



wwPDB X-ray Structure Validation Summary Report

Feb 26, 2014 – 07:46 PM GMT

PDB ID : 4C5O
Title : Flavin monooxygenase from *Stenotrophomonas maltophilia*. Q193R H194T mutant
Authors : Jensen, C.N.; Ali, S.T.; Allen, M.J.; Grogan, G.
Deposited on : 2013-09-13
Resolution : 2.60 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

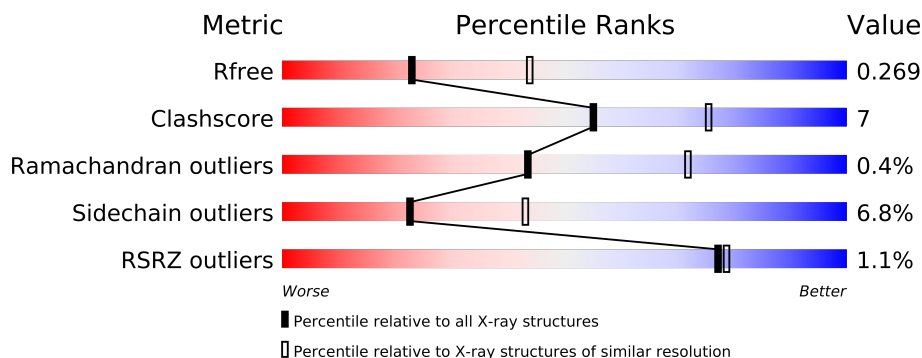
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.60 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}	66092	1718 (2.60-2.60)
Clashscore	79885	2154 (2.60-2.60)
Ramachandran outliers	78287	2113 (2.60-2.60)
Sidechain outliers	78261	2113 (2.60-2.60)
RSRZ outliers	66119	1718 (2.60-2.60)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	357	
1	B	357	
1	C	357	
1	D	357	
1	E	357	
1	F	357	
1	G	357	
1	H	357	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
3	SO4	A	1355	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
3	SO4	B	1355	-	X
3	SO4	B	1357	-	X
3	SO4	C	1355	-	X
3	SO4	C	1356	-	X
3	SO4	C	1357	-	X
3	SO4	D	1355	-	X
3	SO4	D	1356	-	X
3	SO4	D	1358	-	X
3	SO4	E	1355	-	X
3	SO4	F	1356	-	X
3	SO4	F	1357	-	X
3	SO4	G	1355	-	X
3	SO4	H	1355	-	X
3	SO4	H	1356	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 20137 atoms, of which 0 are hydrogen and 0 are deuterium.

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 FLAVIN MONOOXYGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	327	Total	C	N	O	S	0	0	0
			2256	1444	392	414	6			
1	B	330	Total	C	N	O	S	0	0	0
			2388	1533	414	434	7			
1	C	330	Total	C	N	O	S	0	0	0
			2475	1588	436	443	8			
1	D	333	Total	C	N	O	S	0	0	0
			2495	1599	438	451	7			
1	E	330	Total	C	N	O	S	0	0	0
			2448	1574	429	437	8			
1	F	330	Total	C	N	O	S	0	0	0
			2436	1567	422	440	7			
1	G	330	Total	C	N	O	S	0	0	0
			2450	1575	432	436	7			
1	H	331	Total	C	N	O	S	0	0	0
			2494	1597	441	448	8			

There are 16 discrepancies between the modelled and reference sequences:

