



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:35 PM GMT

PDB ID : 4IRN  
Title : Crystal Structure of the Prolyl Acyl Carrier Protein Oxidase AnaB  
Authors : Moncoq, K.; Mann, S.; Regad, L.; Mejean, A.; Ploux, O.  
Deposited on : 2013-01-15  
Resolution : 2.80 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

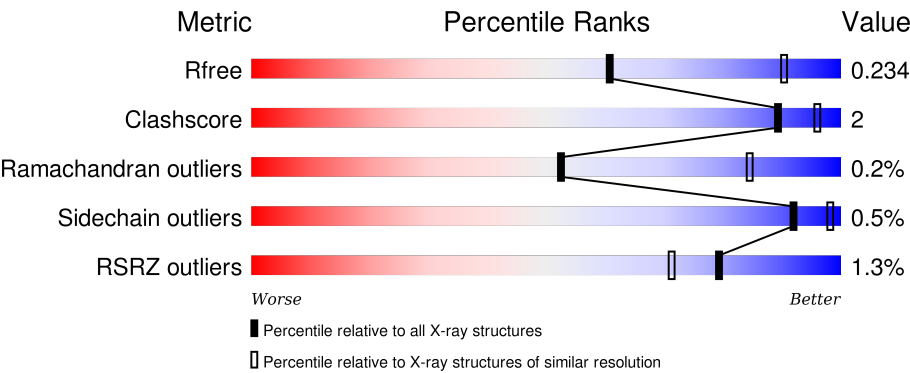
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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 <sub>free</sub>	91344	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

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. 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	416	<div><div></div><div>86%5%9%</div></div>
1	B	416	<div><div>%</div><div>86%5%9%</div></div>
1	C	416	<div><div></div><div>86%5%9%</div></div>
1	D	416	<div><div>%</div><div>85%6%9%</div></div>
1	E	416	<div><div>2%</div><div>87%.9%</div></div>

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Mol	Chain	Length	Quality of chain
1	F	416	<div><div><div>%</div><div><div></div><div></div><div></div></div><div>86%</div><div>5%</div><div>9%</div></div></div>
1	G	416	<div><div><div>2%</div><div><div></div><div></div><div></div></div><div>86%</div><div>5%</div><div>9%</div></div></div>
1	H	416	<div><div><div>%</div><div><div></div><div></div><div></div></div><div>85%</div><div>6%</div><div>9%</div></div></div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 24783 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 Prolyl-ACP dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	378	Total	C	N	O	S	0	0	0
			2988	1911	505	555	17			
1	B	378	Total	C	N	O	S	0	0	0
			2988	1911	505	555	17			
1	C	378	Total	C	N	O	S	0	0	0
			2988	1911	505	555	17			
1	D	378	Total	C	N	O	S	0	0	0
			2988	1911	505	555	17			
1	E	378	Total	C	N	O	S	0	0	0
			2988	1911	505	555	17			
1	F	378	Total	C	N	O	S	0	0	0
			2988	1911	505	555	17			
1	G	378	Total	C	N	O	S	0	0	0
			2988	1911	505	555	17			
1	H	378	Total	C	N	O	S	0	0	0
			2988	1911	505	555	17			

There are 288 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-34	MET	-	EXPRESSION TAG	UNP C4NCB7
A	-33	GLY	-	EXPRESSION TAG	UNP C4NCB7
A	-32	SER	-	EXPRESSION TAG	UNP C4NCB7
A	-31	SER	-	EXPRESSION TAG	UNP C4NCB7
A	-30	HIS	-	EXPRESSION TAG	UNP C4NCB7
A	-29	HIS	-	EXPRESSION TAG	UNP C4NCB7
A	-28	HIS	-	EXPRESSION TAG	UNP C4NCB7
A	-27	HIS	-	EXPRESSION TAG	UNP C4NCB7
A	-26	HIS	-	EXPRESSION TAG	UNP C4NCB7
A	-25	HIS	-	EXPRESSION TAG	UNP C4NCB7
A	-24	SER	-	EXPRESSION TAG	UNP C4NCB7
A	-23	SER	-	EXPRESSION TAG	UNP C4NCB7
A	-22	GLY	-	EXPRESSION TAG	UNP C4NCB7

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-21	LEU	-	EXPRESSION TAG	UNP C4NCB7
A	-20	VAL	-	EXPRESSION TAG	UNP C4NCB7
A	-19	PRO	-	EXPRESSION TAG	UNP C4NCB7
A	-18	ARG	-	EXPRESSION TAG	UNP C4NCB7
A	-17	GLY	-	EXPRESSION TAG	UNP C4NCB7
A	-16	SER	-	EXPRESSION TAG	UNP C4NCB7
A	-15	HIS	-	EXPRESSION TAG	UNP C4NCB7
A	-14	MET	-	EXPRESSION TAG	UNP C4NCB7
A	-13	ALA	-	EXPRESSION TAG	UNP C4NCB7
A	-12	SER	-	EXPRESSION TAG	UNP C4NCB7
A	-11	MET	-	EXPRESSION TAG	UNP C4NCB7
A	-10	THR	-	EXPRESSION TAG	UNP C4NCB7
A	-9	GLY	-	EXPRESSION TAG	UNP C4NCB7
A	-8	GLY	-	EXPRESSION TAG	UNP C4NCB7
A	-7	GLN	-	EXPRESSION TAG	UNP C4NCB7
A	-6	GLN	-	EXPRESSION TAG	UNP C4NCB7
A	-5	MET	-	EXPRESSION TAG	UNP C4NCB7
A	-4	GLY	-	EXPRESSION TAG	UNP C4NCB7
A	-3	ARG	-	EXPRESSION TAG	UNP C4NCB7
A	-2	GLY	-	EXPRESSION TAG	UNP C4NCB7
A	-1	SER	-	EXPRESSION TAG	UNP C4NCB7
A	0	GLU	-	EXPRESSION TAG	UNP C4NCB7
A	1	PHE	-	EXPRESSION TAG	UNP C4NCB7
B	-34	MET	-	EXPRESSION TAG	UNP C4NCB7
B	-33	GLY	-	EXPRESSION TAG	UNP C4NCB7
B	-32	SER	-	EXPRESSION TAG	UNP C4NCB7
B	-31	SER	-	EXPRESSION TAG	UNP C4NCB7
B	-30	HIS	-	EXPRESSION TAG	UNP C4NCB7
B	-29	HIS	-	EXPRESSION TAG	UNP C4NCB7
B	-28	HIS	-	EXPRESSION TAG	UNP C4NCB7
B	-27	HIS	-	EXPRESSION TAG	UNP C4NCB7
B	-26	HIS	-	EXPRESSION TAG	UNP C4NCB7
B	-25	HIS	-	EXPRESSION TAG	UNP C4NCB7
B	-24	SER	-	EXPRESSION TAG	UNP C4NCB7
B	-23	SER	-	EXPRESSION TAG	UNP C4NCB7
B	-22	GLY	-	EXPRESSION TAG	UNP C4NCB7
B	-21	LEU	-	EXPRESSION TAG	UNP C4NCB7
B	-20	VAL	-	EXPRESSION TAG	UNP C4NCB7
B	-19	PRO	-	EXPRESSION TAG	UNP C4NCB7
B	-18	ARG	-	EXPRESSION TAG	UNP C4NCB7
B	-17	GLY	-	EXPRESSION TAG	UNP C4NCB7
B	-16	SER	-	EXPRESSION TAG	UNP C4NCB7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-15	HIS	-	EXPRESSION TAG	UNP C4NCB7
B	-14	MET	-	EXPRESSION TAG	UNP C4NCB7
B	-13	ALA	-	EXPRESSION TAG	UNP C4NCB7
B	-12	SER	-	EXPRESSION TAG	UNP C4NCB7
B	-11	MET	-	EXPRESSION TAG	UNP C4NCB7
B	-10	THR	-	EXPRESSION TAG	UNP C4NCB7
B	-9	GLY	-	EXPRESSION TAG	UNP C4NCB7
B	-8	GLY	-	EXPRESSION TAG	UNP C4NCB7
B	-7	GLN	-	EXPRESSION TAG	UNP C4NCB7
B	-6	GLN	-	EXPRESSION TAG	UNP C4NCB7
B	-5	MET	-	EXPRESSION TAG	UNP C4NCB7
B	-4	GLY	-	EXPRESSION TAG	UNP C4NCB7
B	-3	ARG	-	EXPRESSION TAG	UNP C4NCB7
B	-2	GLY	-	EXPRESSION TAG	UNP C4NCB7
B	-1	SER	-	EXPRESSION TAG	UNP C4NCB7
B	0	GLU	-	EXPRESSION TAG	UNP C4NCB7
B	1	PHE	-	EXPRESSION TAG	UNP C4NCB7
C	-34	MET	-	EXPRESSION TAG	UNP C4NCB7
C	-33	GLY	-	EXPRESSION TAG	UNP C4NCB7
C	-32	SER	-	EXPRESSION TAG	UNP C4NCB7
C	-31	SER	-	EXPRESSION TAG	UNP C4NCB7
C	-30	HIS	-	EXPRESSION TAG	UNP C4NCB7
C	-29	HIS	-	EXPRESSION TAG	UNP C4NCB7
C	-28	HIS	-	EXPRESSION TAG	UNP C4NCB7
C	-27	HIS	-	EXPRESSION TAG	UNP C4NCB7
C	-26	HIS	-	EXPRESSION TAG	UNP C4NCB7
C	-25	HIS	-	EXPRESSION TAG	UNP C4NCB7
C	-24	SER	-	EXPRESSION TAG	UNP C4NCB7
C	-23	SER	-	EXPRESSION TAG	UNP C4NCB7
C	-22	GLY	-	EXPRESSION TAG	UNP C4NCB7
C	-21	LEU	-	EXPRESSION TAG	UNP C4NCB7
C	-20	VAL	-	EXPRESSION TAG	UNP C4NCB7
C	-19	PRO	-	EXPRESSION TAG	UNP C4NCB7
C	-18	ARG	-	EXPRESSION TAG	UNP C4NCB7
C	-17	GLY	-	EXPRESSION TAG	UNP C4NCB7
C	-16	SER	-	EXPRESSION TAG	UNP C4NCB7
C	-15	HIS	-	EXPRESSION TAG	UNP C4NCB7
C	-14	MET	-	EXPRESSION TAG	UNP C4NCB7
C	-13	ALA	-	EXPRESSION TAG	UNP C4NCB7
C	-12	SER	-	EXPRESSION TAG	UNP C4NCB7
C	-11	MET	-	EXPRESSION TAG	UNP C4NCB7
C	-10	THR	-	EXPRESSION TAG	UNP C4NCB7

