



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 09:20 AM GMT

PDB ID : 3I3L  
Title : Crystal structure of CmlS, a flavin-dependent halogenase  
Authors : Podzelinska, K.; Soares, A.; Jia, Z.; Montreal-Kingston Bacterial Structural Genomics Initiative (BSGI)  
Deposited on : 2009-06-30  
Resolution : 2.20 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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

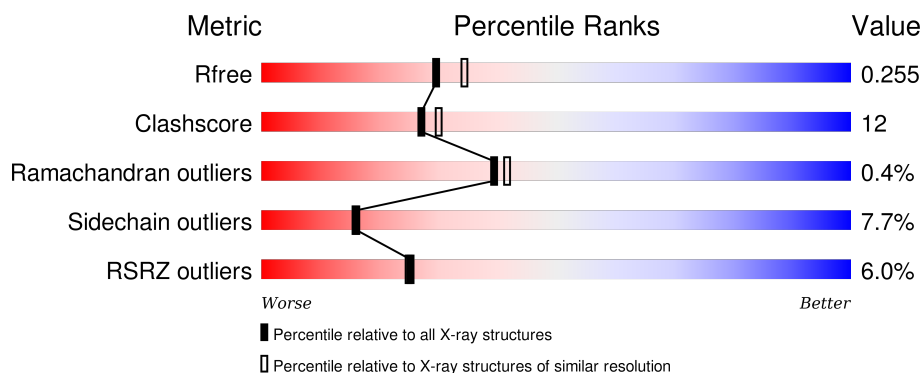
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*


The reported resolution of this entry is 2.20 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	3774 (2.20-2.20)
Clashscore	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)
RSRZ outliers	91569	3781 (2.20-2.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	591	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4641 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.

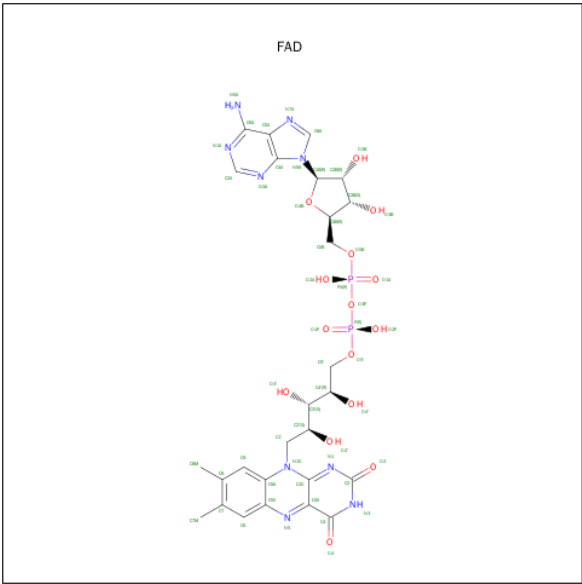
- Molecule 1 is a protein called Alkylhalidase CmlS.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	550	Total	C	N	O	S	0	0	0
			4356	2755	762	828	11			

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	EXPRESSION TAG	UNP Q9AL91
A	-18	GLY	-	EXPRESSION TAG	UNP Q9AL91
A	-17	SER	-	EXPRESSION TAG	UNP Q9AL91
A	-16	SER	-	EXPRESSION TAG	UNP Q9AL91
A	-15	HIS	-	EXPRESSION TAG	UNP Q9AL91
A	-14	HIS	-	EXPRESSION TAG	UNP Q9AL91
A	-13	HIS	-	EXPRESSION TAG	UNP Q9AL91
A	-12	HIS	-	EXPRESSION TAG	UNP Q9AL91
A	-11	HIS	-	EXPRESSION TAG	UNP Q9AL91
A	-10	HIS	-	EXPRESSION TAG	UNP Q9AL91
A	-9	SER	-	EXPRESSION TAG	UNP Q9AL91
A	-8	SER	-	EXPRESSION TAG	UNP Q9AL91
A	-7	GLY	-	EXPRESSION TAG	UNP Q9AL91
A	-6	LEU	-	EXPRESSION TAG	UNP Q9AL91
A	-5	VAL	-	EXPRESSION TAG	UNP Q9AL91
A	-4	PRO	-	EXPRESSION TAG	UNP Q9AL91
A	-3	ARG	-	EXPRESSION TAG	UNP Q9AL91
A	-2	GLY	-	EXPRESSION TAG	UNP Q9AL91
A	-1	SER	-	EXPRESSION TAG	UNP Q9AL91
A	0	HIS	-	EXPRESSION TAG	UNP Q9AL91
A	?	-	ILE	SEE REMARK 999	UNP Q9AL91
A	?	-	PHE	SEE REMARK 999	UNP Q9AL91
A	?	-	ARG	SEE REMARK 999	UNP Q9AL91
A	?	-	ARG	SEE REMARK 999	UNP Q9AL91
A	?	-	SER	SEE REMARK 999	UNP Q9AL91
A	?	-	VAL	SEE REMARK 999	UNP Q9AL91