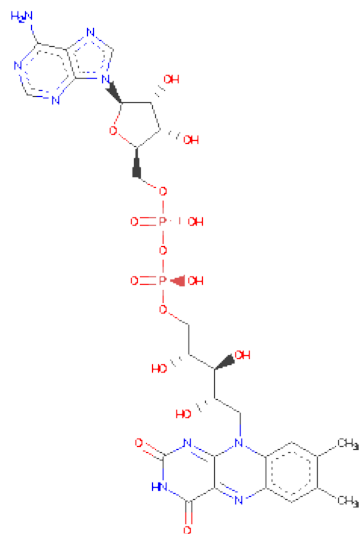
Chain	Residue	Modelled	Actual	Comment	Reference
A	193	ARG	GLN	ENGINEERED MUTATION	UNP B2FRL2
A	194	THR	HIS	ENGINEERED MUTATION	UNP B2FRL2
B	193	ARG	GLN	ENGINEERED MUTATION	UNP B2FRL2
B	194	THR	HIS	ENGINEERED MUTATION	UNP B2FRL2
C	193	ARG	GLN	ENGINEERED MUTATION	UNP B2FRL2
C	194	THR	HIS	ENGINEERED MUTATION	UNP B2FRL2
D	193	ARG	GLN	ENGINEERED MUTATION	UNP B2FRL2
D	194	THR	HIS	ENGINEERED MUTATION	UNP B2FRL2
E	193	ARG	GLN	ENGINEERED MUTATION	UNP B2FRL2
E	194	THR	HIS	ENGINEERED MUTATION	UNP B2FRL2
F	193	ARG	GLN	ENGINEERED MUTATION	UNP B2FRL2
F	194	THR	HIS	ENGINEERED MUTATION	UNP B2FRL2
G	193	ARG	GLN	ENGINEERED MUTATION	UNP B2FRL2

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Chain	Residue	Modelled	Actual	Comment	Reference
G	194	THR	HIS	ENGINEERED MUTATION	UNP B2FRL2
H	193	ARG	GLN	ENGINEERED MUTATION	UNP B2FRL2
H	194	THR	HIS	ENGINEERED MUTATION	UNP B2FRL2

- 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
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		
2	C	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	D	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	E	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	F	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	G	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	H	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		
3	G	1	Total	O	S	0	0
			5	4	1		
3	G	1	Total	O	S	0	0
			5	4	1		
3	G	1	Total	O	S	0	0
			5	4	1		
3	G	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is water.

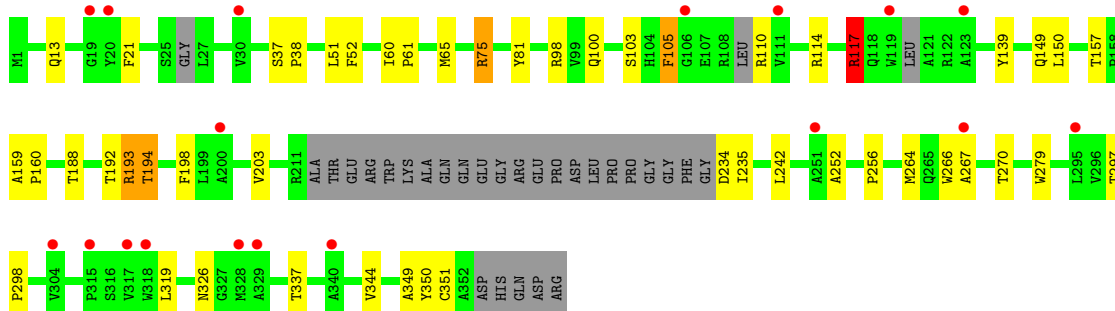
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	5	Total 5	O 5	0	0
4	B	4	Total 4	O 4	0	0
4	C	18	Total 18	O 18	0	0
4	D	12	Total 12	O 12	0	0
4	E	13	Total 13	O 13	0	0
4	F	18	Total 18	O 18	0	0
4	G	15	Total 15	O 15	0	0
4	H	21	Total 21	O 21	0	0

3 Residue-property plots

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.

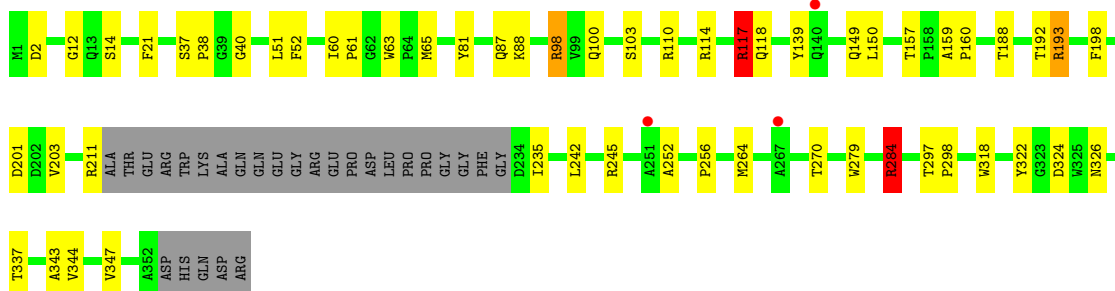
• Molecule 1: FLAVIN MONOOXYGENASE

Chain A: 