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-9	GLY	-	EXPRESSION TAG	UNP C4NCB7
C	-8	GLY	-	EXPRESSION TAG	UNP C4NCB7
C	-7	GLN	-	EXPRESSION TAG	UNP C4NCB7
C	-6	GLN	-	EXPRESSION TAG	UNP C4NCB7
C	-5	MET	-	EXPRESSION TAG	UNP C4NCB7
C	-4	GLY	-	EXPRESSION TAG	UNP C4NCB7
C	-3	ARG	-	EXPRESSION TAG	UNP C4NCB7
C	-2	GLY	-	EXPRESSION TAG	UNP C4NCB7
C	-1	SER	-	EXPRESSION TAG	UNP C4NCB7
C	0	GLU	-	EXPRESSION TAG	UNP C4NCB7
C	1	PHE	-	EXPRESSION TAG	UNP C4NCB7
D	-34	MET	-	EXPRESSION TAG	UNP C4NCB7
D	-33	GLY	-	EXPRESSION TAG	UNP C4NCB7
D	-32	SER	-	EXPRESSION TAG	UNP C4NCB7
D	-31	SER	-	EXPRESSION TAG	UNP C4NCB7
D	-30	HIS	-	EXPRESSION TAG	UNP C4NCB7
D	-29	HIS	-	EXPRESSION TAG	UNP C4NCB7
D	-28	HIS	-	EXPRESSION TAG	UNP C4NCB7
D	-27	HIS	-	EXPRESSION TAG	UNP C4NCB7
D	-26	HIS	-	EXPRESSION TAG	UNP C4NCB7
D	-25	HIS	-	EXPRESSION TAG	UNP C4NCB7
D	-24	SER	-	EXPRESSION TAG	UNP C4NCB7
D	-23	SER	-	EXPRESSION TAG	UNP C4NCB7
D	-22	GLY	-	EXPRESSION TAG	UNP C4NCB7
D	-21	LEU	-	EXPRESSION TAG	UNP C4NCB7
D	-20	VAL	-	EXPRESSION TAG	UNP C4NCB7
D	-19	PRO	-	EXPRESSION TAG	UNP C4NCB7
D	-18	ARG	-	EXPRESSION TAG	UNP C4NCB7
D	-17	GLY	-	EXPRESSION TAG	UNP C4NCB7
D	-16	SER	-	EXPRESSION TAG	UNP C4NCB7
D	-15	HIS	-	EXPRESSION TAG	UNP C4NCB7
D	-14	MET	-	EXPRESSION TAG	UNP C4NCB7
D	-13	ALA	-	EXPRESSION TAG	UNP C4NCB7
D	-12	SER	-	EXPRESSION TAG	UNP C4NCB7
D	-11	MET	-	EXPRESSION TAG	UNP C4NCB7
D	-10	THR	-	EXPRESSION TAG	UNP C4NCB7
D	-9	GLY	-	EXPRESSION TAG	UNP C4NCB7
D	-8	GLY	-	EXPRESSION TAG	UNP C4NCB7
D	-7	GLN	-	EXPRESSION TAG	UNP C4NCB7
D	-6	GLN	-	EXPRESSION TAG	UNP C4NCB7
D	-5	MET	-	EXPRESSION TAG	UNP C4NCB7
D	-4	GLY	-	EXPRESSION TAG	UNP C4NCB7

