



wwPDB X-ray Structure Validation Summary Report ⓘ

May 29, 2020 – 07:53 am BST

PDB ID : 5MGY
Title : Crystal structure of Pseudomonas stutzeri flavinyl transferase ApbE, apo form
Authors : Zhang, L.; Trncik, C.; Andrade, S.L.A.; Einsle, O.
Deposited on : 2016-11-22
Resolution : 2.60 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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
Xtriage (Phenix)	:	1.13
EDS	:	2.11
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

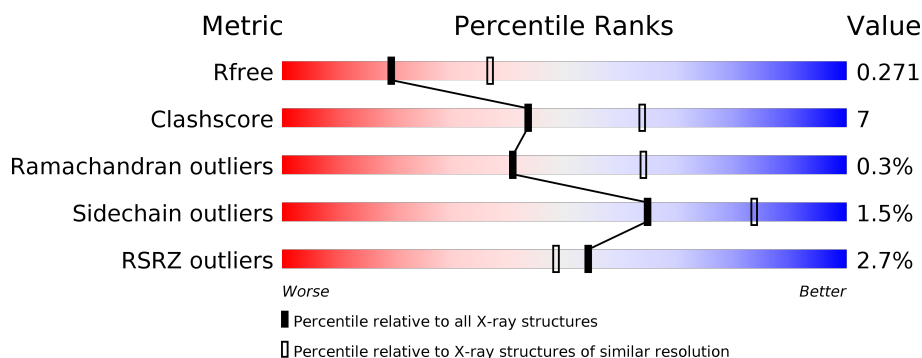
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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}	130704	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (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 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	332	<div> <div>3%</div> <div> <div></div> <div>80%</div> <div>11%</div> <div>• 8%</div> </div> </div>
1	B	332	<div> <div>2%</div> <div> <div></div> <div>79%</div> <div>11%</div> <div>• 9%</div> </div> </div>
1	C	332	<div> <div>2%</div> <div> <div></div> <div>83%</div> <div>10%</div> <div>• 7%</div> </div> </div>
1	D	332	<div> <div>0%</div> <div> <div></div> <div>80%</div> <div>11%</div> <div>• 7%</div> </div> </div>
1	E	332	<div> <div>2%</div> <div> <div></div> <div>83%</div> <div>11%</div> <div>• 5%</div> </div> </div>
1	F	332	<div> <div>2%</div> <div> <div></div> <div>79%</div> <div>15%</div> <div>• 5%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	G	332	<div><div></div><div>5%</div><div>72%</div><div>16%</div><div>•</div><div>10%</div></div>
1	H	332	<div><div></div><div>3%</div><div>83%</div><div>12%</div><div>•</div><div>5%</div></div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 18725 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 FAD:protein FMN transferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	316	Total	C	N	O	S	0	0	0
			2388	1495	415	470	8			
1	B	303	Total	C	N	O	S	0	0	0
			2288	1431	392	457	8			
1	G	299	Total	C	N	O	S	0	0	0
			2261	1422	385	446	8			
1	A	305	Total	C	N	O	S	0	0	0
			2306	1444	395	459	8			
1	C	310	Total	C	N	O	S	0	0	0
			2334	1466	400	460	8			
1	D	309	Total	C	N	O	S	0	0	0
			2330	1464	399	459	8			
1	E	316	Total	C	N	O	S	0	0	0
			2388	1495	415	470	8			
1	F	315	Total	C	N	O	S	0	0	0
			2377	1489	411	469	8			

There are 256 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	27	MET	-	initiating methionine	UNP A0A2N8RKH1
H	28	ALA	-	expression tag	UNP A0A2N8RKH1
H	29	MET	-	expression tag	UNP A0A2N8RKH1
H	30	ASP	-	expression tag	UNP A0A2N8RKH1
H	31	LEU	-	expression tag	UNP A0A2N8RKH1
H	32	PHE	-	expression tag	UNP A0A2N8RKH1
H	33	GLN	-	expression tag	UNP A0A2N8RKH1
H	34	ASP	-	expression tag	UNP A0A2N8RKH1
H	35	LYS	-	expression tag	UNP A0A2N8RKH1
H	36	VAL	-	expression tag	UNP A0A2N8RKH1
H	37	GLU	-	expression tag	UNP A0A2N8RKH1
H	38	ALA	-	expression tag	UNP A0A2N8RKH1
H	39	PHE	-	expression tag	UNP A0A2N8RKH1