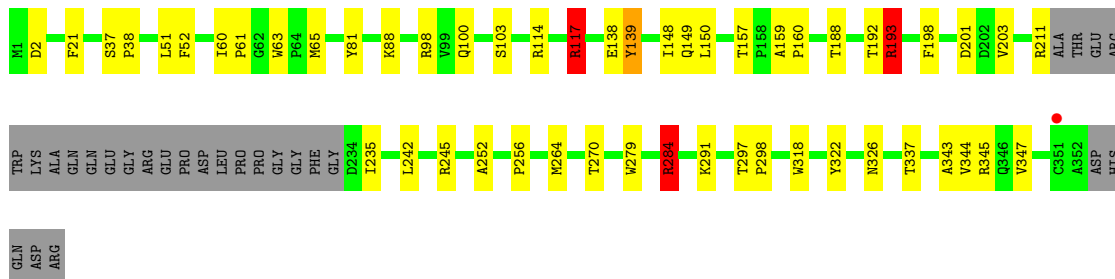
• Molecule 1: FLAVIN MONOOXYGENASE

Chain B: 



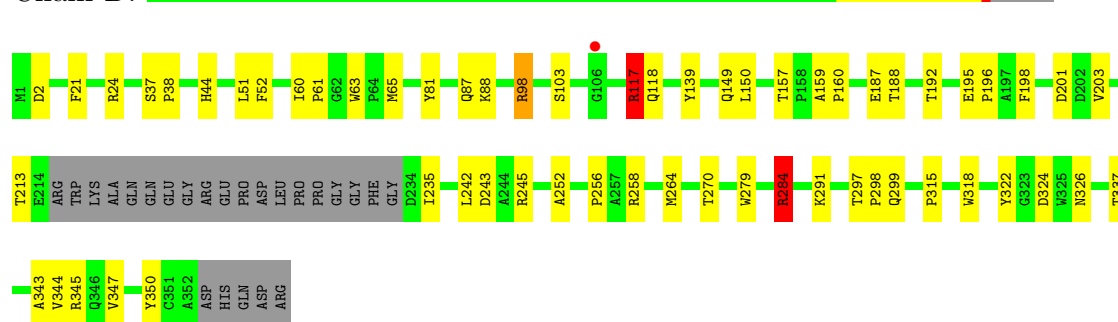
• Molecule 1: FLAVIN MONOOXYGENASE

Chain C: 



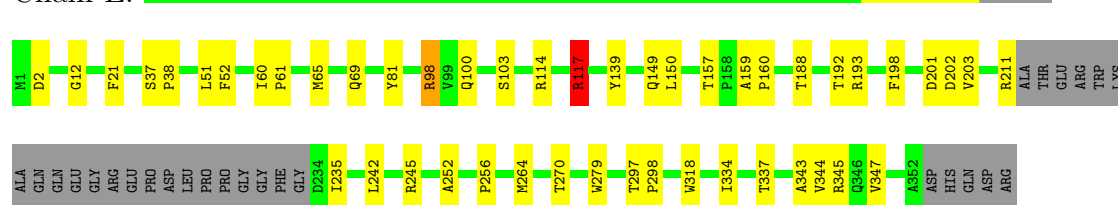
- Molecule 1: FLAVIN MONOOXYGENASE

Chain D:



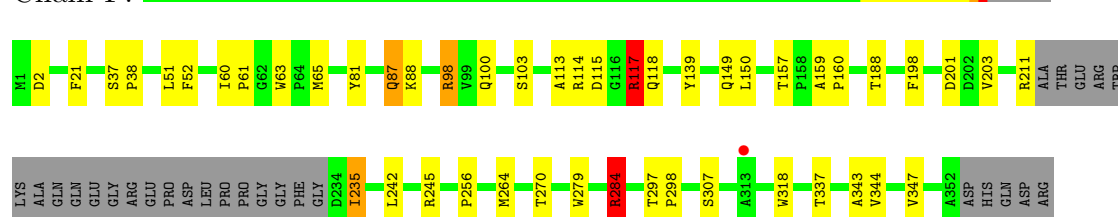
- Molecule 1: FLAVIN MONOOXYGENASE

Chain E:



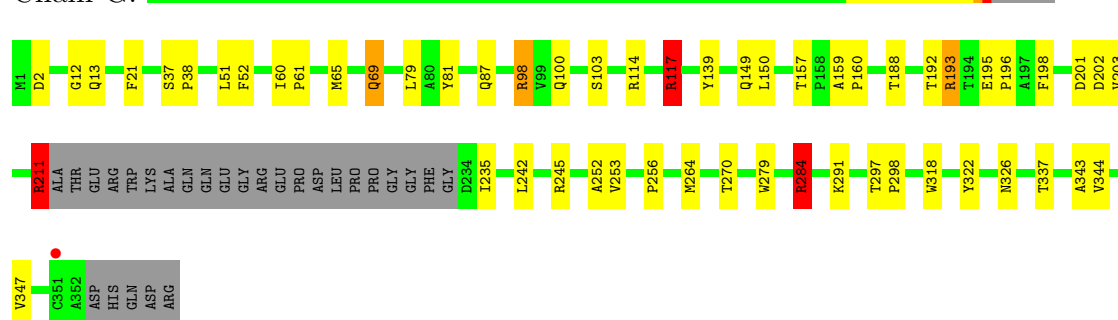
- Molecule 1: FLAVIN MONOOXYGENASE

Chain F:



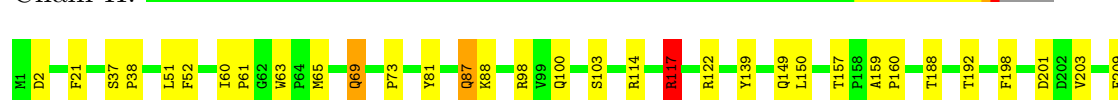
- Molecule 1: FLAVIN MONOOXYGENASE

Chain G:



- Molecule 1: FLAVIN MONOOXYGENASE

Chain H:



E210	R211	A212	THR	GLU	ARG	TRP	LYS	ALA	GLN	GLN	GLU	GLY	ARG	GLU	PRO	ASP	LEU	PRO	PRO	GLY	GLY	PHE	GLY	D234	I235
------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------

HIS	GLN	ASP	ARG
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L242	R245	A252	P256	K264	T270	W279	R284	T297	P298	Y322	N326	T337	A343	Y344	R345	D346	Y347	A352	ASP
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4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	170.54Å 170.54Å 101.76Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	147.69 – 2.60 49.23 – 2.40	Depositor EDS
% Data completeness (in resolution range)	97.2 (147.69-2.60) 97.6 (49.23-2.40)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.78 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.8.0033	Depositor
R, R_{free}	0.255 , 0.295 0.255 , 0.269	Depositor DCC
R_{free} test set	6398 reflections (5.31%)	DCC
Wilson B-factor (Å ²)	46.4	Xtriage
Anisotropy	0.101	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 10.0	EDS
Estimated twinning fraction	0.039 for -h,-k,l 0.057 for h,-h-k,-l 0.044 for -k,-h,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 126991 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	20137	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 71.77 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 2.4807e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, 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	0.59	0/2318	0.77	7/3187 (0.2%)
1	B	0.60	0/2457	0.78	6/3377 (0.2%)
1	C	0.64	0/2546	0.77	6/3483 (0.2%)
1	D	0.65	0/2566	0.79	3/3512 (0.1%)
1	E	0.65	0/2519	0.74	1/3451 (0.0%)
1	F	0.65	0/2507	0.77	4/3439 (0.1%)
1	G	0.64	0/2521	0.77	4/3454 (0.1%)
1	H	0.67	0/2565	0.78	3/3508 (0.1%)
All	All	0.64	0/19999	0.77	34/27411 (0.1%)

There are no bond length outliers.