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-3	ARG	-	EXPRESSION TAG	UNP C4NCB7
D	-2	GLY	-	EXPRESSION TAG	UNP C4NCB7
D	-1	SER	-	EXPRESSION TAG	UNP C4NCB7
D	0	GLU	-	EXPRESSION TAG	UNP C4NCB7
D	1	PHE	-	EXPRESSION TAG	UNP C4NCB7
E	-34	MET	-	EXPRESSION TAG	UNP C4NCB7
E	-33	GLY	-	EXPRESSION TAG	UNP C4NCB7
E	-32	SER	-	EXPRESSION TAG	UNP C4NCB7
E	-31	SER	-	EXPRESSION TAG	UNP C4NCB7
E	-30	HIS	-	EXPRESSION TAG	UNP C4NCB7
E	-29	HIS	-	EXPRESSION TAG	UNP C4NCB7
E	-28	HIS	-	EXPRESSION TAG	UNP C4NCB7
E	-27	HIS	-	EXPRESSION TAG	UNP C4NCB7
E	-26	HIS	-	EXPRESSION TAG	UNP C4NCB7
E	-25	HIS	-	EXPRESSION TAG	UNP C4NCB7
E	-24	SER	-	EXPRESSION TAG	UNP C4NCB7
E	-23	SER	-	EXPRESSION TAG	UNP C4NCB7
E	-22	GLY	-	EXPRESSION TAG	UNP C4NCB7
E	-21	LEU	-	EXPRESSION TAG	UNP C4NCB7
E	-20	VAL	-	EXPRESSION TAG	UNP C4NCB7
E	-19	PRO	-	EXPRESSION TAG	UNP C4NCB7
E	-18	ARG	-	EXPRESSION TAG	UNP C4NCB7
E	-17	GLY	-	EXPRESSION TAG	UNP C4NCB7
E	-16	SER	-	EXPRESSION TAG	UNP C4NCB7
E	-15	HIS	-	EXPRESSION TAG	UNP C4NCB7
E	-14	MET	-	EXPRESSION TAG	UNP C4NCB7
E	-13	ALA	-	EXPRESSION TAG	UNP C4NCB7
E	-12	SER	-	EXPRESSION TAG	UNP C4NCB7
E	-11	MET	-	EXPRESSION TAG	UNP C4NCB7
E	-10	THR	-	EXPRESSION TAG	UNP C4NCB7
E	-9	GLY	-	EXPRESSION TAG	UNP C4NCB7
E	-8	GLY	-	EXPRESSION TAG	UNP C4NCB7
E	-7	GLN	-	EXPRESSION TAG	UNP C4NCB7
E	-6	GLN	-	EXPRESSION TAG	UNP C4NCB7
E	-5	MET	-	EXPRESSION TAG	UNP C4NCB7
E	-4	GLY	-	EXPRESSION TAG	UNP C4NCB7
E	-3	ARG	-	EXPRESSION TAG	UNP C4NCB7
E	-2	GLY	-	EXPRESSION TAG	UNP C4NCB7
E	-1	SER	-	EXPRESSION TAG	UNP C4NCB7
E	0	GLU	-	EXPRESSION TAG	UNP C4NCB7
E	1	PHE	-	EXPRESSION TAG	UNP C4NCB7
F	-34	MET	-	EXPRESSION TAG	UNP C4NCB7

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-33	GLY	-	EXPRESSION TAG	UNP C4NCB7
F	-32	SER	-	EXPRESSION TAG	UNP C4NCB7
F	-31	SER	-	EXPRESSION TAG	UNP C4NCB7
F	-30	HIS	-	EXPRESSION TAG	UNP C4NCB7
F	-29	HIS	-	EXPRESSION TAG	UNP C4NCB7
F	-28	HIS	-	EXPRESSION TAG	UNP C4NCB7
F	-27	HIS	-	EXPRESSION TAG	UNP C4NCB7
F	-26	HIS	-	EXPRESSION TAG	UNP C4NCB7
F	-25	HIS	-	EXPRESSION TAG	UNP C4NCB7
F	-24	SER	-	EXPRESSION TAG	UNP C4NCB7
F	-23	SER	-	EXPRESSION TAG	UNP C4NCB7
F	-22	GLY	-	EXPRESSION TAG	UNP C4NCB7
F	-21	LEU	-	EXPRESSION TAG	UNP C4NCB7
F	-20	VAL	-	EXPRESSION TAG	UNP C4NCB7
F	-19	PRO	-	EXPRESSION TAG	UNP C4NCB7
F	-18	ARG	-	EXPRESSION TAG	UNP C4NCB7
F	-17	GLY	-	EXPRESSION TAG	UNP C4NCB7
F	-16	SER	-	EXPRESSION TAG	UNP C4NCB7
F	-15	HIS	-	EXPRESSION TAG	UNP C4NCB7
F	-14	MET	-	EXPRESSION TAG	UNP C4NCB7
F	-13	ALA	-	EXPRESSION TAG	UNP C4NCB7
F	-12	SER	-	EXPRESSION TAG	UNP C4NCB7
F	-11	MET	-	EXPRESSION TAG	UNP C4NCB7
F	-10	THR	-	EXPRESSION TAG	UNP C4NCB7
F	-9	GLY	-	EXPRESSION TAG	UNP C4NCB7
F	-8	GLY	-	EXPRESSION TAG	UNP C4NCB7
F	-7	GLN	-	EXPRESSION TAG	UNP C4NCB7
F	-6	GLN	-	EXPRESSION TAG	UNP C4NCB7
F	-5	MET	-	EXPRESSION TAG	UNP C4NCB7
F	-4	GLY	-	EXPRESSION TAG	UNP C4NCB7
F	-3	ARG	-	EXPRESSION TAG	UNP C4NCB7
F	-2	GLY	-	EXPRESSION TAG	UNP C4NCB7
F	-1	SER	-	EXPRESSION TAG	UNP C4NCB7
F	0	GLU	-	EXPRESSION TAG	UNP C4NCB7
F	1	PHE	-	EXPRESSION TAG	UNP C4NCB7
G	-34	MET	-	EXPRESSION TAG	UNP C4NCB7
G	-33	GLY	-	EXPRESSION TAG	UNP C4NCB7
G	-32	SER	-	EXPRESSION TAG	UNP C4NCB7
G	-31	SER	-	EXPRESSION TAG	UNP C4NCB7
G	-30	HIS	-	EXPRESSION TAG	UNP C4NCB7
G	-29	HIS	-	EXPRESSION TAG	UNP C4NCB7
G	-28	HIS	-	EXPRESSION TAG	UNP C4NCB7