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Chain	Residue	Modelled	Actual	Comment	Reference
H	40	THR	-	expression tag	UNP A0A2N8RKH1
H	41	GLY	-	expression tag	UNP A0A2N8RKH1
H	42	PRO	-	expression tag	UNP A0A2N8RKH1
H	43	THR	-	expression tag	UNP A0A2N8RKH1
H	60	ALA	SER	conflict	UNP A0A2N8RKH1
H	63	VAL	MET	conflict	UNP A0A2N8RKH1
H	66	GLY	SER	conflict	UNP A0A2N8RKH1
H	71	ILE	LEU	conflict	UNP A0A2N8RKH1
H	74	GLN	GLU	conflict	UNP A0A2N8RKH1
H	114	SER	GLY	conflict	UNP A0A2N8RKH1
H	153	SER	ARG	conflict	UNP A0A2N8RKH1
H	351	VAL	-	expression tag	UNP A0A2N8RKH1
H	352	GLU	-	expression tag	UNP A0A2N8RKH1
H	353	HIS	-	expression tag	UNP A0A2N8RKH1
H	354	HIS	-	expression tag	UNP A0A2N8RKH1
H	355	HIS	-	expression tag	UNP A0A2N8RKH1
H	356	HIS	-	expression tag	UNP A0A2N8RKH1
H	357	HIS	-	expression tag	UNP A0A2N8RKH1
H	358	HIS	-	expression tag	UNP A0A2N8RKH1
B	27	MET	-	initiating methionine	UNP A0A2N8RKH1
B	28	ALA	-	expression tag	UNP A0A2N8RKH1
B	29	MET	-	expression tag	UNP A0A2N8RKH1
B	30	ASP	-	expression tag	UNP A0A2N8RKH1
B	31	LEU	-	expression tag	UNP A0A2N8RKH1
B	32	PHE	-	expression tag	UNP A0A2N8RKH1
B	33	GLN	-	expression tag	UNP A0A2N8RKH1
B	34	ASP	-	expression tag	UNP A0A2N8RKH1
B	35	LYS	-	expression tag	UNP A0A2N8RKH1
B	36	VAL	-	expression tag	UNP A0A2N8RKH1
B	37	GLU	-	expression tag	UNP A0A2N8RKH1
B	38	ALA	-	expression tag	UNP A0A2N8RKH1
B	39	PHE	-	expression tag	UNP A0A2N8RKH1
B	40	THR	-	expression tag	UNP A0A2N8RKH1
B	41	GLY	-	expression tag	UNP A0A2N8RKH1
B	42	PRO	-	expression tag	UNP A0A2N8RKH1
B	43	THR	-	expression tag	UNP A0A2N8RKH1
B	60	ALA	SER	conflict	UNP A0A2N8RKH1
B	63	VAL	MET	conflict	UNP A0A2N8RKH1
B	66	GLY	SER	conflict	UNP A0A2N8RKH1
B	71	ILE	LEU	conflict	UNP A0A2N8RKH1
B	74	GLN	GLU	conflict	UNP A0A2N8RKH1
B	114	SER	GLY	conflict	UNP A0A2N8RKH1

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Chain	Residue	Modelled	Actual	Comment	Reference
B	153	SER	ARG	conflict	UNP A0A2N8RKH1
B	351	VAL	-	expression tag	UNP A0A2N8RKH1
B	352	GLU	-	expression tag	UNP A0A2N8RKH1
B	353	HIS	-	expression tag	UNP A0A2N8RKH1
B	354	HIS	-	expression tag	UNP A0A2N8RKH1
B	355	HIS	-	expression tag	UNP A0A2N8RKH1
B	356	HIS	-	expression tag	UNP A0A2N8RKH1
B	357	HIS	-	expression tag	UNP A0A2N8RKH1
B	358	HIS	-	expression tag	UNP A0A2N8RKH1
G	27	MET	-	initiating methionine	UNP A0A2N8RKH1
G	28	ALA	-	expression tag	UNP A0A2N8RKH1
G	29	MET	-	expression tag	UNP A0A2N8RKH1
G	30	ASP	-	expression tag	UNP A0A2N8RKH1
G	31	LEU	-	expression tag	UNP A0A2N8RKH1
G	32	PHE	-	expression tag	UNP A0A2N8RKH1
G	33	GLN	-	expression tag	UNP A0A2N8RKH1
G	34	ASP	-	expression tag	UNP A0A2N8RKH1
G	35	LYS	-	expression tag	UNP A0A2N8RKH1
G	36	VAL	-	expression tag	UNP A0A2N8RKH1
G	37	GLU	-	expression tag	UNP A0A2N8RKH1
G	38	ALA	-	expression tag	UNP A0A2N8RKH1
G	39	PHE	-	expression tag	UNP A0A2N8RKH1
G	40	THR	-	expression tag	UNP A0A2N8RKH1
G	41	GLY	-	expression tag	UNP A0A2N8RKH1
G	42	PRO	-	expression tag	UNP A0A2N8RKH1
G	43	THR	-	expression tag	UNP A0A2N8RKH1
G	60	ALA	SER	conflict	UNP A0A2N8RKH1
G	63	VAL	MET	conflict	UNP A0A2N8RKH1
G	66	GLY	SER	conflict	UNP A0A2N8RKH1
G	71	ILE	LEU	conflict	UNP A0A2N8RKH1
G	74	GLN	GLU	conflict	UNP A0A2N8RKH1
G	114	SER	GLY	conflict	UNP A0A2N8RKH1
G	153	SER	ARG	conflict	UNP A0A2N8RKH1
G	351	VAL	-	expression tag	UNP A0A2N8RKH1
G	352	GLU	-	expression tag	UNP A0A2N8RKH1
G	353	HIS	-	expression tag	UNP A0A2N8RKH1
G	354	HIS	-	expression tag	UNP A0A2N8RKH1
G	355	HIS	-	expression tag	UNP A0A2N8RKH1
G	356	HIS	-	expression tag	UNP A0A2N8RKH1
G	357	HIS	-	expression tag	UNP A0A2N8RKH1
G	358	HIS	-	expression tag	UNP A0A2N8RKH1
A	27	MET	-	initiating methionine	UNP A0A2N8RKH1