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula:  $C_{27}H_{33}N_9O_{15}P_2$ ).



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

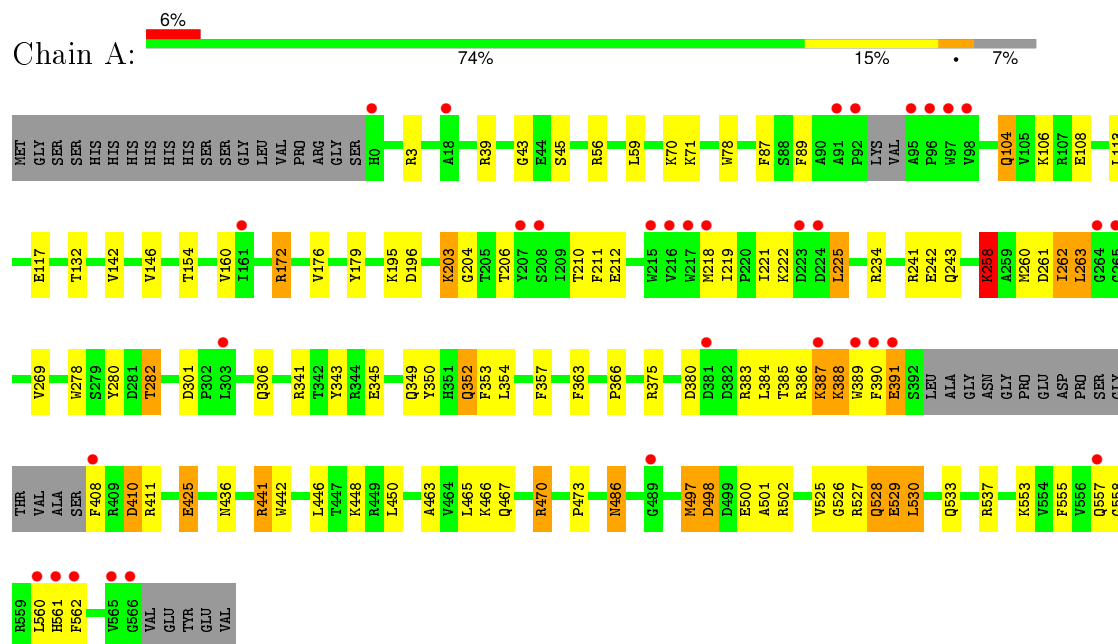
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	232	Total	O	0	0
			232	232		

### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: Alkylhalidase CmlS



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	208.09 Å   57.74 Å   59.88 Å 90.00°   97.47°   90.00°	Depositor
Resolution (Å)	30.00 – 2.20 26.25 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.4 (30.00-2.20) 99.5 (26.25-2.20)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.08	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.21 (at 2.20 Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, $R_{free}$	0.200   ,   0.261 0.197   ,   0.255	Depositor DCC
$R_{free}$ test set	1786 reflections (5.24%)	DCC
Wilson B-factor (Å <sup>2</sup> )	36.0	Xtriage
Anisotropy	0.432	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 42.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 35864 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4641	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.74% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: FAD

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	0.98	1/4456 (0.0%)	0.79	4/6024 (0.1%)

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

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	258	LYS	CE-NZ	6.13	1.64	1.49

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	380	ASP	CB-CG-OD1	6.32	123.99	118.30
1	A	3	ARG	NE-CZ-NH2	-5.64	117.48	120.30
1	A	113	LEU	CA-CB-CG	5.52	128.00	115.30
1	A	375	ARG	NE-CZ-NH1	5.37	122.98	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	387	LYS	Peptide

## 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	4356	0	4196	103	0
2	A	53	0	30	2	0
3	A	232	0	0	5	0
All	All	4641	0	4226	104	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 12.