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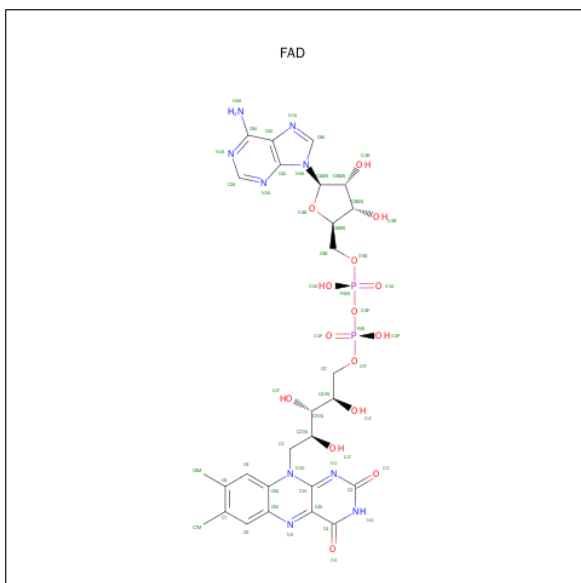
Chain	Residue	Modelled	Actual	Comment	Reference
G	-27	HIS	-	EXPRESSION TAG	UNP C4NCB7
G	-26	HIS	-	EXPRESSION TAG	UNP C4NCB7
G	-25	HIS	-	EXPRESSION TAG	UNP C4NCB7
G	-24	SER	-	EXPRESSION TAG	UNP C4NCB7
G	-23	SER	-	EXPRESSION TAG	UNP C4NCB7
G	-22	GLY	-	EXPRESSION TAG	UNP C4NCB7
G	-21	LEU	-	EXPRESSION TAG	UNP C4NCB7
G	-20	VAL	-	EXPRESSION TAG	UNP C4NCB7
G	-19	PRO	-	EXPRESSION TAG	UNP C4NCB7
G	-18	ARG	-	EXPRESSION TAG	UNP C4NCB7
G	-17	GLY	-	EXPRESSION TAG	UNP C4NCB7
G	-16	SER	-	EXPRESSION TAG	UNP C4NCB7
G	-15	HIS	-	EXPRESSION TAG	UNP C4NCB7
G	-14	MET	-	EXPRESSION TAG	UNP C4NCB7
G	-13	ALA	-	EXPRESSION TAG	UNP C4NCB7
G	-12	SER	-	EXPRESSION TAG	UNP C4NCB7
G	-11	MET	-	EXPRESSION TAG	UNP C4NCB7
G	-10	THR	-	EXPRESSION TAG	UNP C4NCB7
G	-9	GLY	-	EXPRESSION TAG	UNP C4NCB7
G	-8	GLY	-	EXPRESSION TAG	UNP C4NCB7
G	-7	GLN	-	EXPRESSION TAG	UNP C4NCB7
G	-6	GLN	-	EXPRESSION TAG	UNP C4NCB7
G	-5	MET	-	EXPRESSION TAG	UNP C4NCB7
G	-4	GLY	-	EXPRESSION TAG	UNP C4NCB7
G	-3	ARG	-	EXPRESSION TAG	UNP C4NCB7
G	-2	GLY	-	EXPRESSION TAG	UNP C4NCB7
G	-1	SER	-	EXPRESSION TAG	UNP C4NCB7
G	0	GLU	-	EXPRESSION TAG	UNP C4NCB7
G	1	PHE	-	EXPRESSION TAG	UNP C4NCB7
H	-34	MET	-	EXPRESSION TAG	UNP C4NCB7
H	-33	GLY	-	EXPRESSION TAG	UNP C4NCB7
H	-32	SER	-	EXPRESSION TAG	UNP C4NCB7
H	-31	SER	-	EXPRESSION TAG	UNP C4NCB7
H	-30	HIS	-	EXPRESSION TAG	UNP C4NCB7
H	-29	HIS	-	EXPRESSION TAG	UNP C4NCB7
H	-28	HIS	-	EXPRESSION TAG	UNP C4NCB7
H	-27	HIS	-	EXPRESSION TAG	UNP C4NCB7
H	-26	HIS	-	EXPRESSION TAG	UNP C4NCB7
H	-25	HIS	-	EXPRESSION TAG	UNP C4NCB7
H	-24	SER	-	EXPRESSION TAG	UNP C4NCB7
H	-23	SER	-	EXPRESSION TAG	UNP C4NCB7
H	-22	GLY	-	EXPRESSION TAG	UNP C4NCB7

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Chain	Residue	Modelled	Actual	Comment	Reference
H	-21	LEU	-	EXPRESSION TAG	UNP C4NCB7
H	-20	VAL	-	EXPRESSION TAG	UNP C4NCB7
H	-19	PRO	-	EXPRESSION TAG	UNP C4NCB7
H	-18	ARG	-	EXPRESSION TAG	UNP C4NCB7
H	-17	GLY	-	EXPRESSION TAG	UNP C4NCB7
H	-16	SER	-	EXPRESSION TAG	UNP C4NCB7
H	-15	HIS	-	EXPRESSION TAG	UNP C4NCB7
H	-14	MET	-	EXPRESSION TAG	UNP C4NCB7
H	-13	ALA	-	EXPRESSION TAG	UNP C4NCB7
H	-12	SER	-	EXPRESSION TAG	UNP C4NCB7
H	-11	MET	-	EXPRESSION TAG	UNP C4NCB7
H	-10	THR	-	EXPRESSION TAG	UNP C4NCB7
H	-9	GLY	-	EXPRESSION TAG	UNP C4NCB7
H	-8	GLY	-	EXPRESSION TAG	UNP C4NCB7
H	-7	GLN	-	EXPRESSION TAG	UNP C4NCB7
H	-6	GLN	-	EXPRESSION TAG	UNP C4NCB7
H	-5	MET	-	EXPRESSION TAG	UNP C4NCB7
H	-4	GLY	-	EXPRESSION TAG	UNP C4NCB7
H	-3	ARG	-	EXPRESSION TAG	UNP C4NCB7
H	-2	GLY	-	EXPRESSION TAG	UNP C4NCB7
H	-1	SER	-	EXPRESSION TAG	UNP C4NCB7
H	0	GLU	-	EXPRESSION TAG	UNP C4NCB7
H	1	PHE	-	EXPRESSION TAG	UNP C4NCB7

- 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 water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	83	Total	O	0	0
			83	83		
3	B	56	Total	O	0	0
			56	56		
3	C	80	Total	O	0	0
			80	80		
3	D	57	Total	O	0	0
			57	57		
3	E	36	Total	O	0	0
			36	36		
3	F	51	Total	O	0	0
			51	51		
3	G	47	Total	O	0	0
			47	47		
3	H	45	Total	O	0	0
			45	45		

### 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.

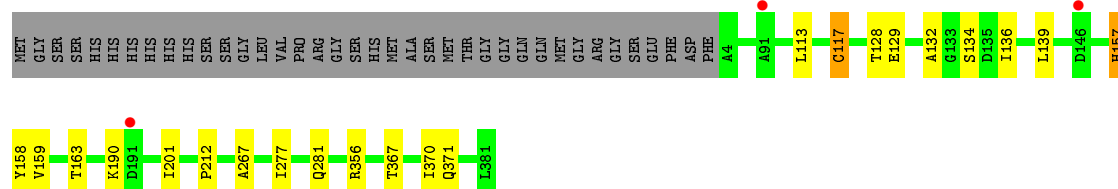
#### • Molecule 1: Prolyl-ACP dehydrogenase

Chain A: 



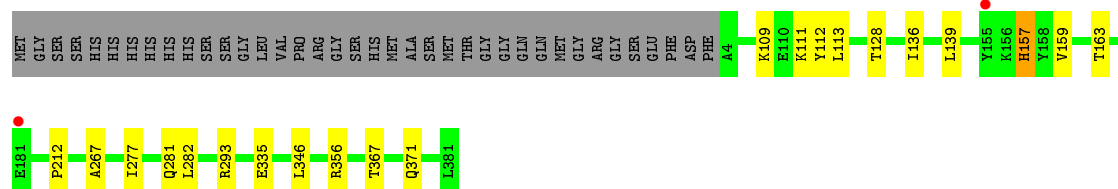
#### • Molecule 1: Prolyl-ACP dehydrogenase

Chain B: 




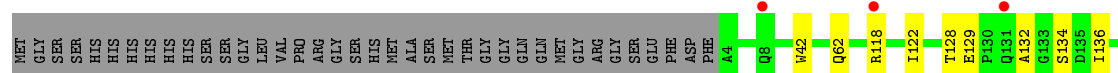
#### • Molecule 1: Prolyl-ACP dehydrogenase

Chain C: 



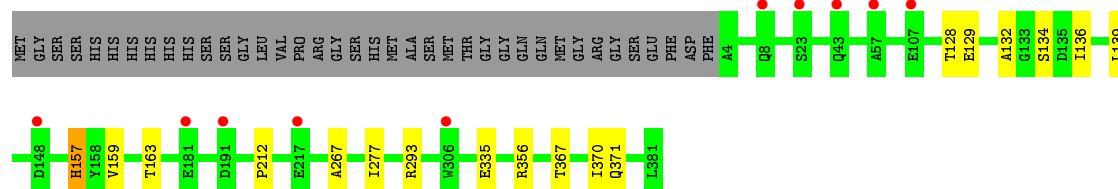
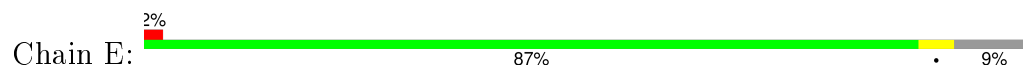
#### • Molecule 1: Prolyl-ACP dehydrogenase

