58	1.10	1 (1%)	68,89,89	1.69	15 (22%)
2	FAD	A	601	3,1	53,58,58	1.03	3 (5%)	68,89,89	1.64	14 (20%)
3	K6Q	B	602	2	19,19,19	1.62	4 (21%)	20,24,24	1.81	6 (30%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
4	C15	B	603	-	10,10,21	3.01	2 (20%)	14,15,26	1.43	2 (14%)
4	C15	A	603	-	14,14,21	2.40	2 (14%)	18,19,26	1.41	2 (11%)

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	K6Q	A	602	2	-	2/8/18/18	0/2/2/2
2	FAD	B	601	3,1	-	1/30/50/50	0/6/6/6
2	FAD	A	601	3,1	-	3/30/50/50	0/6/6/6
3	K6Q	B	602	2	-	0/8/18/18	0/2/2/2
4	C15	B	603	-	-	1/8/8/21	-
4	C15	A	603	-	-	0/14/14/21	-

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	603	C15	C1-S1	-6.92	1.67	1.77
4	B	603	C15	O2S-S1	6.61	1.64	1.45
4	B	603	C15	C1-S1	-6.54	1.68	1.77
4	A	603	C15	O3S-S1	4.97	1.65	1.47
3	B	602	K6Q	CAF-CAC	3.84	1.43	1.32
3	A	602	K6Q	CAF-CAC	3.75	1.43	1.32
2	B	601	FAD	C4X-N5	3.37	1.37	1.30
3	A	602	K6Q	CAF-NAS	3.32	1.44	1.33
3	A	602	K6Q	CAR-CAE	3.02	1.56	1.50
2	A	601	FAD	C4-N3	-2.72	1.33	1.38
3	B	602	K6Q	CAF-NAS	2.70	1.42	1.33
3	A	602	K6Q	CAJ-CAH	-2.53	1.34	1.38
3	B	602	K6Q	CAJ-CAH	-2.37	1.34	1.38
2	A	601	FAD	C4X-N5	2.32	1.35	1.30
2	A	601	FAD	C9A-N10	-2.24	1.37	1.41
3	B	602	K6Q	CAI-CAQ	-2.04	1.35	1.39

All (42) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	602	K6Q	CAO-NAS-CAF	-4.57	111.25	121.58
2	B	601	FAD	N3A-C2A-N1A	-4.32	121.92	128.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	601	FAD	C9A-C5X-N5	-4.23	117.83	122.43
2	A	601	FAD	N3A-C2A-N1A	-4.12	122.24	128.68
2	B	601	FAD	C9A-C5X-N5	-4.03	118.05	122.43
4	A	603	C15	O3S-S1-C1	3.95	112.16	105.77
4	B	603	C15	O2S-S1-C1	3.64	111.30	106.92
2	B	601	FAD	C9-C9A-N10	3.53	126.60	121.84
2	B	601	FAD	C4-C4X-N5	3.41	123.09	118.23
2	A	601	FAD	O4B-C1B-C2B	-3.39	101.97	106.93
3	B	602	K6Q	CAO-NAS-CAF	-3.36	113.98	121.58
3	A	602	K6Q	CAR-CAE-CAD	-3.31	117.99	126.40
2	B	601	FAD	C10-C4X-N5	-3.29	117.87	124.86
3	B	602	K6Q	CAN-NAS-CAO	3.28	119.42	114.08
2	A	601	FAD	C4-N3-C2	-3.27	119.60	125.64
3	B	602	K6Q	CAR-CAE-CAD	-3.27	118.11	126.40
4	B	603	C15	O3S-S1-C1	3.14	110.85	105.77
4	A	603	C15	O2S-S1-C1	3.14	110.70	106.92
2	B	601	FAD	C4-N3-C2	-3.04	120.03	125.64
2	B	601	FAD	C10-N1-C2	2.98	122.87	116.90
2	B	601	FAD	C4X-C4-N3	2.95	120.67	113.19
2	A	601	FAD	C4X-C10-N1	-2.94	117.91	124.73
2	B	601	FAD	C4X-C10-N1	-2.90	117.99	124.73
2	A	601	FAD	C4X-C4-N3	2.81	120.32	113.19
2	A	601	FAD	C10-C4X-N5	-2.78	118.96	124.86
2	B	601	FAD	O4B-C1B-C2B	-2.72	102.95	106.93
2	A	601	FAD	C9-C9A-N10	2.66	125.44	121.84
2	B	601	FAD	O4-C4-C4X	-2.57	119.78	126.60
2	A	601	FAD	C9A-N10-C10	-2.51	116.86	120.77
2	B	601	FAD	C6-C5X-C9A	2.44	122.39	118.94
3	A	602	K6Q	CAM-CAR-CAE	-2.43	106.08	111.72
2	A	601	FAD	C4A-C5A-N7A	-2.43	106.87	109.40
2	B	601	FAD	C9A-N10-C10	-2.25	117.26	120.77
2	A	601	FAD	O4-C4-C4X	-2.24	120.64	126.60
2	A	601	FAD	C1B-N9A-C4A	-2.24	122.70	126.64
3	B	602	K6Q	CAL-CAR-CAE	2.23	116.90	111.72
3	B	602	K6Q	CAH-CAP-CAG	-2.22	119.87	122.83
3	B	602	K6Q	CAN-NAS-CAF	2.20	126.57	121.58
2	B	601	FAD	C9-C9A-C5X	-2.20	115.95	120.11
2	A	601	FAD	C9-C9A-C5X	-2.14	116.07	120.11
2	A	601	FAD	C4-C4X-C10	2.13	120.36	116.79
2	B	601	FAD	C4'-C3'-C2'	2.02	117.56	113.36

There are no chirality outliers.