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Chain	Residue	Modelled	Actual	Comment	Reference
A	28	ALA	-	expression tag	UNP A0A2N8RKH1
A	29	MET	-	expression tag	UNP A0A2N8RKH1
A	30	ASP	-	expression tag	UNP A0A2N8RKH1
A	31	LEU	-	expression tag	UNP A0A2N8RKH1
A	32	PHE	-	expression tag	UNP A0A2N8RKH1
A	33	GLN	-	expression tag	UNP A0A2N8RKH1
A	34	ASP	-	expression tag	UNP A0A2N8RKH1
A	35	LYS	-	expression tag	UNP A0A2N8RKH1
A	36	VAL	-	expression tag	UNP A0A2N8RKH1
A	37	GLU	-	expression tag	UNP A0A2N8RKH1
A	38	ALA	-	expression tag	UNP A0A2N8RKH1
A	39	PHE	-	expression tag	UNP A0A2N8RKH1
A	40	THR	-	expression tag	UNP A0A2N8RKH1
A	41	GLY	-	expression tag	UNP A0A2N8RKH1
A	42	PRO	-	expression tag	UNP A0A2N8RKH1
A	43	THR	-	expression tag	UNP A0A2N8RKH1
A	60	ALA	SER	conflict	UNP A0A2N8RKH1
A	63	VAL	MET	conflict	UNP A0A2N8RKH1
A	66	GLY	SER	conflict	UNP A0A2N8RKH1
A	71	ILE	LEU	conflict	UNP A0A2N8RKH1
A	74	GLN	GLU	conflict	UNP A0A2N8RKH1
A	114	SER	GLY	conflict	UNP A0A2N8RKH1
A	153	SER	ARG	conflict	UNP A0A2N8RKH1
A	351	VAL	-	expression tag	UNP A0A2N8RKH1
A	352	GLU	-	expression tag	UNP A0A2N8RKH1
A	353	HIS	-	expression tag	UNP A0A2N8RKH1
A	354	HIS	-	expression tag	UNP A0A2N8RKH1
A	355	HIS	-	expression tag	UNP A0A2N8RKH1
A	356	HIS	-	expression tag	UNP A0A2N8RKH1
A	357	HIS	-	expression tag	UNP A0A2N8RKH1
A	358	HIS	-	expression tag	UNP A0A2N8RKH1
C	27	MET	-	initiating methionine	UNP A0A2N8RKH1
C	28	ALA	-	expression tag	UNP A0A2N8RKH1
C	29	MET	-	expression tag	UNP A0A2N8RKH1
C	30	ASP	-	expression tag	UNP A0A2N8RKH1
C	31	LEU	-	expression tag	UNP A0A2N8RKH1
C	32	PHE	-	expression tag	UNP A0A2N8RKH1
C	33	GLN	-	expression tag	UNP A0A2N8RKH1
C	34	ASP	-	expression tag	UNP A0A2N8RKH1
C	35	LYS	-	expression tag	UNP A0A2N8RKH1
C	36	VAL	-	expression tag	UNP A0A2N8RKH1
C	37	GLU	-	expression tag	UNP A0A2N8RKH1

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Chain	Residue	Modelled	Actual	Comment	Reference
C	38	ALA	-	expression tag	UNP A0A2N8RKH1
C	39	PHE	-	expression tag	UNP A0A2N8RKH1
C	40	THR	-	expression tag	UNP A0A2N8RKH1
C	41	GLY	-	expression tag	UNP A0A2N8RKH1
C	42	PRO	-	expression tag	UNP A0A2N8RKH1
C	43	THR	-	expression tag	UNP A0A2N8RKH1
C	60	ALA	SER	conflict	UNP A0A2N8RKH1
C	63	VAL	MET	conflict	UNP A0A2N8RKH1
C	66	GLY	SER	conflict	UNP A0A2N8RKH1
C	71	ILE	LEU	conflict	UNP A0A2N8RKH1
C	74	GLN	GLU	conflict	UNP A0A2N8RKH1
C	114	SER	GLY	conflict	UNP A0A2N8RKH1
C	153	SER	ARG	conflict	UNP A0A2N8RKH1
C	351	VAL	-	expression tag	UNP A0A2N8RKH1
C	352	GLU	-	expression tag	UNP A0A2N8RKH1
C	353	HIS	-	expression tag	UNP A0A2N8RKH1
C	354	HIS	-	expression tag	UNP A0A2N8RKH1
C	355	HIS	-	expression tag	UNP A0A2N8RKH1
C	356	HIS	-	expression tag	UNP A0A2N8RKH1
C	357	HIS	-	expression tag	UNP A0A2N8RKH1
C	358	HIS	-	expression tag	UNP A0A2N8RKH1
D	27	MET	-	initiating methionine	UNP A0A2N8RKH1
D	28	ALA	-	expression tag	UNP A0A2N8RKH1
D	29	MET	-	expression tag	UNP A0A2N8RKH1
D	30	ASP	-	expression tag	UNP A0A2N8RKH1
D	31	LEU	-	expression tag	UNP A0A2N8RKH1
D	32	PHE	-	expression tag	UNP A0A2N8RKH1
D	33	GLN	-	expression tag	UNP A0A2N8RKH1
D	34	ASP	-	expression tag	UNP A0A2N8RKH1
D	35	LYS	-	expression tag	UNP A0A2N8RKH1
D	36	VAL	-	expression tag	UNP A0A2N8RKH1
D	37	GLU	-	expression tag	UNP A0A2N8RKH1
D	38	ALA	-	expression tag	UNP A0A2N8RKH1
D	39	PHE	-	expression tag	UNP A0A2N8RKH1
D	40	THR	-	expression tag	UNP A0A2N8RKH1
D	41	GLY	-	expression tag	UNP A0A2N8RKH1
D	42	PRO	-	expression tag	UNP A0A2N8RKH1
D	43	THR	-	expression tag	UNP A0A2N8RKH1
D	60	ALA	SER	conflict	UNP A0A2N8RKH1
D	63	VAL	MET	conflict	UNP A0A2N8RKH1
D	66	GLY	SER	conflict	UNP A0A2N8RKH1
D	71	ILE	LEU	conflict	UNP A0A2N8RKH1