Chain D: 

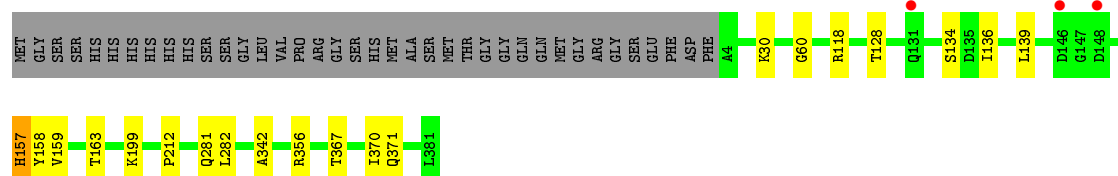
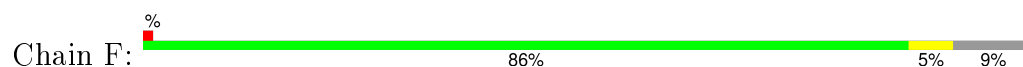




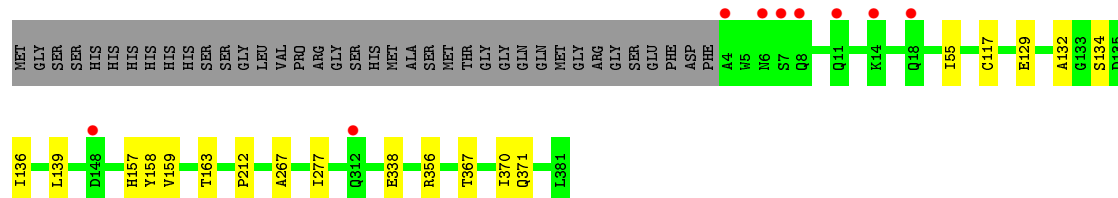
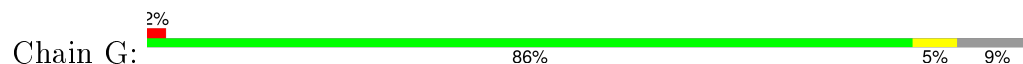
- Molecule 1: Prolyl-ACP dehydrogenase



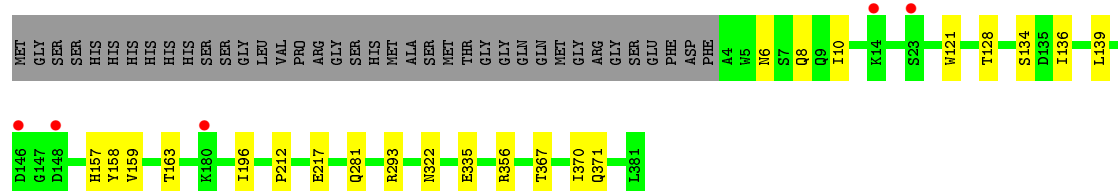
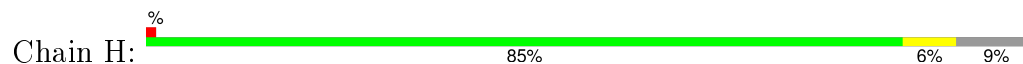
- Molecule 1: Prolyl-ACP dehydrogenase



- Molecule 1: Prolyl-ACP dehydrogenase



- Molecule 1: Prolyl-ACP dehydrogenase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	64.44Å 191.18Å 132.49Å 90.00° 98.94° 90.00°	Depositor
Resolution (Å)	30.00 – 2.80 29.74 – 2.80	Depositor EDS
% Data completeness (in resolution range)	98.8 (30.00-2.80) 98.8 (29.74-2.80)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.12	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.84 (at 2.80Å)	Xtriage
Refinement program	BUSTER 2.10.0	Depositor
R, $R_{free}$	0.188 , 0.219 0.205 , 0.234	Depositor DCC
$R_{free}$ test set	3857 reflections (5.29%)	DCC
Wilson B-factor (Å <sup>2</sup> )	29.0	Xtriage
Anisotropy	0.723	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 50.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.27$	Xtriage
Outliers	2 of 76749 reflections (0.003%)	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	24783	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	29.0	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 20.01 % 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 9.5562e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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 [i](#)

### 5.1 Standard geometry [i](#)

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	0.44	0/3049	0.63	0/4112
1	B	0.42	0/3049	0.61	0/4112
1	C	0.44	0/3049	0.61	0/4112
1	D	0.43	0/3049	0.60	0/4112
1	E	0.42	0/3049	0.61	0/4112
1	F	0.44	0/3049	0.63	0/4112
1	G	0.42	0/3049	0.61	0/4112
1	H	0.42	0/3049	0.62	0/4112
All	All	0.43	0/24392	0.61	0/32896

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 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	2988	0	2985	14	0
1	B	2988	0	2985	14	0
1	C	2988	0	2985	15	0
1	D	2988	0	2985	17	0
1	E	2988	0	2985	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	2988	0	2985	14	0
1	G	2988	0	2985	10	0
1	H	2988	0	2985	16	0
2	A	53	0	31	3	0
2	B	53	0	31	4	0
2	C	53	0	31	4	0
2	D	53	0	31	4	0
2	E	53	0	31	4	0
2	F	53	0	31	4	0
2	G	53	0	31	2	0
2	H	53	0	31	4	0
3	A	83	0	0	0	0
3	B	56	0	0	0	0
3	C	80	0	0	0	0
3	D	57	0	0	0	0
3	E	36	0	0	0	0
3	F	51	0	0	0	0
3	G	47	0	0	0	0
3	H	45	0	0	0	0
All	All	24783	0	24128	118	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 2.