All (7) torsion outliers are listed below:

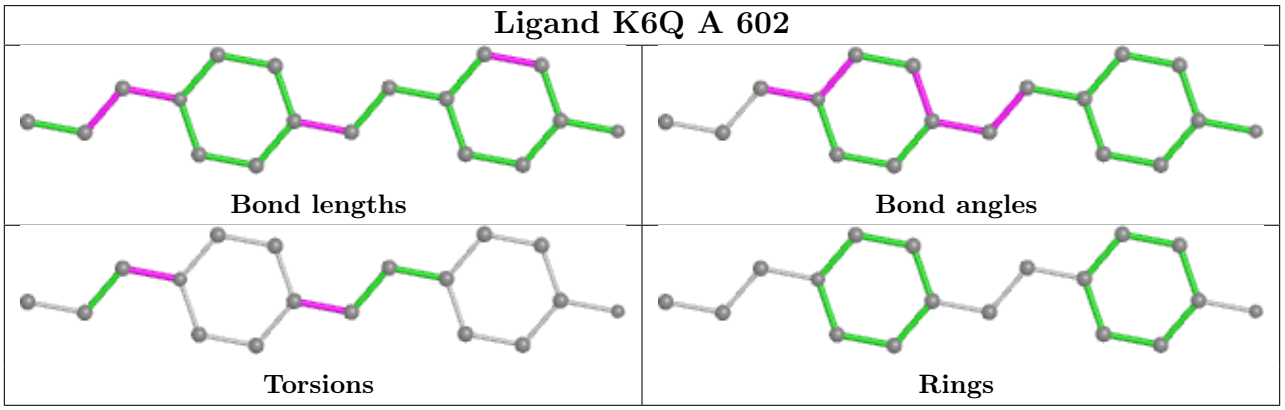
Mol	Chain	Res	Type	Atoms
3	A	602	K6Q	CAC-CAF-NAS-CAO
4	B	603	C15	S1-C1-C2-C3
2	A	601	FAD	C2'-C1'-N10-C10
2	B	601	FAD	O4B-C4B-C5B-O5B
3	A	602	K6Q	CAD-CAE-CAR-CAM
2	A	601	FAD	C5B-O5B-PA-O1A
2	A	601	FAD	O4B-C4B-C5B-O5B

There are no ring outliers.

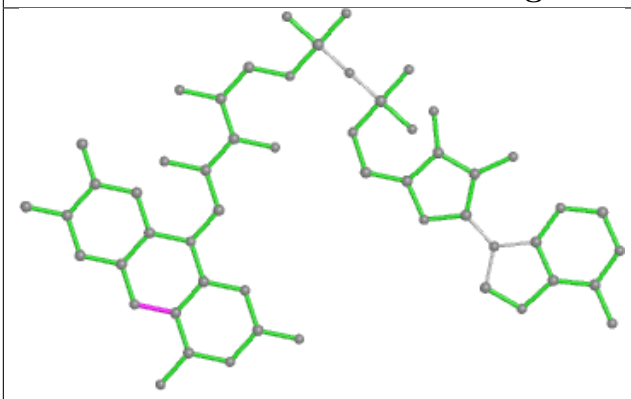
2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	601	FAD	1	0
2	A	601	FAD	1	0

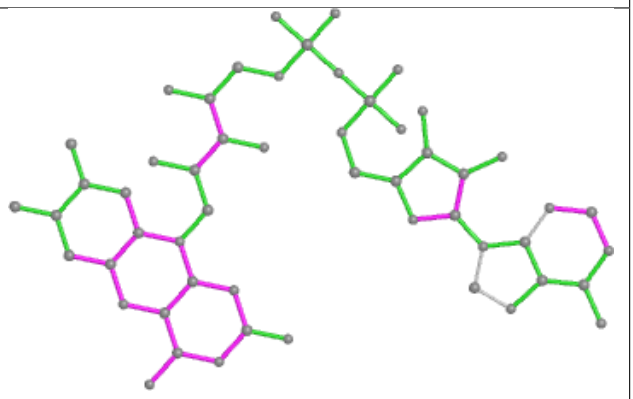
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