All (104) 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:441:ARG:HH11	1:A:441:ARG:HG3	1.06	1.14
1:A:529:GLU:CD	1:A:529:GLU:H	1.63	1.01
1:A:206:THR:HG23	1:A:219:ILE:CD1	1.90	1.01
1:A:206:THR:HG23	1:A:219:ILE:HD11	1.42	0.99
1:A:441:ARG:NH1	1:A:441:ARG:HG3	1.72	0.96
1:A:218:MET:SD	1:A:262:ILE:CD1	2.54	0.95
1:A:218:MET:SD	1:A:262:ILE:HD12	2.08	0.93
1:A:470:ARG:HG3	1:A:470:ARG:HH11	1.32	0.93
1:A:59:LEU:HD21	1:A:117:GLU:HG2	1.52	0.91
1:A:218:MET:SD	1:A:262:ILE:HD11	2.20	0.81
1:A:203:LYS:HD3	1:A:204:GLY:N	1.99	0.78
1:A:497:MET:HE3	1:A:527:ARG:CZ	2.13	0.78
1:A:441:ARG:HH11	1:A:441:ARG:CG	1.94	0.78
1:A:470:ARG:CG	1:A:470:ARG:HH11	1.98	0.74
1:A:529:GLU:CD	1:A:529:GLU:N	2.41	0.70
1:A:425:GLU:HB3	3:A:751:HOH:O	1.90	0.70
1:A:408:PHE:N	1:A:411:ARG:HB2	2.08	0.69
1:A:262:ILE:HD13	1:A:263:LEU:N	2.10	0.66
1:A:176:VAL:HG23	1:A:282:THR:CG2	2.28	0.64
1:A:497:MET:CE	1:A:527:ARG:CZ	2.78	0.61
1:A:258:LYS:O	1:A:261:ASP:HB3	2.02	0.60
1:A:410:ASP:HB3	1:A:557:GLN:NE2	2.17	0.60
1:A:486:ASN:HD22	1:A:486:ASN:C	2.06	0.59
1:A:87:PHE:HZ	1:A:561:HIS:HD1	1.48	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:260:MET:HA	1:A:260:MET:HE2	1.85	0.58
1:A:260:MET:CE	1:A:263:LEU:HD23	2.34	0.58
1:A:87:PHE:CD2	1:A:562:PHE:CE1	2.92	0.58
1:A:87:PHE:CD2	1:A:562:PHE:CZ	2.92	0.57
1:A:526:GLY:HA2	1:A:528:GLN:HE22	1.70	0.57
1:A:172:ARG:C	1:A:172:ARG:HD3	2.25	0.57
1:A:206:THR:CG2	1:A:219:ILE:HD11	2.27	0.56
1:A:497:MET:HE3	1:A:527:ARG:NH1	2.19	0.56
1:A:500:GLU:HG2	1:A:525:VAL:HG21	1.87	0.56
1:A:71:LYS:HE3	1:A:89:PHE:HE2	1.71	0.55
1:A:352:GLN:HG2	1:A:353:PHE:N	2.20	0.55
1:A:258:LYS:HE2	3:A:576:HOH:O	2.06	0.54
1:A:353:PHE:CZ	1:A:357:PHE:HE1	2.25	0.54
1:A:526:GLY:C	1:A:528:GLN:NE2	2.61	0.54
1:A:203:LYS:C	1:A:203:LYS:HD3	2.27	0.54
1:A:353:PHE:CE1	1:A:357:PHE:CE1	2.97	0.53
1:A:387:LYS:HG2	1:A:387:LYS:O	2.09	0.53
1:A:470:ARG:NH1	1:A:470:ARG:CG	2.68	0.52
1:A:526:GLY:CA	1:A:528:GLN:HE22	2.22	0.52
1:A:301:ASP:HB3	1:A:354:LEU:HD21	1.92	0.52
1:A:260:MET:CE	1:A:260:MET:HA	2.40	0.51
1:A:172:ARG:O	1:A:172:ARG:HD3	2.11	0.50
1:A:106:LYS:HG2	1:A:108:GLU:HG2	1.92	0.50
1:A:206:THR:CG2	1:A:219:ILE:CD1	2.78	0.50
1:A:553:LYS:HD2	1:A:555:PHE:CE1	2.47	0.50
1:A:466:LYS:HG2	1:A:467:GLN:N	2.26	0.50
1:A:104:GLN:HE21	1:A:104:GLN:HA	1.77	0.50
1:A:211:PHE:HB2	3:A:610:HOH:O	2.10	0.50