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	211	ARG	N-CA-C	8.91	135.06	111.00
1	H	117	ARG	NE-CZ-NH1	8.48	124.54	120.30
1	C	284	ARG	NE-CZ-NH1	8.34	124.47	120.30
1	D	284	ARG	NE-CZ-NH1	8.33	124.47	120.30
1	G	117	ARG	NE-CZ-NH1	8.12	124.36	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the

chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2256	0	2032	29	0
1	B	2388	0	2265	34	0
1	C	2475	0	2413	31	0
1	D	2495	0	2425	35	0
1	E	2448	0	2370	27	0
1	F	2436	0	2339	30	0
1	G	2450	0	2375	35	0
1	H	2494	0	2434	39	0
2	A	53	0	31	4	0
2	B	53	0	31	4	0
2	C	53	0	31	0	0
2	D	53	0	31	1	0
2	E	53	0	31	2	0
2	F	53	0	31	0	0
2	G	53	0	31	3	0
2	H	53	0	31	2	0
3	A	15	0	0	1	0
3	B	20	0	0	2	0
3	C	25	0	0	1	0
3	D	30	0	0	3	0
3	E	15	0	0	2	0
3	F	20	0	0	3	0
3	G	20	0	0	2	0
3	H	20	0	0	1	0
4	A	5	0	0	1	0
4	B	4	0	0	1	0
4	C	18	0	0	0	0
4	D	12	0	0	1	0
4	E	13	0	0	0	0
4	F	18	0	0	1	0
4	G	15	0	0	0	0
4	H	21	0	0	0	0
All	All	20137	0	18901	259	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 7.

The worst 5 of 259 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:H:210:GLU:C	1:H:212:ALA:HB3	1.59	1.22

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:H:210:GLU:O	1:H:212:ALA:HB3	1.52	1.10
1:A:266:TRP:O	1:D:315:PRO:HG2	1.68	0.92
1:H:210:GLU:C	1:H:212:ALA:CB	2.40	0.89
1:D:117:ARG:HG3	1:D:117:ARG:HH11	1.39	0.86

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	317/357 (89%)	296 (93%)	18 (6%)	3 (1%)	25	49
1	B	326/357 (91%)	309 (95%)	16 (5%)	1 (0%)	50	77
1	C	326/357 (91%)	310 (95%)	15 (5%)	1 (0%)	50	77
1	D	329/357 (92%)	316 (96%)	12 (4%)	1 (0%)	50	77
1	E	326/357 (91%)	311 (95%)	14 (4%)	1 (0%)	50	77
1	F	326/357 (91%)	311 (95%)	14 (4%)	1 (0%)	50	77
1	G	326/357 (91%)	312 (96%)	13 (4%)	1 (0%)	50	77
1	H	327/357 (92%)	312 (95%)	14 (4%)	1 (0%)	50	77
All	All	2603/2856 (91%)	2477 (95%)	116 (4%)	10 (0%)	43	72

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	139	TYR
1	A	350	TYR
1	B	139	TYR
1	C	139	TYR
1	D	139	TYR

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	193/272 (71%)	181 (94%)	12 (6%)	26	49
1	B	225/272 (83%)	211 (94%)	14 (6%)	26	49
1	C	244/272 (90%)	228 (93%)	16 (7%)	24	45
1	D	246/272 (90%)	226 (92%)	20 (8%)	17	32
1	E	238/272 (88%)	223 (94%)	15 (6%)	25	49
1	F	235/272 (86%)	220 (94%)	15 (6%)	25	47
1	G	237/272 (87%)	219 (92%)	18 (8%)	19	36
1	H	247/272 (91%)	230 (93%)	17 (7%)	22	42
All	All	1865/2176 (86%)	1738 (93%)	127 (7%)	22	43

5 of 127 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	270	THR
1	E	203	VAL
1	H	117	ARG
1	D	291	LYS
1	E	52	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	326	ASN
1	E	301	GLN
1	H	299	GLN
1	E	149	GLN
1	E	326	ASN