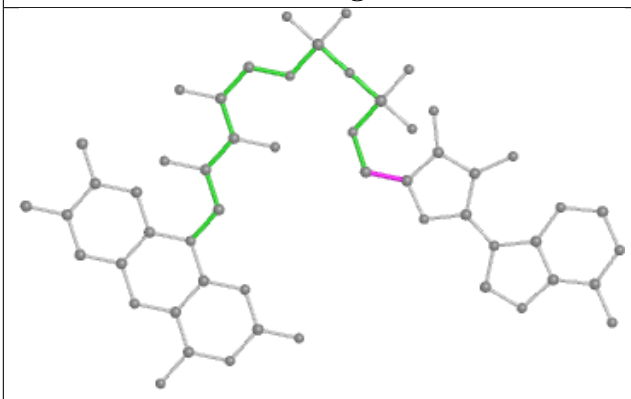
Ligand FAD B 601



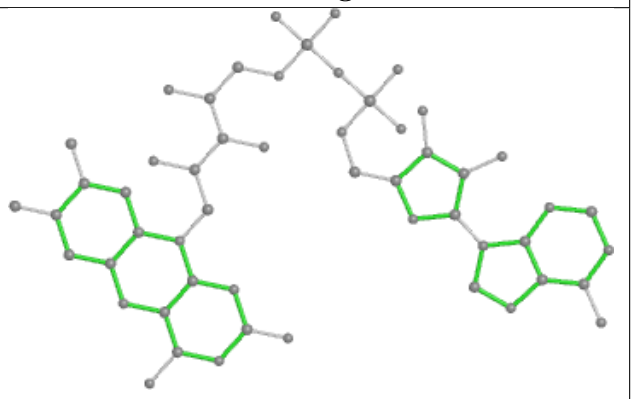
Bond lengths



Bond angles

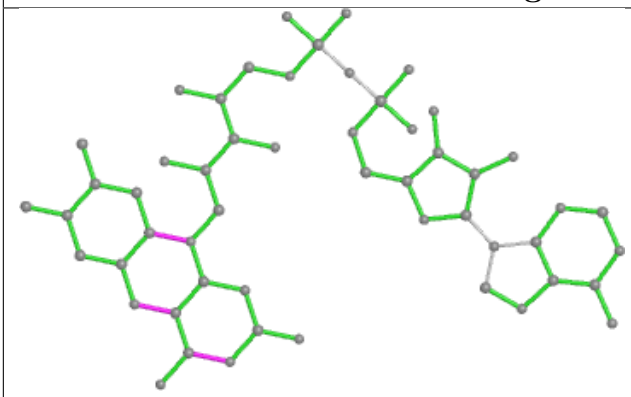


Torsions

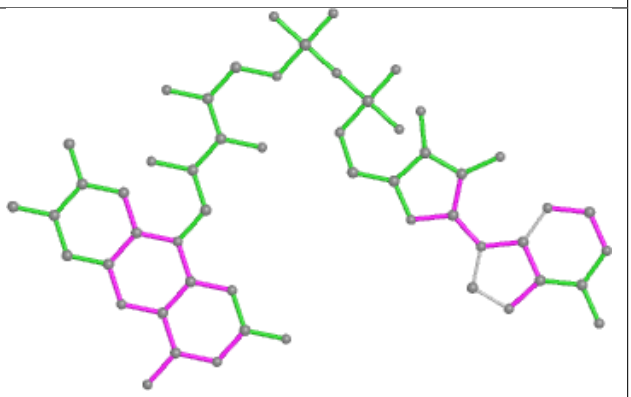


Rings

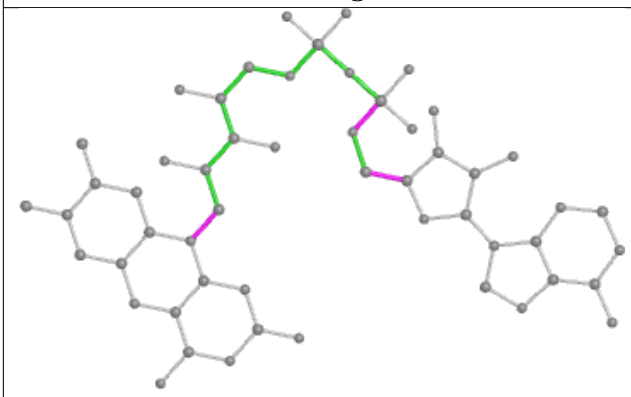
Ligand FAD A 601



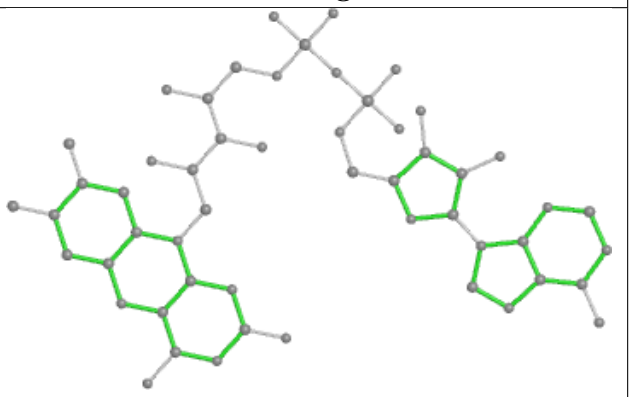
Bond lengths



Bond angles

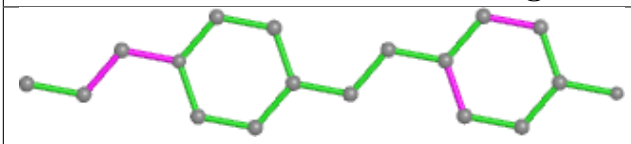


Torsions

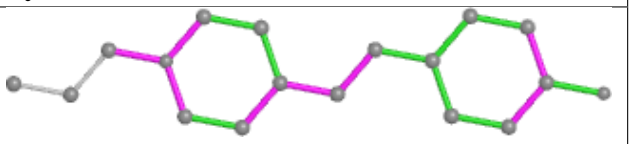


Rings

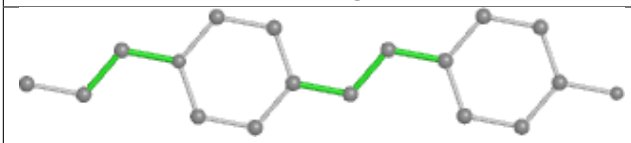
Ligand K6Q B 602



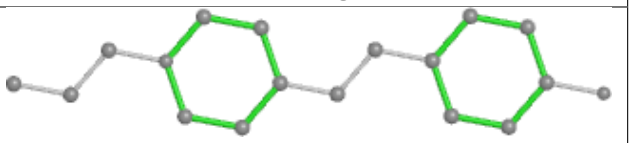
Bond lengths



Bond angles

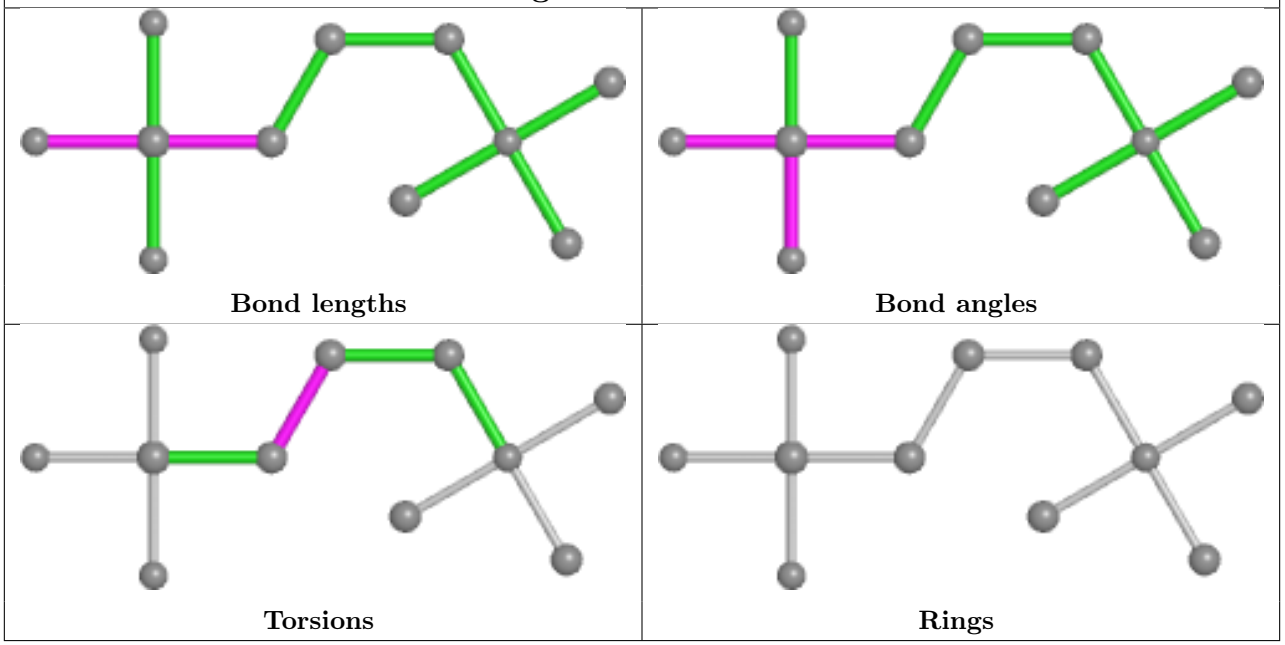


Torsions