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Chain	Residue	Modelled	Actual	Comment	Reference
D	74	GLN	GLU	conflict	UNP A0A2N8RKH1
D	114	SER	GLY	conflict	UNP A0A2N8RKH1
D	153	SER	ARG	conflict	UNP A0A2N8RKH1
D	351	VAL	-	expression tag	UNP A0A2N8RKH1
D	352	GLU	-	expression tag	UNP A0A2N8RKH1
D	353	HIS	-	expression tag	UNP A0A2N8RKH1
D	354	HIS	-	expression tag	UNP A0A2N8RKH1
D	355	HIS	-	expression tag	UNP A0A2N8RKH1
D	356	HIS	-	expression tag	UNP A0A2N8RKH1
D	357	HIS	-	expression tag	UNP A0A2N8RKH1
D	358	HIS	-	expression tag	UNP A0A2N8RKH1
E	27	MET	-	initiating methionine	UNP A0A2N8RKH1
E	28	ALA	-	expression tag	UNP A0A2N8RKH1
E	29	MET	-	expression tag	UNP A0A2N8RKH1
E	30	ASP	-	expression tag	UNP A0A2N8RKH1
E	31	LEU	-	expression tag	UNP A0A2N8RKH1
E	32	PHE	-	expression tag	UNP A0A2N8RKH1
E	33	GLN	-	expression tag	UNP A0A2N8RKH1
E	34	ASP	-	expression tag	UNP A0A2N8RKH1
E	35	LYS	-	expression tag	UNP A0A2N8RKH1
E	36	VAL	-	expression tag	UNP A0A2N8RKH1
E	37	GLU	-	expression tag	UNP A0A2N8RKH1
E	38	ALA	-	expression tag	UNP A0A2N8RKH1
E	39	PHE	-	expression tag	UNP A0A2N8RKH1
E	40	THR	-	expression tag	UNP A0A2N8RKH1
E	41	GLY	-	expression tag	UNP A0A2N8RKH1
E	42	PRO	-	expression tag	UNP A0A2N8RKH1
E	43	THR	-	expression tag	UNP A0A2N8RKH1
E	60	ALA	SER	conflict	UNP A0A2N8RKH1
E	63	VAL	MET	conflict	UNP A0A2N8RKH1
E	66	GLY	SER	conflict	UNP A0A2N8RKH1
E	71	ILE	LEU	conflict	UNP A0A2N8RKH1
E	74	GLN	GLU	conflict	UNP A0A2N8RKH1
E	114	SER	GLY	conflict	UNP A0A2N8RKH1
E	153	SER	ARG	conflict	UNP A0A2N8RKH1
E	351	VAL	-	expression tag	UNP A0A2N8RKH1
E	352	GLU	-	expression tag	UNP A0A2N8RKH1
E	353	HIS	-	expression tag	UNP A0A2N8RKH1
E	354	HIS	-	expression tag	UNP A0A2N8RKH1
E	355	HIS	-	expression tag	UNP A0A2N8RKH1
E	356	HIS	-	expression tag	UNP A0A2N8RKH1
E	357	HIS	-	expression tag	UNP A0A2N8RKH1

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Chain	Residue	Modelled	Actual	Comment	Reference
E	358	HIS	-	expression tag	UNP A0A2N8RKH1
F	27	MET	-	initiating methionine	UNP A0A2N8RKH1
F	28	ALA	-	expression tag	UNP A0A2N8RKH1
F	29	MET	-	expression tag	UNP A0A2N8RKH1
F	30	ASP	-	expression tag	UNP A0A2N8RKH1
F	31	LEU	-	expression tag	UNP A0A2N8RKH1
F	32	PHE	-	expression tag	UNP A0A2N8RKH1
F	33	GLN	-	expression tag	UNP A0A2N8RKH1
F	34	ASP	-	expression tag	UNP A0A2N8RKH1
F	35	LYS	-	expression tag	UNP A0A2N8RKH1
F	36	VAL	-	expression tag	UNP A0A2N8RKH1
F	37	GLU	-	expression tag	UNP A0A2N8RKH1
F	38	ALA	-	expression tag	UNP A0A2N8RKH1
F	39	PHE	-	expression tag	UNP A0A2N8RKH1
F	40	THR	-	expression tag	UNP A0A2N8RKH1
F	41	GLY	-	expression tag	UNP A0A2N8RKH1
F	42	PRO	-	expression tag	UNP A0A2N8RKH1
F	43	THR	-	expression tag	UNP A0A2N8RKH1
F	60	ALA	SER	conflict	UNP A0A2N8RKH1
F	63	VAL	MET	conflict	UNP A0A2N8RKH1
F	66	GLY	SER	conflict	UNP A0A2N8RKH1
F	71	ILE	LEU	conflict	UNP A0A2N8RKH1
F	74	GLN	GLU	conflict	UNP A0A2N8RKH1
F	114	SER	GLY	conflict	UNP A0A2N8RKH1
F	153	SER	ARG	conflict	UNP A0A2N8RKH1
F	351	VAL	-	expression tag	UNP A0A2N8RKH1
F	352	GLU	-	expression tag	UNP A0A2N8RKH1
F	353	HIS	-	expression tag	UNP A0A2N8RKH1
F	354	HIS	-	expression tag	UNP A0A2N8RKH1
F	355	HIS	-	expression tag	UNP A0A2N8RKH1
F	356	HIS	-	expression tag	UNP A0A2N8RKH1
F	357	HIS	-	expression tag	UNP A0A2N8RKH1
F	358	HIS	-	expression tag	UNP A0A2N8RKH1