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

41 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	$\# Z > 2$
2	FAD	A	1353	-	58,58,58	1.78	11 (18%)	85,89,89	2.56	20 (23%)
3	SO4	A	1354	-	4,4,4	0.45	0	6,6,6	0.83	0
3	SO4	A	1355	-	4,4,4	0.60	0	6,6,6	0.14	0
3	SO4	A	1356	-	4,4,4	0.73	0	6,6,6	0.58	0
2	FAD	B	1353	-	58,58,58	1.84	12 (20%)	85,89,89	2.63	23 (27%)
3	SO4	B	1354	-	4,4,4	0.49	0	6,6,6	0.54	0
3	SO4	B	1355	-	4,4,4	0.69	0	6,6,6	0.31	0
3	SO4	B	1356	-	4,4,4	0.73	0	6,6,6	0.59	0
3	SO4	B	1357	-	4,4,4	0.46	0	6,6,6	0.18	0
2	FAD	C	1353	-	58,58,58	1.85	10 (17%)	85,89,89	2.75	23 (27%)
3	SO4	C	1354	-	4,4,4	0.58	0	6,6,6	0.43	0
3	SO4	C	1355	-	4,4,4	0.56	0	6,6,6	0.27	0
3	SO4	C	1356	-	4,4,4	0.48	0	6,6,6	0.25	0
3	SO4	C	1357	-	4,4,4	0.72	0	6,6,6	0.56	0
3	SO4	C	1358	-	4,4,4	0.64	0	6,6,6	0.37	0
2	FAD	D	1353	-	58,58,58	1.54	11 (18%)	85,89,89	2.70	27 (31%)
3	SO4	D	1354	-	4,4,4	0.62	0	6,6,6	0.38	0
3	SO4	D	1355	-	4,4,4	0.72	0	6,6,6	0.21	0
3	SO4	D	1356	-	4,4,4	0.63	0	6,6,6	0.16	0
3	SO4	D	1357	-	4,4,4	0.88	0	6,6,6	0.33	0
3	SO4	D	1358	-	4,4,4	0.47	0	6,6,6	0.17	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SO4	D	1359	-	4,4,4	0.38	0	6,6,6	0.81	0
2	FAD	E	1353	-	58,58,58	1.75	15 (25%)	85,89,89	2.50	18 (21%)
3	SO4	E	1354	-	4,4,4	0.99	0	6,6,6	0.48	0
3	SO4	E	1355	-	4,4,4	0.81	0	6,6,6	0.52	0
3	SO4	E	1356	-	4,4,4	0.82	0	6,6,6	0.95	0
2	FAD	F	1353	-	58,58,58	1.56	10 (17%)	85,89,89	2.60	25 (29%)
3	SO4	F	1354	-	4,4,4	0.47	0	6,6,6	0.67	0
3	SO4	F	1355	-	4,4,4	0.51	0	6,6,6	0.47	0
3	SO4	F	1356	-	4,4,4	0.67	0	6,6,6	0.54	0
3	SO4	F	1357	-	4,4,4	0.62	0	6,6,6	0.65	0
2	FAD	G	1353	-	58,58,58	1.70	10 (17%)	85,89,89	2.56	23 (27%)
3	SO4	G	1354	-	4,4,4	0.31	0	6,6,6	0.24	0
3	SO4	G	1355	-	4,4,4	0.56	0	6,6,6	0.23	0
3	SO4	G	1356	-	4,4,4	0.80	0	6,6,6	0.65	0
3	SO4	G	1357	-	4,4,4	0.75	0	6,6,6	0.38	0
2	FAD	H	1353	-	58,58,58	1.81	16 (27%)	85,89,89	2.82	28 (32%)
3	SO4	H	1354	-	4,4,4	0.77	0	6,6,6	0.67	0
3	SO4	H	1355	-	4,4,4	0.59	0	6,6,6	0.35	0
3	SO4	H	1356	-	4,4,4	0.53	0	6,6,6	0.17	0
3	SO4	H	1357	-	4,4,4	0.47	0	6,6,6	0.94	0