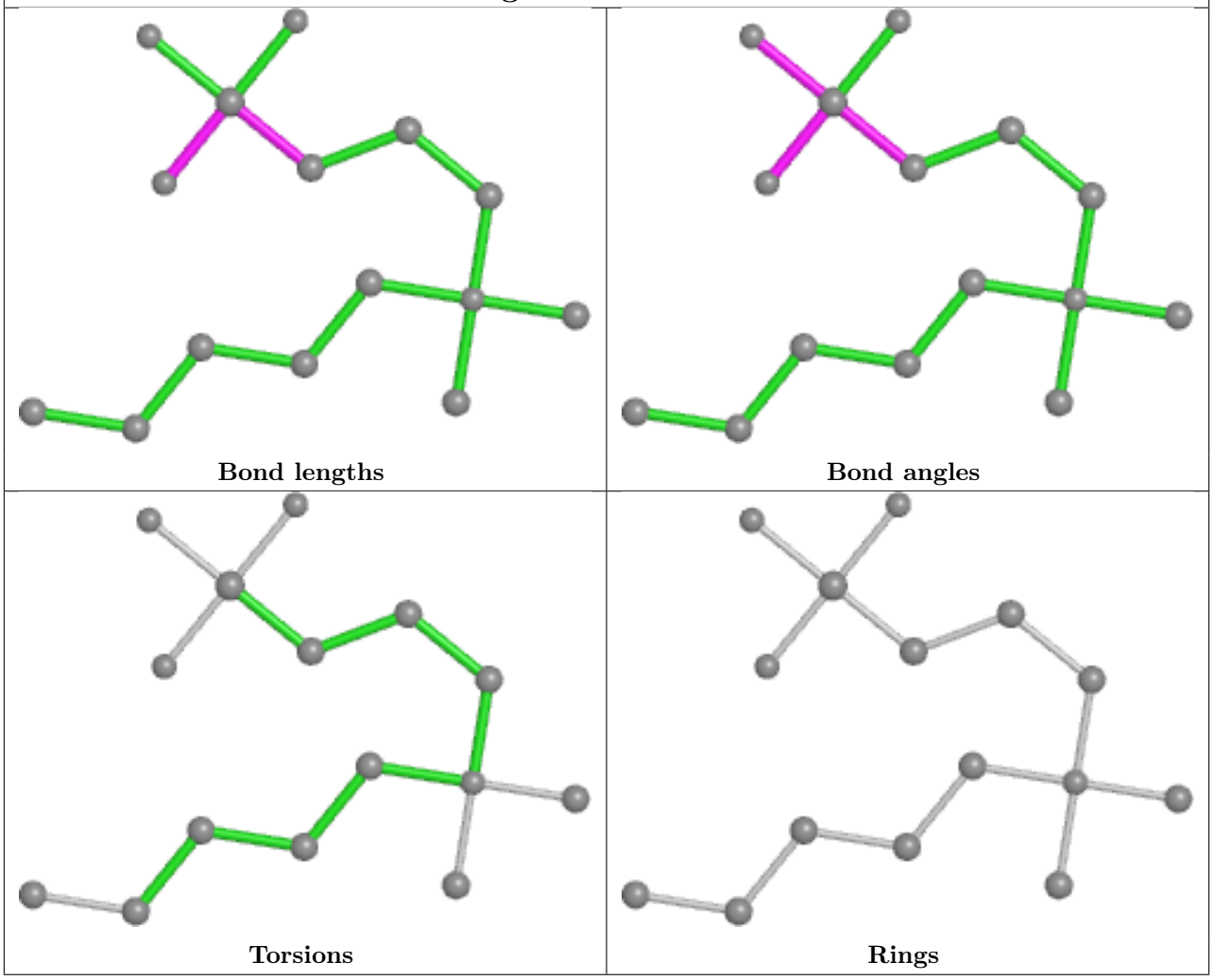


Rings

Ligand C15 B 603



Ligand C15 A 603



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, 95^{th} 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	499/520 (95%)	-0.42	7 (1%)	75	80	14, 23, 43, 109	0
1	B	494/520 (95%)	-0.51	1 (0%)	95	96	13, 21, 39, 77	0
All	All	993/1040 (95%)	-0.46	8 (0%)	86	89	13, 22, 42, 109	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	501	ILE	6.5
1	A	500	THR	5.6
1	A	499	THR	5.3
1	A	498	LEU	4.3
1	A	496	ILE	2.9
1	B	496	ILE	2.6
1	A	495	LEU	2.5
1	A	494	ARG	2.0

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

There are no monosaccharides in this entry.