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	G	1	Total Mg 1 1	0	0
2	D	1	Total Mg 1 1	0	0
2	E	1	Total Mg 1 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	H	1	Total 1	Mg 1	0	0
2	B	1	Total 1	Mg 1	0	0
2	C	1	Total 1	Mg 1	0	0
2	A	1	Total 1	Mg 1	0	0
2	F	1	Total 1	Mg 1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	H	6	Total 6	O 6	0	0
3	B	9	Total 9	O 9	0	0
3	G	3	Total 3	O 3	0	0
3	A	12	Total 12	O 12	0	0
3	C	3	Total 3	O 3	0	0
3	D	5	Total 5	O 5	0	0
3	E	5	Total 5	O 5	0	0
3	F	2	Total 2	O 2	0	0

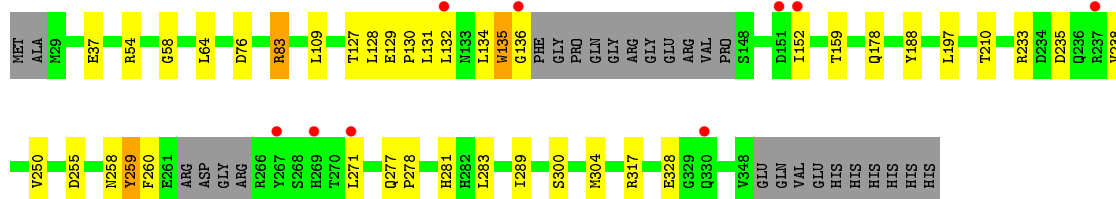
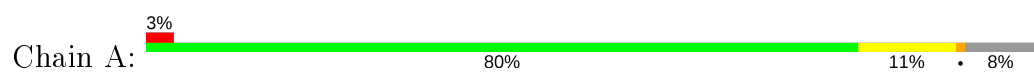
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are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

- Chain H:
-
- | Position | Amino Acid | Conservation (bits) |
|----------|------------|---------------------|
| 1 | MET | 0.00 |
| 2 | ALA | 0.00 |
| 3 | H29 | 0.00 |
| 4 | E37 | 0.00 |
| 5 | K44 | 0.20 |
| 6 | Y52 | 0.00 |
| 7 | A60 | 0.00 |
| 8 | V63 | 0.00 |
| 9 | L64 | 0.00 |
| 10 | E67 | 0.00 |
| 11 | I71 | 0.00 |
| 12 | D76 | 0.00 |
| 13 | K78 | 0.00 |
| 14 | Q78 | 0.00 |
| 15 | L94 | 0.00 |
| 16 | M105 | 0.00 |
| 17 | L128 | 0.00 |
| 18 | L134 | 0.00 |
| 19 | M135 | 0.00 |
| 20 | G136 | 0.00 |
| 21 | R142 | 0.00 |
| 22 | G143 | 0.00 |
| 23 | E144 | 0.20 |
| 24 | R145 | 0.00 |
| 25 | V146 | 0.00 |
| 26 | P147 | 0.00 |
| 27 | I152 | 0.00 |
| 28 | Y188 | 0.00 |
| 29 | L192 | 0.00 |
| 30 | L197 | 0.00 |
| 31 | V207 | 0.00 |
| 32 | E208 | 0.00 |
| 33 | P223 | 0.00 |
| 34 | P224 | 0.00 |
| 35 | R233 | 0.20 |
| 36 | ASP | 0.00 |
| 37 | ASP | 0.00 |
| 38 | GLN | 0.00 |
| 39 | ARG | 0.00 |
| 40 | V238 | 0.20 |