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	1353	-	-	0/34/50/50	0/1/6/6
3	SO4	A	1354	-	-	0/0/0/0	0/0/0/0
3	SO4	A	1355	-	-	0/0/0/0	0/0/0/0
3	SO4	A	1356	-	-	0/0/0/0	0/0/0/0
2	FAD	B	1353	-	-	0/34/50/50	0/1/6/6
3	SO4	B	1354	-	-	0/0/0/0	0/0/0/0
3	SO4	B	1355	-	-	0/0/0/0	0/0/0/0
3	SO4	B	1356	-	-	0/0/0/0	0/0/0/0
3	SO4	B	1357	-	-	0/0/0/0	0/0/0/0
2	FAD	C	1353	-	-	0/34/50/50	0/1/6/6
3	SO4	C	1354	-	-	0/0/0/0	0/0/0/0
3	SO4	C	1355	-	-	0/0/0/0	0/0/0/0
3	SO4	C	1356	-	-	0/0/0/0	0/0/0/0
3	SO4	C	1357	-	-	0/0/0/0	0/0/0/0
3	SO4	C	1358	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	FAD	D	1353	-	-	0/34/50/50	0/1/6/6
3	SO4	D	1354	-	-	0/0/0/0	0/0/0/0
3	SO4	D	1355	-	-	0/0/0/0	0/0/0/0
3	SO4	D	1356	-	-	0/0/0/0	0/0/0/0
3	SO4	D	1357	-	-	0/0/0/0	0/0/0/0
3	SO4	D	1358	-	-	0/0/0/0	0/0/0/0
3	SO4	D	1359	-	-	0/0/0/0	0/0/0/0
2	FAD	E	1353	-	-	0/34/50/50	0/1/6/6
3	SO4	E	1354	-	-	0/0/0/0	0/0/0/0
3	SO4	E	1355	-	-	0/0/0/0	0/0/0/0
3	SO4	E	1356	-	-	0/0/0/0	0/0/0/0
2	FAD	F	1353	-	-	0/34/50/50	0/1/6/6
3	SO4	F	1354	-	-	0/0/0/0	0/0/0/0
3	SO4	F	1355	-	-	0/0/0/0	0/0/0/0
3	SO4	F	1356	-	-	0/0/0/0	0/0/0/0
3	SO4	F	1357	-	-	0/0/0/0	0/0/0/0
2	FAD	G	1353	-	-	0/34/50/50	0/1/6/6
3	SO4	G	1354	-	-	0/0/0/0	0/0/0/0
3	SO4	G	1355	-	-	0/0/0/0	0/0/0/0
3	SO4	G	1356	-	-	0/0/0/0	0/0/0/0
3	SO4	G	1357	-	-	0/0/0/0	0/0/0/0
2	FAD	H	1353	-	-	0/34/50/50	0/1/6/6
3	SO4	H	1354	-	-	0/0/0/0	0/0/0/0
3	SO4	H	1355	-	-	0/0/0/0	0/0/0/0
3	SO4	H	1356	-	-	0/0/0/0	0/0/0/0
3	SO4	H	1357	-	-	0/0/0/0	0/0/0/0

The worst 5 of 95 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1353	FAD	C4-C4X	6.45	1.51	1.41
2	A	1353	FAD	C4-C4X	6.02	1.51	1.41
2	H	1353	FAD	C4-C4X	5.84	1.50	1.41
2	A	1353	FAD	C9A-C5X	5.25	1.53	1.42
2	B	1353	FAD	C4-C4X	5.07	1.49	1.41

The worst 5 of 187 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	1353	FAD	C2'-C1'-N10	11.05	127.11	112.45
2	B	1353	FAD	C2'-C1'-N10	10.58	126.49	112.45
2	A	1353	FAD	C2-N1-C10	10.30	125.36	114.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1353	FAD	C2'-C1'-N10	10.25	126.06	112.45
2	H	1353	FAD	O4B-C1B-N9A	9.86	117.61	108.44

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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	327/357 (91%)	0.25	18 (5%) 24 20	40, 79, 111, 127	0
1	B	330/357 (92%)	-0.21	3 (0%) 81 82	31, 65, 95, 135	0
1	C	330/357 (92%)	-0.45	1 (0%) 91 92	26, 45, 69, 86	0
1	D	333/357 (93%)	-0.43	1 (0%) 91 92	25, 46, 74, 94	0
1	E	330/357 (92%)	-0.47	0 100 100	22, 46, 70, 110	0
1	F	330/357 (92%)	-0.32	1 (0%) 91 92	29, 48, 74, 101	0
1	G	330/357 (92%)	-0.42	1 (0%) 91 92	24, 46, 77, 108	0
1	H	331/357 (92%)	-0.53	0 100 100	20, 40, 67, 96	0
All	All	2641/2856 (92%)	-0.32	25 (0%) 77 82	20, 49, 90, 135	0