6.4 Ligands

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,

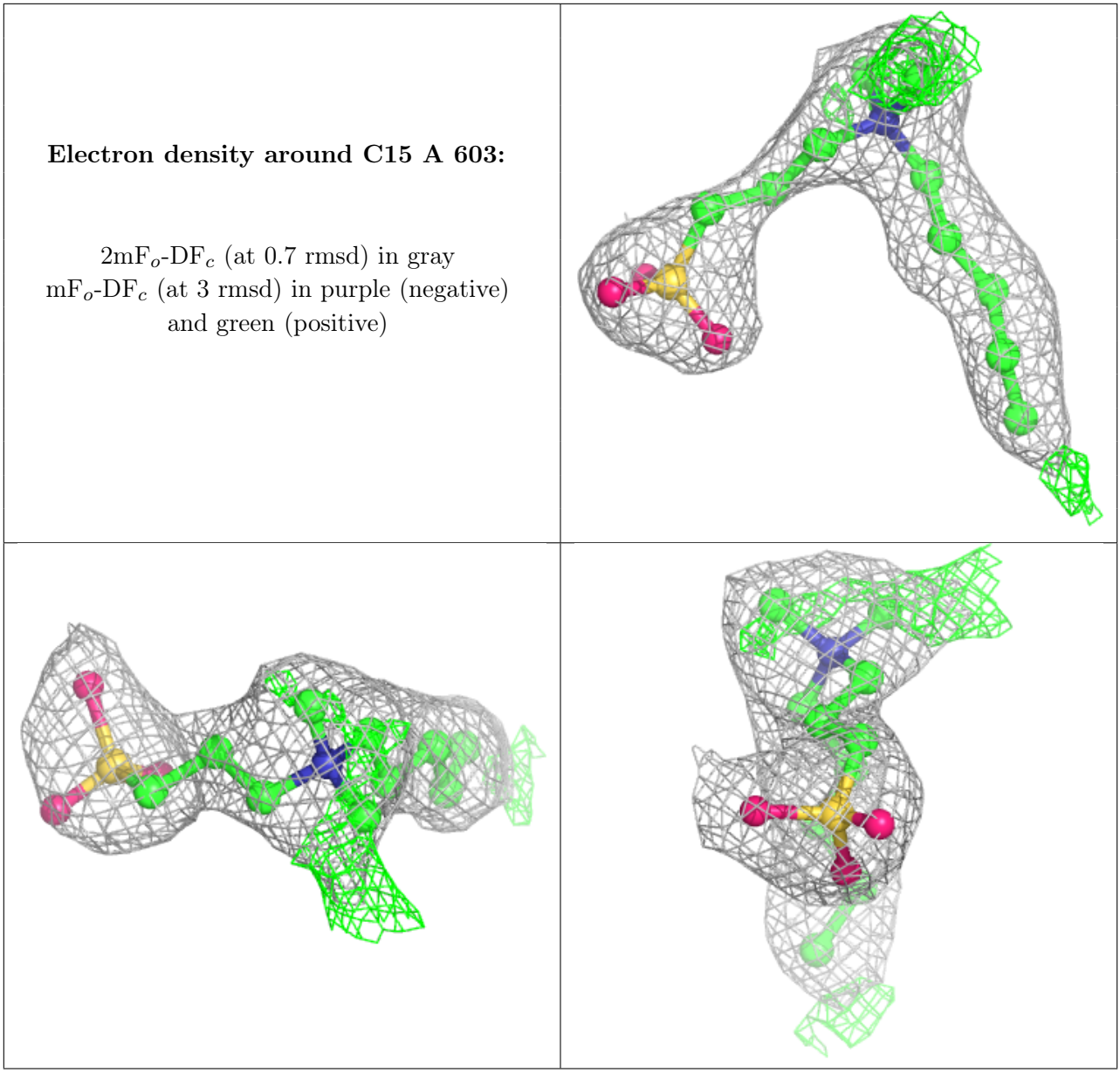
median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	C15	A	603	15/22	0.77	0.19	44,50,73,74	0
4	C15	B	603	11/22	0.86	0.16	50,54,67,69	0
3	K6Q	A	602	18/18	0.95	0.15	23,27,29,31	0
3	K6Q	B	602	18/18	0.95	0.12	21,24,26,26	0
2	FAD	A	601	53/53	0.98	0.10	14,16,17,17	0
2	FAD	B	601	53/53	0.98	0.11	12,13,15,15	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.