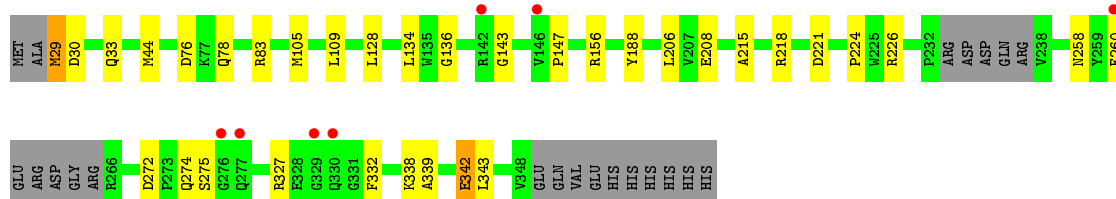
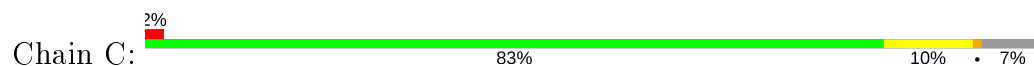
- Chain B:
-
- Sequence logo for Chain B. The y-axis represents information content in bits (0.00 to 0.25). The x-axis lists amino acids. A horizontal bar at the top shows the overall conservation: 29% (red), 79% (green), 11% (yellow), and 9% (grey).
- | Amino Acid | Information Content (bits) |
|------------|----------------------------|
| MET | 0.00 |
| ALA | 0.00 |
| P29 | 0.00 |
| D34 | 0.00 |
| E37 | 0.00 |
| M44 | 0.00 |
| Y52 | 0.00 |
| Q74 | 0.00 |
| L75 | 0.00 |
| Q78 | 0.00 |
| R83 | 0.00 |
| S84 | 0.00 |
| P103 | 0.00 |
| D104 | 0.00 |
| M105 | 0.00 |
| V106 | 0.00 |
| L107 | 0.00 |
| E108 | 0.00 |
| D109 | 0.00 |
| L128 | 0.00 |
| E129 | 0.00 |
| P130 | 0.00 |
| L131 | 0.00 |
| L132 | 0.00 |
| M133 | 0.00 |
| L134 | 0.00 |
| TRP | 0.00 |
| GLY | 0.00 |
| PHE | 0.00 |
| GLY | 0.00 |
| PRO | 0.00 |
| PRO | 0.00 |
| GLN | 0.00 |
| GLY | 0.00 |
| ARG | 0.00 |
| GLY | 0.00 |
| GLU | 0.00 |
| ARG | 0.00 |
| VAL | 0.00 |
| PRO | 0.00 |
| S148 | 0.00 |
| I152 | 0.00 |
| L158 | 0.00 |
| R170 | 0.00 |
| A176 | 0.00 |
| D180 | 0.00 |
| E181 | 0.00 |
| M192 | 0.00 |
| Y198 | 0.00 |
| T210 | 0.00 |
| R233 | 0.00 |
| R237 | 0.00 |
| D255 | 0.00 |
| N258 | 0.00 |
| Y259 | 0.00 |
| P260 | 0.00 |
| E261 | 0.00 |
| ARG | 0.00 |
| ASP | 0.00 |
| GLY | 0.00 |
| ARG | 0.00 |
| R266 | 0.00 |
| R269 | 0.00 |
| T270 | 0.00 |
| L271 | 0.00 |
| D272 | 0.00 |
| D273 | 0.00 |
| Q274 | 0.00 |
| S275 | 0.00 |
| G276 | 0.00 |
| Q277 | 0.00 |
| P278 | 0.00 |
| H281 | 0.00 |
| F282 | 0.00 |
| L283 | 0.00 |
| D290 | 0.00 |
| L294 | 0.00 |
| R295 | 0.00 |
| L312 | 0.00 |
| T335 | 0.00 |
| V343 | 0.00 |
| GLU | 0.00 |
| GLN | 0.00 |
| VAL | 0.00 |
| GLU | 0.00 |
| HIS | 0.00 |
| HIS | 0.00 |
| HIS | 0.00 |
| HIS | 0.00 |
| HIS | 0.00 |

- Chain G:
-
- Sequence logo for Chain G. The y-axis represents frequency in bits (0.00 to 0.15). The x-axis lists amino acids. A color scale at the top indicates frequency percentages: 5% (red), 72% (green), 16% (yellow), and 10% (grey).
- | Position | Amino Acid | Frequency (bits) |
|----------|------------|------------------|
| 1 | Met | 0.00 |
| 2 | Ala | 0.00 |
| 3 | Met | 0.00 |
| 4 | Met | 0.00 |
| 5 | Met | 0.00 |
| 6 | Met | 0.00 |
| 7 | Met | 0.00 |
| 8 | Met | 0.00 |
| 9 | Met | 0.00 |
| 10 | Met | 0.00 |
| 11 | Met | 0.00 |
| 12 | Met | 0.00 |
| 13 | Met | 0.00 |
| 14 | Met | 0.00 |
| 15 | Met | 0.00 |
| 16 | Met | 0.00 |
| 17 | Met | 0.00 |
| 18 | Met | 0.00 |
| 19 | Met | 0.00 |
| 20 | Met | 0.00 |
| 21 | Met | 0.00 |
| 22 | Met | 0.00 |
| 23 | Met | 0.00 |
| 24 | Met | 0.00 |
| 25 | Met | 0.00 |
| 26 | Met | 0.00 |
| 27 | Met | 0.00 |
| 28 | Met | 0.00 |
| 29 | Met | 0.00 |
| 30 | Met | 0.00 |
| 31 | Met | 0.00 |
| 32 | Met | 0.00 |
| 33 | Met | 0.00 |
| 34 | Met | 0.00 |
| 35 | Met | 0.00 |