The worst 5 of 25 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	318	TRP	7.7
1	A	251	ALA	6.6
1	A	304	VAL	4.9
1	G	351	CYS	3.7
1	A	267	ALA	3.6

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 carbohydrates 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. 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, 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	SO4	D	1356	5/5	0.40	30.31	145,150,156,159	0
3	SO4	C	1355	5/5	0.59	29.30	98,122,126,127	0
3	SO4	B	1357	5/5	0.36	24.28	132,135,144,151	0
3	SO4	H	1356	5/5	0.32	17.79	123,129,130,138	0
3	SO4	A	1355	5/5	0.53	16.94	137,139,145,159	0
3	SO4	E	1355	5/5	0.30	16.16	93,94,105,111	0
3	SO4	D	1358	5/5	0.34	14.41	137,141,153,154	0
3	SO4	H	1355	5/5	0.26	9.11	105,117,124,131	0
3	SO4	B	1355	5/5	0.40	8.50	112,113,123,131	0
3	SO4	C	1356	5/5	0.39	6.35	106,114,117,127	0
3	SO4	G	1355	5/5	0.42	6.23	132,142,147,158	0
3	SO4	F	1357	5/5	0.28	5.69	83,88,97,113	0
3	SO4	F	1356	5/5	0.22	5.66	76,83,93,111	0
3	SO4	D	1355	5/5	0.20	3.56	86,89,99,100	0
3	SO4	C	1357	5/5	0.21	2.37	90,91,104,108	0
3	SO4	A	1354	5/5	0.15	0.38	50,52,61,62	0
3	SO4	B	1356	5/5	0.21	0.34	87,90,105,107	0
2	FAD	H	1353	53/53	0.12	0.04	18,25,30,32	0
3	SO4	D	1359	5/5	0.13	0.00	50,56,58,64	0
3	SO4	E	1354	5/5	0.12	-0.11	36,42,44,45	0
2	FAD	F	1353	53/53	0.12	-0.30	23,29,33,43	0
3	SO4	G	1357	5/5	0.12	-0.33	66,73,80,83	0
3	SO4	H	1357	5/5	0.12	-0.35	42,47,51,54	0
3	SO4	C	1354	5/5	0.11	-0.46	37,39,40,42	0
2	FAD	D	1353	53/53	0.12	-0.49	22,28,36,44	0
2	FAD	E	1353	53/53	0.11	-0.50	21,26,33,36	0
2	FAD	C	1353	53/53	0.11	-0.58	23,29,37,38	0
2	FAD	G	1353	53/53	0.11	-0.72	24,30,34,39	0
2	FAD	A	1353	53/53	0.13	-0.89	33,48,57,59	0
2	FAD	B	1353	53/53	0.11	-0.95	25,31,39,44	0
3	SO4	G	1356	5/5	0.08	-1.07	54,56,67,75	0
3	SO4	E	1356	5/5	0.11	-1.21	42,50,51,55	0
3	SO4	F	1355	5/5	0.10	-1.25	46,56,58,68	0
3	SO4	B	1354	5/5	0.09	-1.74	48,49,59,63	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	SO4	C	1358	5/5	0.08	-2.03	59,60,68,70	0
3	SO4	D	1354	5/5	0.07	-2.06	36,40,49,50	0
3	SO4	A	1356	5/5	0.10	-2.32	57,66,83,83	0
3	SO4	F	1354	5/5	0.09	-2.38	33,36,41,45	0
3	SO4	D	1357	5/5	0.08	-2.55	58,60,68,69	0
3	SO4	H	1354	5/5	0.07	-4.74	34,41,44,45	0
3	SO4	G	1354	5/5	0.09	-6.29	47,48,52,52	0

6.5 Other polymers ⓘ

There are no such residues in this entry.