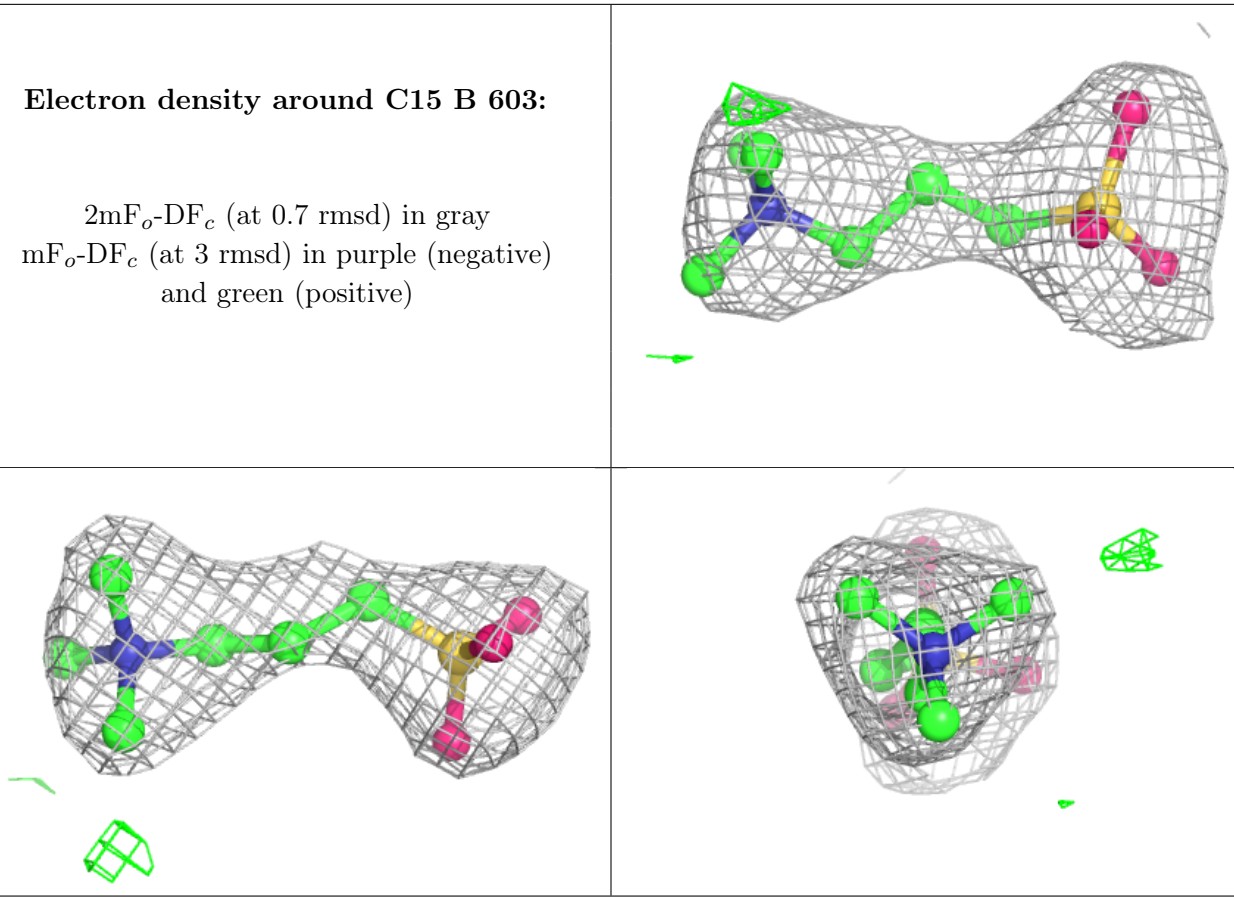
Electron density around C15 A 603:

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



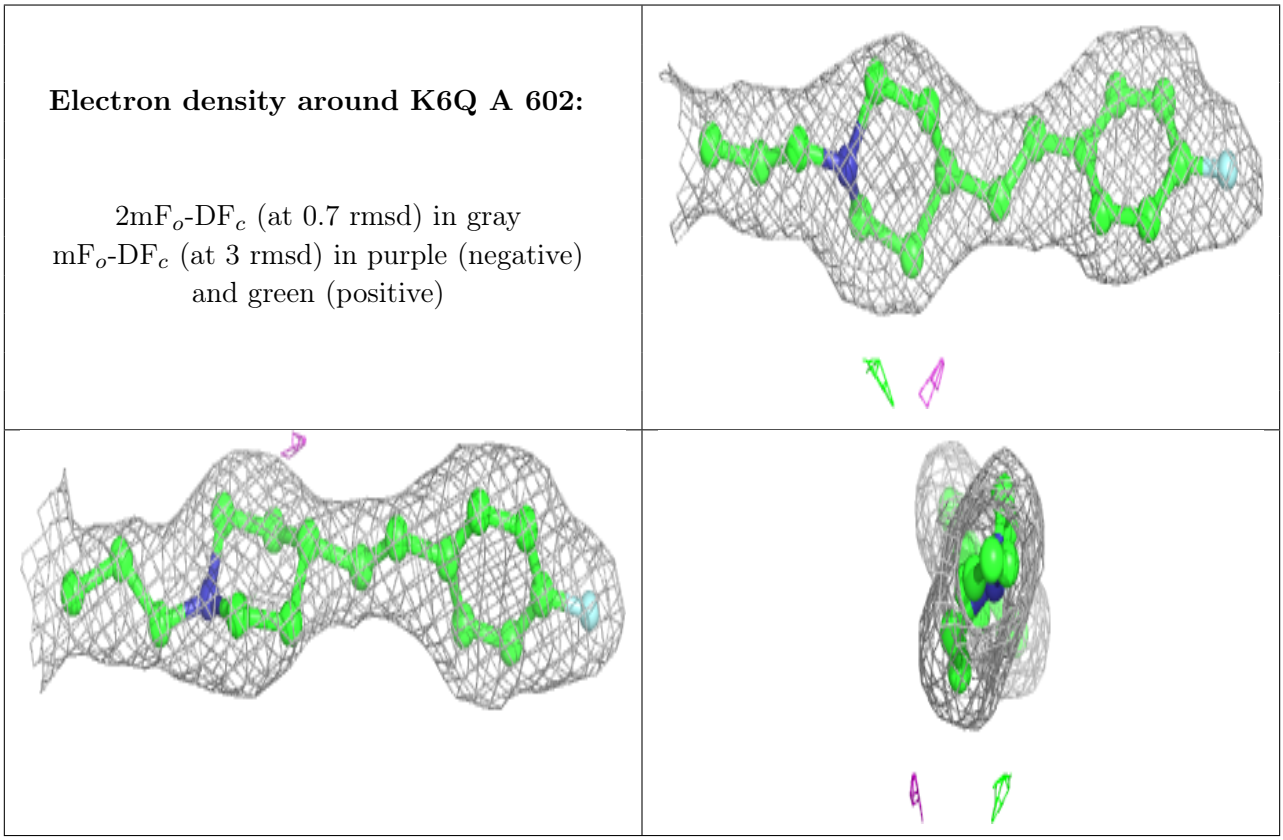
Electron density around C15 B 603:

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



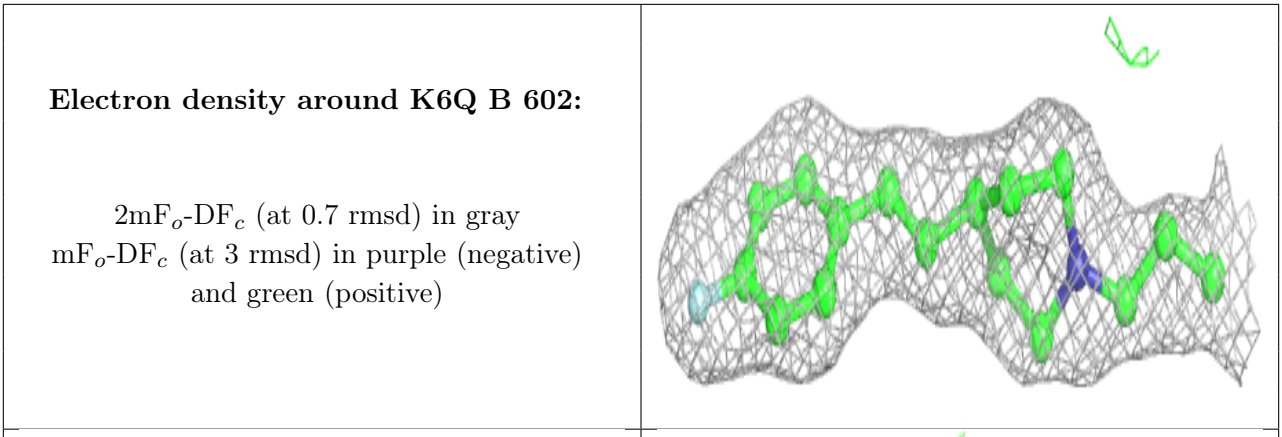
Electron density around K6Q A 602:

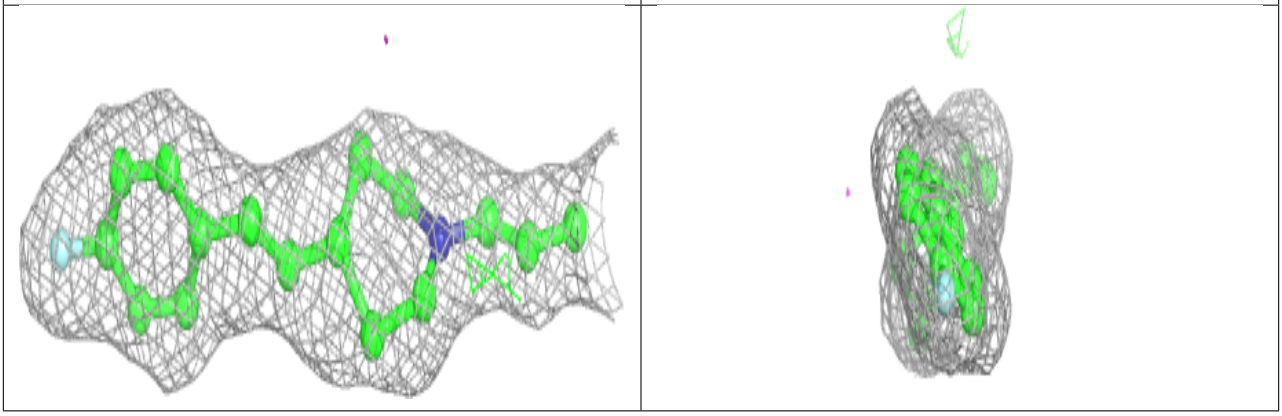
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



Electron density around K6Q B 602:

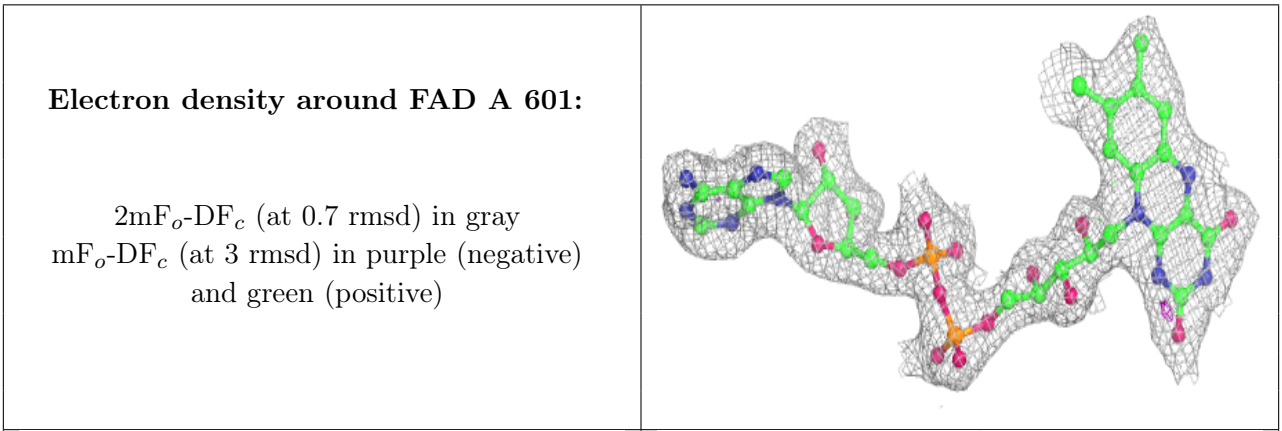
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