All (118) 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:H:322:ASN:HD22	1:H:371:GLN:NE2	1.66	0.92
1:H:322:ASN:ND2	1:H:371:GLN:NE2	2.34	0.73
1:H:322:ASN:ND2	1:H:371:GLN:HE22	1.95	0.64
1:B:163:THR:HG23	1:B:212:PRO:HG3	1.85	0.59
1:H:163:THR:HG23	1:H:212:PRO:HG3	1.85	0.58
1:C:136:ILE:O	1:C:139:LEU:HG	2.04	0.58
1:A:136:ILE:O	1:A:139:LEU:HG	2.04	0.57
1:D:159:VAL:O	1:D:212:PRO:HD2	2.05	0.56
1:H:136:ILE:O	1:H:139:LEU:HG	2.05	0.56
2:B:400:FAD:H9	2:B:400:FAD:H2'	1.88	0.56
1:D:136:ILE:O	1:D:139:LEU:HG	2.06	0.56
1:E:136:ILE:O	1:E:139:LEU:HG	2.06	0.56
1:B:159:VAL:O	1:B:212:PRO:HD2	2.06	0.56
2:B:400:FAD:C9	2:B:400:FAD:H2'	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:136:ILE:O	1:G:139:LEU:HG	2.06	0.55
1:D:42:TRP:CZ2	1:D:122:ILE:HG12	2.41	0.55
1:E:163:THR:HG23	1:E:212:PRO:HG3	1.89	0.55
1:E:159:VAL:O	1:E:212:PRO:HD2	2.07	0.55
2:F:400:FAD:H2'	2:F:400:FAD:H9	1.88	0.55
1:G:163:THR:HG23	1:G:212:PRO:HG3	1.90	0.54
1:C:159:VAL:O	1:C:212:PRO:HD2	2.06	0.54
2:C:400:FAD:C9	2:C:400:FAD:H2'	2.36	0.54
2:C:400:FAD:H2'	2:C:400:FAD:H9	1.89	0.54
1:F:159:VAL:O	1:F:212:PRO:HD2	2.06	0.54
1:A:159:VAL:O	1:A:212:PRO:HD2	2.06	0.54
2:F:400:FAD:C9	2:F:400:FAD:H2'	2.36	0.54
1:G:159:VAL:O	1:G:212:PRO:HD2	2.08	0.54
1:D:163:THR:HG23	1:D:212:PRO:HG3	1.90	0.54
1:H:159:VAL:O	1:H:212:PRO:HD2	2.07	0.54
1:D:62:GLN:NE2	1:D:118:ARG:HH21	2.06	0.54
2:E:400:FAD:H2'	2:E:400:FAD:C9	2.39	0.53
2:A:400:FAD:H2'	2:A:400:FAD:H9	1.90	0.53
2:H:400:FAD:C9	2:H:400:FAD:H2'	2.38	0.53
2:E:400:FAD:H2'	2:E:400:FAD:H9	1.91	0.52
2:A:400:FAD:H2'	2:A:400:FAD:C9	2.38	0.52
1:D:62:GLN:NE2	1:D:118:ARG:NH2	2.57	0.52
2:H:400:FAD:H2'	2:H:400:FAD:H9	1.91	0.52
2:D:400:FAD:H2'	2:D:400:FAD:C9	2.39	0.52
1:A:163:THR:HG23	1:A:212:PRO:HG3	1.91	0.52
1:A:281:GLN:HB2	1:C:281:GLN:HB2	1.92	0.51
2:D:400:FAD:H9	2:D:400:FAD:H2'	1.93	0.51
1:A:60:GLY:O	1:A:118:ARG:HD2	2.11	0.51
1:F:281:GLN:HB2	1:H:281:GLN:HB2	1.93	0.50
1:C:163:THR:HG23	1:C:212:PRO:HG3	1.92	0.50
1:F:163:THR:HG23	1:F:212:PRO:HG3	1.92	0.50
1:B:136:ILE:O	1:B:139:LEU:HG	2.12	0.50
1:C:111:LYS:HD3	1:C:112:TYR:CE2	2.46	0.49
2:G:400:FAD:H2'	2:G:400:FAD:C9	2.42	0.49
1:F:60:GLY:O	1:F:118:ARG:HD2	2.13	0.48
1:D:129:GLU:HB2	1:D:132:ALA:HB3	1.94	0.48
1:D:62:GLN:HE21	1:D:118:ARG:HH21	1.62	0.48
1:F:136:ILE:O	1:F:139:LEU:HG	2.14	0.47
2:G:400:FAD:H2'	2:G:400:FAD:H9	1.97	0.47
1:B:113:LEU:O	1:B:117:CYS:HB2	2.16	0.46
1:A:281:GLN:HB3	1:C:282:LEU:HG	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:338:GLU:O	2:H:400:FAD:O3B	2.33	0.46
1:C:367:THR:O	1:C:371:GLN:HG2	2.16	0.46
1:C:356:ARG:HD3	1:D:356:ARG:HD3	1.97	0.46
1:B:267:ALA:HA	1:B:277:ILE:HG13	1.97	0.46
1:B:129:GLU:HB2	1:B:132:ALA:HB3	1.98	0.45
1:C:346:LEU:HD22	1:D:201:ILE:CG2	2.46	0.45
1:E:129:GLU:HB2	1:E:132:ALA:HB3	1.98	0.45
1:B:128:THR:HG23	1:B:157:HIS:O	2.17	0.45
1:D:134:SER:HB3	1:D:370:ILE:HD11	1.99	0.45
2:B:400:FAD:C2'	2:B:400:FAD:H9	2.46	0.44
1:H:196:ILE:CD1	1:H:217:GLU:HG3	2.47	0.44
1:F:128:THR:HG23	1:F:157:HIS:O	2.17	0.44
1:D:128:THR:HG21	2:D:400:FAD:H1'1	1.99	0.44
1:E:128:THR:HG23	1:E:157:HIS:O	2.17	0.44
1:A:128:THR:HG21	2:A:400:FAD:H1'1	1.99	0.44
1:H:128:THR:HG21	2:H:400:FAD:H1'1	1.99	0.44
1:E:367:THR:O	1:E:371:GLN:HG2	2.17	0.44
2:E:400:FAD:O3'	1:F:342:ALA:HB2	2.18	0.44
1:D:367:THR:O	1:D:371:GLN:HG2	2.17	0.44
1:E:134:SER:HB3	1:E:370:ILE:HD11	2.00	0.44
1:C:267:ALA:HA	1:C:277:ILE:HG13	2.00	0.44
1:A:134:SER:HB3	1:A:370:ILE:HD11	1.99	0.44
1:C:293:ARG:NH2	1:C:335:GLU:OE1	2.51	0.44
1:E:267:ALA:HA	1:E:277:ILE:HG13	1.98	0.44
1:H:134:SER:HB3	1:H:370:ILE:HD11	1.99	0.43
1:E:293:ARG:NH2	1:E:335:GLU:OE1	2.51	0.43
1:H:293:ARG:NH2	1:H:335:GLU:OE1	2.51	0.43
1:F:367:THR:O	1:F:371:GLN:HG2	2.18	0.43
1:B:134:SER:HB3	1:B:370:ILE:HD11	2.00	0.43
1:G:129:GLU:HB2	1:G:132:ALA:HB3	2.01	0.43
1:A:113:LEU:O	1:A:117:CYS:HB2	2.18	0.43
1:B:128:THR:HG21	2:B:400:FAD:H1'1	2.01	0.43
1:G:134:SER:HB3	1:G:370:ILE:HD11	2.00	0.43
1:F:199:LYS:HE2	1:F:199:LYS:HB2	1.83	0.43
1:B:190:LYS:HE2	1:F:30:LYS:HD2	2.02	0.42
1:G:367:THR:O	1:G:371:GLN:HG2	2.18	0.42
1:H:367:THR:O	1:H:371:GLN:HG2	2.18	0.42
2:F:400:FAD:C2'	2:F:400:FAD:H9	2.47	0.42
2:C:400:FAD:C2'	2:C:400:FAD:H9	2.47	0.42
1:A:367:THR:O	1:A:371:GLN:HG2	2.19	0.42
1:C:128:THR:HG21	2:C:400:FAD:H1'1	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:128:THR:HG23	1:A:157:HIS:O	2.19	0.42
1:A:346:LEU:HD22	1:B:201:ILE:CG2	2.50	0.42
2:E:400:FAD:C2'	2:E:400:FAD:H9	2.48	0.41
1:E:356:ARG:HD3	1:F:356:ARG:HD3	2.03	0.41
1:G:267:ALA:HA	1:G:277:ILE:HG13	2.01	0.41
1:F:128:THR:HG21	2:F:400:FAD:H1'1	2.02	0.41
1:A:356:ARG:HD3	1:B:356:ARG:HD3	2.02	0.41
1:C:346:LEU:HD22	1:D:201:ILE:HG22	2.02	0.41
1:B:281:GLN:HB3	1:D:282:LEU:HG	2.01	0.41
1:B:367:THR:O	1:B:371:GLN:HG2	2.19	0.41
1:H:371:GLN:H	1:H:371:GLN:HG2	1.64	0.41
1:D:293:ARG:NH2	1:D:335:GLU:OE1	2.53	0.41
1:F:134:SER:HB3	1:F:370:ILE:HD11	2.01	0.41
1:C:128:THR:HG23	1:C:157:HIS:O	2.20	0.41
2:D:400:FAD:H9	2:D:400:FAD:C2'	2.50	0.41
1:F:282:LEU:HG	1:H:281:GLN:HB3	2.02	0.41
1:A:284:ALA:O	1:A:288:VAL:HG23	2.21	0.41
1:G:55:ILE:HG21	1:G:117:CYS:SG	2.61	0.40
1:D:128:THR:HG23	1:D:157:HIS:O	2.21	0.40
1:C:109:LYS:O	1:C:113:LEU:HB2	2.21	0.40
1:G:356:ARG:HD3	1:H:356:ARG:HD3	2.03	0.40
1:H:6:ASN:O	1:H:10:ILE:HG12	2.21	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	376/416 (90%)	360 (96%)	15 (4%)	1 (0%)	46	79
1	B	376/416 (90%)	360 (96%)	15 (4%)	1 (0%)	46	79
1	C	376/416 (90%)	359 (96%)	17 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	376/416 (90%)	359 (96%)	16 (4%)	1 (0%)	46	79
1	E	376/416 (90%)	360 (96%)	16 (4%)	0	100	100
1	F	376/416 (90%)	359 (96%)	16 (4%)	1 (0%)	46	79
1	G	376/416 (90%)	361 (96%)	14 (4%)	1 (0%)	46	79
1	H	376/416 (90%)	359 (96%)	16 (4%)	1 (0%)	46	79
All	All	3008/3328 (90%)	2877 (96%)	125 (4%)	6 (0%)	52	84