1:A:260:MET:HE1	1:A:263:LEU:HD23	1.94	0.49
1:A:222:LYS:HB2	1:A:225:LEU:HB2	1.94	0.49
1:A:442:TRP:HZ2	1:A:558:GLY:HA2	1.78	0.49
1:A:218:MET:CE	1:A:262:ILE:HD12	2.44	0.48
1:A:446:LEU:HD23	1:A:446:LEU:O	2.14	0.47
1:A:212:GLU:HG3	1:A:366:PRO:HG2	1.97	0.47
1:A:262:ILE:C	1:A:262:ILE:HD13	2.35	0.47
1:A:221:ILE:HD11	1:A:225:LEU:HD13	1.97	0.47
1:A:43:GLY:HA2	2:A:600:FAD:C4X	2.45	0.46
1:A:529:GLU:N	1:A:529:GLU:OE1	2.47	0.46
1:A:498:ASP:OD1	1:A:500:GLU:HB3	2.16	0.46
1:A:497:MET:HE1	1:A:527:ARG:NE	2.31	0.46
1:A:388:LYS:O	1:A:391:GLU:OE1	2.34	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:278:TRP:N	1:A:278:TRP:CD1	2.83	0.45
1:A:353:PHE:CE1	1:A:357:PHE:HE1	2.33	0.45
1:A:179:TYR:HA	1:A:280:TYR:HB3	1.98	0.45
1:A:537:ARG:HD3	1:A:537:ARG:HA	1.66	0.45
1:A:56:ARG:HD2	1:A:473:PRO:O	2.16	0.45
1:A:176:VAL:HG23	1:A:282:THR:HG23	1.99	0.45
1:A:528:GLN:H	1:A:528:GLN:NE2	2.14	0.45
1:A:225:LEU:HA	1:A:225:LEU:HD23	1.82	0.45
1:A:78:TRP:CE3	1:A:210:THR:HG23	2.53	0.44
1:A:45:SER:CB	1:A:104:GLN:HE22	2.30	0.44
1:A:386:ARG:C	1:A:388:LYS:H	2.21	0.44
1:A:363:PHE:HZ	1:A:386:ARG:HD2	1.83	0.44
1:A:465:LEU:HD11	1:A:498:ASP:C	2.38	0.43
1:A:446:LEU:CD2	1:A:450:LEU:HD12	2.48	0.43
2:A:600:FAD:H1'1	2:A:600:FAD:H9	1.48	0.43
1:A:441:ARG:NH1	1:A:441:ARG:CG	2.55	0.43
1:A:529:GLU:OE1	1:A:530:LEU:HD22	2.18	0.43
1:A:497:MET:HE2	1:A:501:ALA:CB	2.49	0.43
1:A:526:GLY:C	1:A:528:GLN:HE21	2.22	0.43
1:A:470:ARG:NH1	1:A:470:ARG:HG3	2.13	0.43
1:A:306:GLN:HG3	1:A:350:TYR:CE1	2.54	0.42
1:A:497:MET:HE2	1:A:501:ALA:HB3	2.00	0.42
1:A:446:LEU:HD23	1:A:446:LEU:C	2.39	0.42
1:A:526:GLY:CA	1:A:528:GLN:NE2	2.82	0.42
1:A:195:LYS:O	1:A:196:ASP:C	2.58	0.42
1:A:388:LYS:HG2	1:A:388:LYS:O	2.20	0.42
1:A:301:ASP:CB	1:A:354:LEU:HD21	2.49	0.41
1:A:385:THR:O	1:A:388:LYS:N	2.53	0.41
1:A:203:LYS:HD2	3:A:622:HOH:O	2.19	0.41
1:A:142:VAL:HG11	1:A:160:VAL:HB	2.02	0.41
1:A:341:ARG:O	1:A:345:GLU:HG3	2.20	0.41
1:A:486:ASN:C	1:A:486:ASN:ND2	2.72	0.41
1:A:533:GLN:OE1	1:A:533:GLN:N	2.52	0.41
1:A:463:ALA:O	1:A:502:ARG:HD2	2.21	0.41
1:A:389:TRP:C	1:A:391:GLU:H	2.23	0.41
1:A:436:ASN:HA	1:A:436:ASN:HD22	1.60	0.41
1:A:497:MET:HB3	1:A:497:MET:HE2	1.77	0.40
1:A:70:LYS:HG3	3:A:732:HOH:O	2.21	0.40
1:A:45:SER:HA	1:A:104:GLN:NE2	2.36	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	544/591 (92%)	520 (96%)	22 (4%)	2 (0%)	39	42