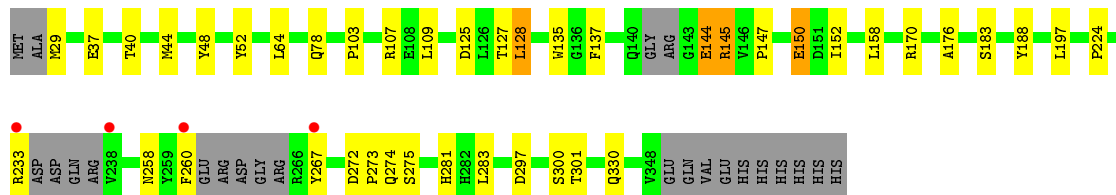
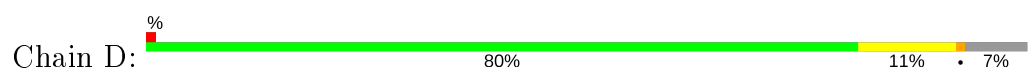
- 
- WORLD WIDE
PDB
PROTEIN DATA BANK



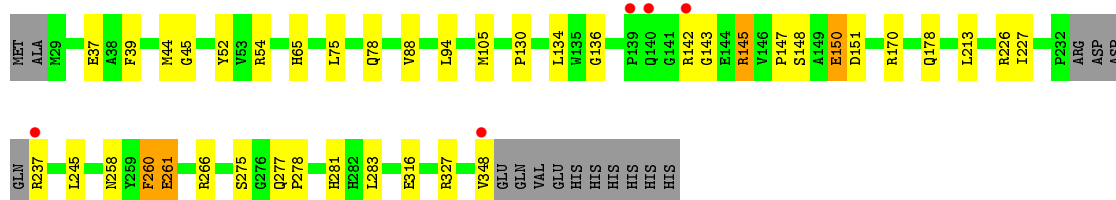
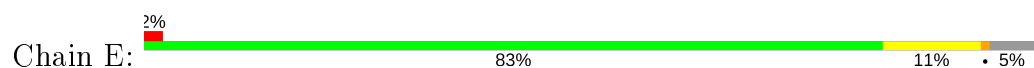
- Molecule 1: FAD:protein FMN transferase



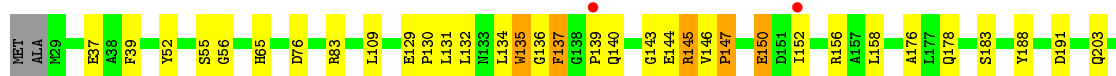
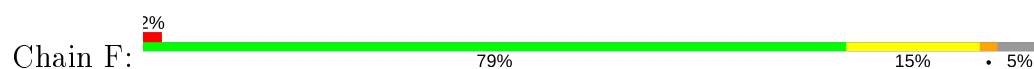
- Molecule 1: FAD:protein FMN transferase

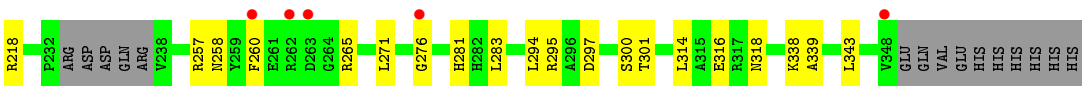


- Molecule 1: FAD:protein FMN transferase



- Molecule 1: FAD:protein FMN transferase





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	135.66Å 91.98Å 138.06Å 90.00° 90.41° 90.00°	Depositor
Resolution (Å)	138.06 – 2.60 138.06 – 2.46	Depositor EDS
% Data completeness (in resolution range)	100.0 (138.06-2.60) 100.0 (138.06-2.46)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.12 (at 2.45Å)	Xtriage
Refinement program	REFMAC 5.8.0155	Depositor
R, R_{free}	0.232 , 0.274 0.233 , 0.271	Depositor DCC
R_{free} test set	5960 reflections (4.84%)	wwPDB-VP
Wilson B-factor (Å ²)	39.9	Xtriage
Anisotropy	0.214	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 21.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.000 for l,k,-h 0.000 for h,-k,-l 0.000 for l,-k,h	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	18725	wwPDB-VP
Average B, all atoms (Å ²)	60.0	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 48.34 % 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 8.7302e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: MG

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	1.04	3/2343 (0.1%)	1.05	6/3171 (0.2%)
1	B	0.95	1/2323 (0.0%)	1.06	12/3143 (0.4%)
1	C	0.88	1/2374 (0.0%)	0.97	5/3214 (0.2%)
1	D	0.91	3/2369 (0.1%)	1.02	8/3206 (0.2%)
1	E	0.87	0/2429	1.04	10/3287 (0.3%)
1	F	0.92	2/2418 (0.1%)	1.10	10/3273 (0.3%)
1	G	1.04	3/2299 (0.1%)	1.08	11/3110 (0.4%)
1	H	0.92	1/2429 (0.0%)	1.05	11/3287 (0.3%)
All	All	0.94	14/18984 (0.1%)	1.05	73/25691 (0.3%)

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	281	HIS	C-N	24.09	1.89	1.34
1	A	259	TYR	C-N	18.56	1.76	1.34
1	D	150	GLU	CG-CD	8.63	1.64	1.51
1	C	342	GLU	CD-OE2	-7.88	1.17	1.25
1	B	74	GLN	CG-CD	-7.76	1.33	1.51