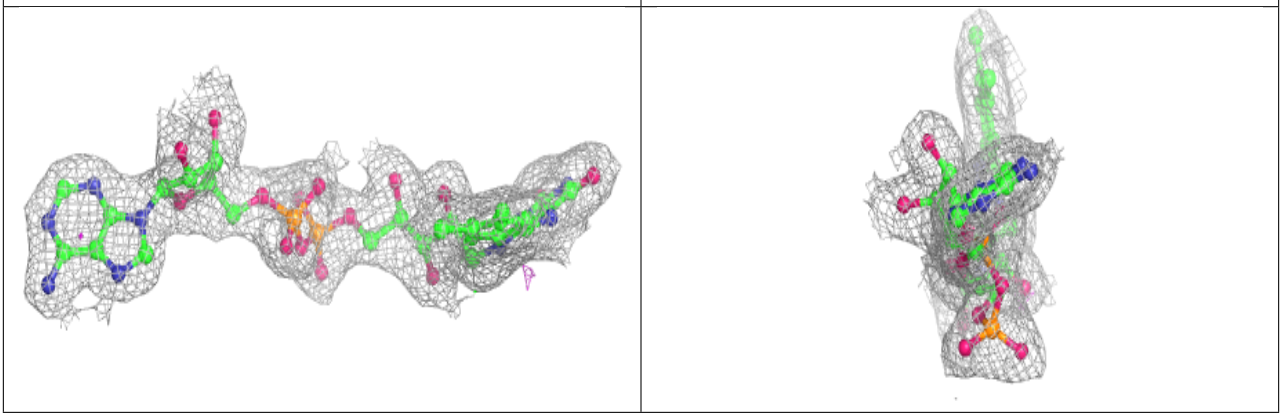




Electron density around FAD A 601:

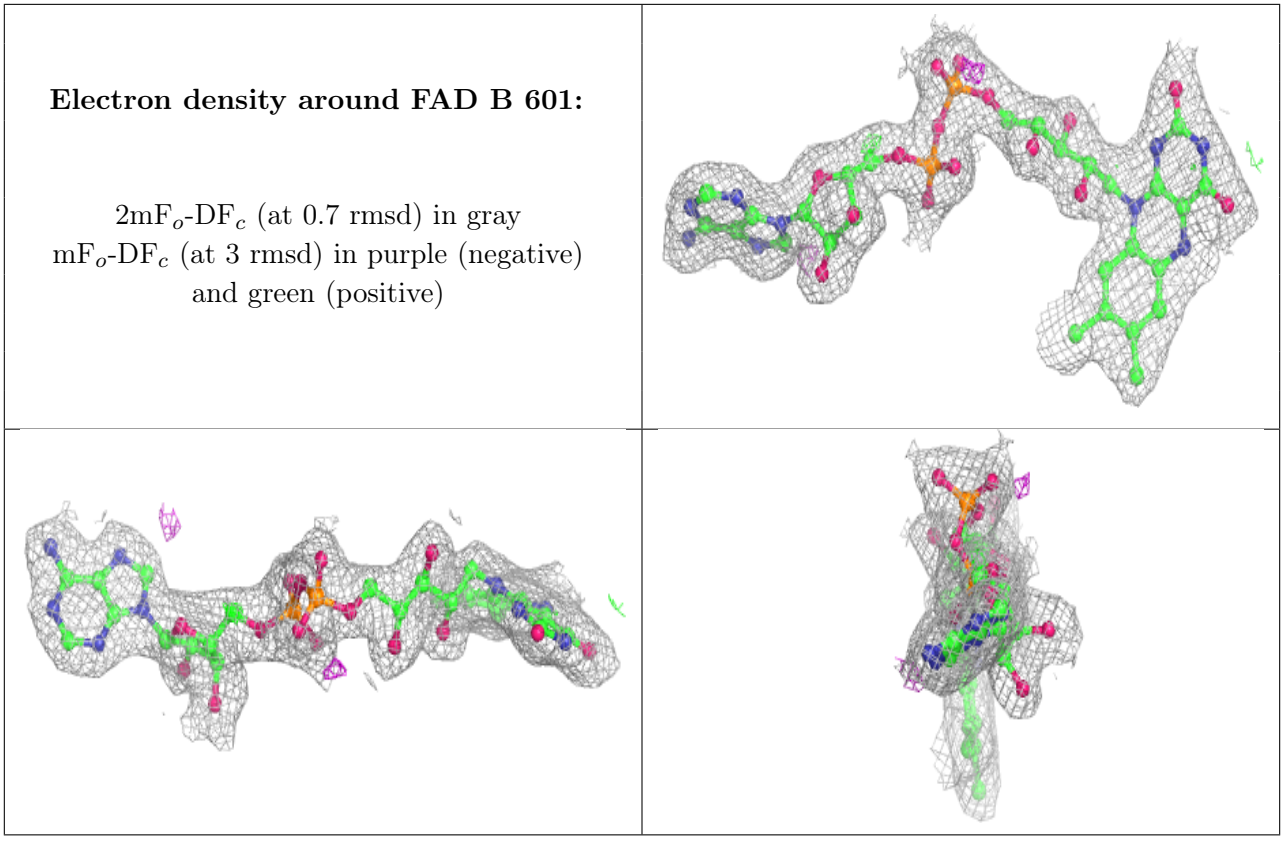
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)





Electron density around FAD B 601:

$2mF_o$-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.