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	158	TYR
1	B	158	TYR
1	D	158	TYR
1	H	158	TYR
1	F	158	TYR
1	G	158	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	310/340 (91%)	309 (100%)	1 (0%)	94	99
1	B	310/340 (91%)	308 (99%)	2 (1%)	90	98
1	C	310/340 (91%)	309 (100%)	1 (0%)	94	99
1	D	310/340 (91%)	308 (99%)	2 (1%)	90	98
1	E	310/340 (91%)	309 (100%)	1 (0%)	94	99
1	F	310/340 (91%)	309 (100%)	1 (0%)	94	99
1	G	310/340 (91%)	309 (100%)	1 (0%)	94	99
1	H	310/340 (91%)	307 (99%)	3 (1%)	82	96
All	All	2480/2720 (91%)	2468 (100%)	12 (0%)	92	98

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	157	HIS
1	B	117	CYS
1	B	157	HIS
1	C	157	HIS
1	D	157	HIS
1	D	190	LYS
1	E	157	HIS
1	F	157	HIS
1	G	157	HIS
1	H	8	GLN
1	H	121	TRP
1	H	157	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	296	ASN
1	B	18	GLN
1	B	296	ASN
1	D	18	GLN
1	D	62	GLN
1	D	296	ASN
1	E	296	ASN
1	G	239	HIS
1	G	296	ASN
1	G	340	HIS
1	H	371	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

8 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	400	-	48,58,58	1.10	5 (10%)	54,89,89	2.44	8 (14%)
2	FAD	B	400	-	48,58,58	1.06	5 (10%)	54,89,89	2.26	8 (14%)
2	FAD	C	400	-	48,58,58	1.09	5 (10%)	54,89,89	2.42	8 (14%)
2	FAD	D	400	-	48,58,58	1.05	5 (10%)	54,89,89	2.29	7 (12%)
2	FAD	E	400	-	48,58,58	1.11	5 (10%)	54,89,89	2.48	10 (18%)
2	FAD	F	400	-	48,58,58	1.09	5 (10%)	54,89,89	2.43	8 (14%)
2	FAD	G	400	-	48,58,58	1.06	5 (10%)	54,89,89	2.36	7 (12%)
2	FAD	H	400	-	48,58,58	1.06	5 (10%)	54,89,89	2.43	9 (16%)

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	400	-	-	0/30/50/50	0/6/6/6
2	FAD	B	400	-	-	0/30/50/50	0/6/6/6
2	FAD	C	400	-	-	0/30/50/50	0/6/6/6
2	FAD	D	400	-	-	0/30/50/50	0/6/6/6
2	FAD	E	400	-	-	0/30/50/50	0/6/6/6
2	FAD	F	400	-	-	0/30/50/50	0/6/6/6
2	FAD	G	400	-	-	0/30/50/50	0/6/6/6
2	FAD	H	400	-	-	0/30/50/50	0/6/6/6

All (40) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	400	FAD	C4X-C10	2.26	1.45	1.41
2	D	400	FAD	C4-N3	2.42	1.37	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	400	FAD	C4-N3	2.44	1.37	1.33
2	H	400	FAD	C9A-N10	2.51	1.42	1.38
2	B	400	FAD	C4-N3	2.53	1.37	1.33
2	H	400	FAD	C4-N3	2.53	1.37	1.33
2	C	400	FAD	C4-N3	2.53	1.37	1.33
2	A	400	FAD	C4-N3	2.55	1.37	1.33
2	E	400	FAD	C9A-N10	2.55	1.42	1.38
2	G	400	FAD	C4-N3	2.57	1.37	1.33
2	B	400	FAD	C4X-C10	2.59	1.45	1.41
2	G	400	FAD	C9A-N10	2.60	1.42	1.38
2	E	400	FAD	C4X-C10	2.70	1.46	1.41
2	H	400	FAD	C4X-C10	2.72	1.46	1.41
2	C	400	FAD	C9A-N10	2.74	1.42	1.38
2	B	400	FAD	C9A-N10	2.75	1.42	1.38
2	G	400	FAD	C4X-C10	2.76	1.46	1.41
2	A	400	FAD	C4-C4X	2.79	1.46	1.41
2	E	400	FAD	C4-N3	2.79	1.38	1.33
2	D	400	FAD	C9A-N10	2.79	1.42	1.38
2	F	400	FAD	C9A-N10	2.81	1.42	1.38
2	B	400	FAD	C5X-N5	2.83	1.39	1.35
2	G	400	FAD	C5X-N5	2.89	1.39	1.35
2	A	400	FAD	C5X-N5	2.91	1.40	1.35
2	A	400	FAD	C9A-N10	2.93	1.42	1.38
2	H	400	FAD	C5X-N5	2.97	1.40	1.35
2	F	400	FAD	C5X-N5	2.98	1.40	1.35
2	C	400	FAD	C5X-N5	3.01	1.40	1.35
2	F	400	FAD	C4X-C10	3.01	1.46	1.41
2	C	400	FAD	C4X-C10	3.04	1.46	1.41
2	C	400	FAD	C4-C4X	3.06	1.47	1.41
2	D	400	FAD	C5X-N5	3.08	1.40	1.35
2	E	400	FAD	C4-C4X	3.17	1.47	1.41
2	D	400	FAD	C4-C4X	3.18	1.47	1.41
2	B	400	FAD	C4-C4X	3.18	1.47	1.41
2	H	400	FAD	C4-C4X	3.23	1.47	1.41
2	F	400	FAD	C4-C4X	3.24	1.47	1.41
2	G	400	FAD	C4-C4X	3.27	1.47	1.41
2	A	400	FAD	C4X-C10	3.30	1.47	1.41
2	E	400	FAD	C5X-N5	3.44	1.40	1.35