The worst 5 of 73 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	145	ARG	NE-CZ-NH2	-17.41	111.60	120.30
1	G	145	ARG	NE-CZ-NH1	-13.63	113.48	120.30
1	D	145	ARG	NE-CZ-NH2	11.78	126.19	120.30
1	F	146	VAL	C-N-CD	-10.91	96.59	120.60
1	H	76	ASP	CB-CG-OD2	10.39	127.65	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	2306	0	2261	31	1
1	B	2288	0	2250	26	1
1	C	2334	0	2295	19	0
1	D	2330	0	2292	21	0
1	E	2388	0	2349	30	0
1	F	2377	0	2336	53	0
1	G	2261	0	2220	61	0
1	H	2388	0	2349	34	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
3	A	12	0	0	1	0
3	B	9	0	0	0	0
3	C	3	0	0	0	0
3	D	5	0	0	0	0
3	E	5	0	0	0	0
3	F	2	0	0	0	0
3	G	3	0	0	0	0
3	H	6	0	0	0	0
All	All	18725	0	18352	248	1

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 7.

The worst 5 of 248 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:F:134:LEU:HD11	1:F:147:PRO:CB	1.27	1.54
1:A:259:TYR:C	1:A:260:PHE:N	1.76	1.38
1:F:134:LEU:CD1	1:F:147:PRO:CB	2.02	1.37

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:281:HIS:C	1:G:282:HIS:N	1.89	1.24
1:F:134:LEU:CD1	1:F:147:PRO:CG	2.20	1.18

All (1) 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)
1:B:84:SER:OG	1:A:328:GLU:OE1[2_646]	2.18	0.02

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	299/332 (90%)	283 (95%)	14 (5%)	2 (1%)	22	43
1	B	297/332 (90%)	279 (94%)	18 (6%)	0	100	100
1	C	304/332 (92%)	289 (95%)	14 (5%)	1 (0%)	41	64
1	D	301/332 (91%)	291 (97%)	9 (3%)	1 (0%)	41	64
1	E	312/332 (94%)	297 (95%)	15 (5%)	0	100	100
1	F	311/332 (94%)	298 (96%)	11 (4%)	2 (1%)	25	47
1	G	291/332 (88%)	275 (94%)	15 (5%)	1 (0%)	41	64
1	H	312/332 (94%)	301 (96%)	11 (4%)	0	100	100
All	All	2427/2656 (91%)	2313 (95%)	107 (4%)	7 (0%)	41	64

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	235	ASP
1	G	148	SER
1	F	276	GLY

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Mol	Chain	Res	Type
1	C	221	ASP
1	D	330	GLN

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	243/265 (92%)	241 (99%)	2 (1%)	81	92
1	B	242/265 (91%)	238 (98%)	4 (2%)	60	81
1	C	245/265 (92%)	243 (99%)	2 (1%)	81	92
1	D	245/265 (92%)	243 (99%)	2 (1%)	81	92
1	E	250/265 (94%)	243 (97%)	7 (3%)	43	69
1	F	249/265 (94%)	245 (98%)	4 (2%)	62	82
1	G	239/265 (90%)	235 (98%)	4 (2%)	60	81
1	H	250/265 (94%)	245 (98%)	5 (2%)	55	78
All	All	1963/2120 (93%)	1933 (98%)	30 (2%)	65	83

5 of 30 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	128	LEU
1	C	128	LEU
1	F	144	GLU
1	C	29	MET
1	D	128	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	281	HIS
1	D	65	HIS
1	F	281	HIS

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Mol	Chain	Res	Type
1	C	240	GLN
1	C	281	HIS

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, 8 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	G	1
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	G	281:HIS	C	282:HIS	N	1.89
1	A	259:TYR	C	260:PHE	N	1.76

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
1	A	305/332 (91%)	-0.19	9 (2%)	50	43	26, 48, 106, 146	0
1	B	303/332 (91%)	-0.21	8 (2%)	56	50	25, 44, 109, 143	0
1	C	310/332 (93%)	-0.21	7 (2%)	60	54	29, 54, 106, 141	0
1	D	309/332 (93%)	-0.22	4 (1%)	77	73	28, 49, 106, 144	0
1	E	316/332 (95%)	-0.17	5 (1%)	72	68	31, 53, 113, 145	0
1	F	315/332 (94%)	-0.17	7 (2%)	62	56	27, 52, 131, 170	0
1	G	299/332 (90%)	0.11	17 (5%)	23	18	29, 69, 116, 154	0
1	H	316/332 (95%)	-0.20	11 (3%)	44	36	26, 50, 107, 154	0
All	All	2473/2656 (93%)	-0.16	68 (2%)	54	48	25, 51, 113, 170	0

The worst 5 of 68 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	331	GLY	9.4
1	G	282	HIS	8.6
1	G	326	VAL	5.1
1	D	260	PHE	4.9
1	E	140	GLN	4.7

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
2	MG	H	401	1/1	0.83	0.11	51,51,51,51	0
2	MG	F	401	1/1	0.83	0.07	46,46,46,46	0
2	MG	B	401	1/1	0.92	0.11	45,45,45,45	0
2	MG	G	401	1/1	0.94	0.08	61,61,61,61	0
2	MG	D	401	1/1	0.95	0.13	51,51,51,51	0
2	MG	E	401	1/1	0.95	0.11	51,51,51,51	0
2	MG	A	401	1/1	0.97	0.08	40,40,40,40	0
2	MG	C	401	1/1	0.99	0.05	38,38,38,38	0

6.5 Other polymers [i](#)

There are no such residues in this entry.