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	560	LEU
1	A	390	PHE

### 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	452/492 (92%)	417 (92%)	35 (8%)	16	16

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	39	ARG
1	A	104	GLN
1	A	132	THR
1	A	146	VAL
1	A	154	THR
1	A	172	ARG
1	A	203	LYS
1	A	225	LEU
1	A	234	ARG

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Mol	Chain	Res	Type
1	A	241	ARG
1	A	242	GLU
1	A	243	GLN
1	A	258	LYS
1	A	262	ILE
1	A	263	LEU
1	A	269	VAL
1	A	282	THR
1	A	343	TYR
1	A	349	GLN
1	A	352	GLN
1	A	383	ARG
1	A	384	LEU
1	A	388	LYS
1	A	391	GLU
1	A	410	ASP
1	A	425	GLU
1	A	441	ARG
1	A	448	LYS
1	A	470	ARG
1	A	486	ASN
1	A	497	MET
1	A	498	ASP
1	A	528	GLN
1	A	529	GLU
1	A	530	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	23	HIS
1	A	55	ASN
1	A	66	GLN
1	A	104	GLN
1	A	126	HIS
1	A	243	GLN
1	A	268	GLN
1	A	436	ASN
1	A	451	ASN
1	A	486	ASN
1	A	528	GLN
1	A	557	GLN

### 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 ⓘ

1 ligand is 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$
2	FAD	A	600	1	48,58,58	1.30	7 (14%)	54,89,89	2.40	8 (14%)

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	FAD	A	600	1	-	0/30/50/50	0/6/6/6

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	600	FAD	C10-N10	-3.73	1.34	1.39
2	A	600	FAD	C9A-C5X	-2.64	1.37	1.42
2	A	600	FAD	O2'-C2'	-2.60	1.37	1.43
2	A	600	FAD	C2A-N1A	2.02	1.37	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	600	FAD	C4-N3	2.33	1.37	1.33
2	A	600	FAD	C2A-N3A	2.46	1.36	1.32
2	A	600	FAD	C4X-N5	2.50	1.37	1.33

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	600	FAD	N3A-C2A-N1A	-12.54	119.30	128.89
2	A	600	FAD	C4X-C4-N3	-3.78	118.43	123.59
2	A	600	FAD	C1'-N10-C9A	-2.33	116.25	118.86
2	A	600	FAD	C9A-C5X-N5	-2.20	119.10	122.36
2	A	600	FAD	C4X-N5-C5X	2.32	119.44	116.76
2	A	600	FAD	C2B-C1B-N9A	2.39	117.94	114.29
2	A	600	FAD	C5X-C9A-N10	6.05	122.22	117.62
2	A	600	FAD	C4-N3-C2	6.29	120.68	115.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	600	FAD	2	0

## 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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	550/591 (93%)	0.16	33 (6%) 25 25	19, 36, 60, 80	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	97	TRP	6.2
1	A	96	PRO	5.6
1	A	562	PHE	5.0
1	A	408	PHE	4.5
1	A	92	PRO	4.2
1	A	389	TRP	4.1
1	A	560	LEU	4.1
1	A	98	VAL	3.9
1	A	265	GLY	3.8
1	A	91	ALA	3.8
1	A	561	HIS	3.6
1	A	95	ALA	3.4
1	A	390	PHE	3.4
1	A	391	GLU	3.1
1	A	208	SER	2.7
1	A	217	TRP	2.7
1	A	303	LEU	2.7
1	A	224	ASP	2.7
1	A	566	GLY	2.6
1	A	489	GLY	2.6
1	A	381	ASP	2.5
1	A	387	LYS	2.5
1	A	161	ILE	2.5
1	A	264	GLY	2.4
1	A	565	VAL	2.3
1	A	223	ASP	2.3
1	A	218	MET	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	215	TRP	2.2
1	A	18	ALA	2.2
1	A	216	VAL	2.1
1	A	0	HIS	2.1
1	A	207	TYR	2.0
1	A	557	GLN	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	FAD	A	600	53/53	0.98	0.13	-0.42	19,26,30,32	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.