All (65) bond angle outliers are listed below:

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	400	FAD	C4X-C4-N3	-6.71	114.42	123.59
2	G	400	FAD	C4X-C4-N3	-6.67	114.47	123.59
2	E	400	FAD	C4X-C4-N3	-6.64	114.51	123.59
2	C	400	FAD	C4X-C4-N3	-6.64	114.51	123.59
2	F	400	FAD	C4X-C4-N3	-6.63	114.52	123.59
2	H	400	FAD	C4X-C4-N3	-6.60	114.57	123.59
2	B	400	FAD	C4X-C4-N3	-6.56	114.61	123.59
2	D	400	FAD	C4X-C4-N3	-6.53	114.66	123.59
2	G	400	FAD	C4X-C10-N10	-5.11	117.51	120.52
2	A	400	FAD	C4X-C10-N10	-4.94	117.61	120.52
2	C	400	FAD	C4X-C10-N10	-4.85	117.66	120.52
2	B	400	FAD	C4X-C10-N10	-4.83	117.67	120.52
2	F	400	FAD	C4X-C10-N10	-4.76	117.71	120.52
2	H	400	FAD	C4X-C10-N10	-4.64	117.79	120.52
2	E	400	FAD	C4X-C10-N10	-4.56	117.83	120.52
2	D	400	FAD	C4X-C10-N10	-4.51	117.86	120.52
2	E	400	FAD	C4-C4X-C10	-3.63	117.62	119.94
2	H	400	FAD	C4-C4X-C10	-3.42	117.75	119.94
2	D	400	FAD	C4-C4X-C10	-3.38	117.78	119.94
2	A	400	FAD	C4-C4X-C10	-3.36	117.79	119.94
2	F	400	FAD	C4-C4X-C10	-3.31	117.82	119.94
2	G	400	FAD	C4-C4X-C10	-3.30	117.83	119.94
2	B	400	FAD	C4-C4X-C10	-3.20	117.89	119.94
2	C	400	FAD	C4-C4X-C10	-3.20	117.90	119.94
2	H	400	FAD	P-O3P-PA	-2.89	124.61	132.73
2	F	400	FAD	P-O3P-PA	-2.82	124.80	132.73
2	E	400	FAD	P-O3P-PA	-2.82	124.81	132.73
2	E	400	FAD	O2P-P-O5'	-2.77	94.50	108.46
2	D	400	FAD	P-O3P-PA	-2.73	125.07	132.73
2	C	400	FAD	P-O3P-PA	-2.71	125.12	132.73
2	G	400	FAD	P-O3P-PA	-2.56	125.55	132.73
2	A	400	FAD	P-O3P-PA	-2.53	125.64	132.73
2	H	400	FAD	O2P-P-O5'	-2.51	95.79	108.46
2	A	400	FAD	O2P-P-O5'	-2.37	96.50	108.46
2	F	400	FAD	O2P-P-O5'	-2.37	96.51	108.46
2	C	400	FAD	O2P-P-O5'	-2.36	96.57	108.46
2	B	400	FAD	O2P-P-O5'	-2.20	97.35	108.46
2	E	400	FAD	C2B-C1B-N9A	-2.10	111.08	114.29
2	B	400	FAD	O3P-P-O5'	2.01	108.28	102.94
2	H	400	FAD	O2P-P-O3P	2.03	114.29	105.09
2	E	400	FAD	O2P-P-O3P	2.10	114.62	105.09

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	400	FAD	O2P-P-O1P	2.47	125.92	112.53
2	D	400	FAD	O3P-P-O5'	2.50	109.57	102.94
2	G	400	FAD	O3P-P-O5'	2.69	110.08	102.94
2	B	400	FAD	O3P-PA-O5B	4.40	114.61	102.94
2	E	400	FAD	O3P-PA-O5B	4.80	115.67	102.94
2	H	400	FAD	O3P-PA-O5B	5.20	116.73	102.94
2	C	400	FAD	O3P-P-O5'	5.40	117.25	102.94
2	A	400	FAD	O3P-PA-O5B	5.40	117.27	102.94
2	C	400	FAD	O3P-PA-O5B	5.41	117.28	102.94
2	F	400	FAD	O3P-PA-O5B	5.51	117.55	102.94
2	F	400	FAD	O3P-P-O5'	5.52	117.59	102.94
2	A	400	FAD	O3P-P-O5'	5.60	117.78	102.94
2	H	400	FAD	O3P-P-O5'	5.72	118.11	102.94
2	D	400	FAD	O3P-PA-O5B	5.89	118.57	102.94
2	G	400	FAD	O3P-PA-O5B	6.21	119.41	102.94
2	E	400	FAD	O3P-P-O5'	6.29	119.63	102.94
2	B	400	FAD	C4-N3-C2	11.74	125.40	115.25
2	D	400	FAD	C4-N3-C2	11.76	125.41	115.25
2	C	400	FAD	C4-N3-C2	11.77	125.42	115.25
2	H	400	FAD	C4-N3-C2	11.81	125.45	115.25
2	F	400	FAD	C4-N3-C2	11.82	125.47	115.25
2	G	400	FAD	C4-N3-C2	11.84	125.48	115.25
2	A	400	FAD	C4-N3-C2	11.90	125.53	115.25
2	E	400	FAD	C4-N3-C2	11.99	125.61	115.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

8 monomers are involved in 29 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	400	FAD	3	0
2	B	400	FAD	4	0
2	C	400	FAD	4	0
2	D	400	FAD	4	0
2	E	400	FAD	4	0
2	F	400	FAD	4	0
2	G	400	FAD	2	0
2	H	400	FAD	4	0

## 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, 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	378/416 (90%)	-0.44	1 (0%) 94 92	9, 22, 42, 55	0
1	B	378/416 (90%)	-0.29	3 (0%) 87 81	10, 25, 44, 54	0
1	C	378/416 (90%)	-0.31	2 (0%) 91 88	12, 23, 42, 59	0
1	D	378/416 (90%)	-0.21	6 (1%) 74 66	10, 27, 47, 56	0
1	E	378/416 (90%)	-0.13	10 (2%) 59 47	15, 31, 49, 66	0
1	F	378/416 (90%)	-0.17	3 (0%) 87 81	15, 30, 50, 61	0
1	G	378/416 (90%)	-0.06	9 (2%) 62 50	15, 31, 51, 69	0
1	H	378/416 (90%)	-0.15	5 (1%) 79 71	16, 32, 52, 61	0
All	All	3024/3328 (90%)	-0.22	39 (1%) 79 71	9, 28, 49, 69	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	8	GLN	4.5
1	D	148	ASP	3.3
1	G	148	ASP	3.0
1	G	7	SER	2.9
1	B	146	ASP	2.8
1	C	181	GLU	2.8
1	G	312	GLN	2.8
1	G	18	GLN	2.6
1	E	148	ASP	2.6
1	H	23	SER	2.6
1	E	43	GLN	2.6
1	G	8	GLN	2.6
1	H	14	LYS	2.6
1	E	306	TRP	2.6
1	G	4	ALA	2.5
1	F	148	ASP	2.5

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Mol	Chain	Res	Type	RSRZ
1	E	23	SER	2.4
1	D	155	TYR	2.4
1	H	146	ASP	2.4
1	G	14	LYS	2.4
1	H	148	ASP	2.4
1	G	11	GLN	2.3
1	D	131	GLN	2.2
1	D	118	ARG	2.2
1	E	107	GLU	2.2
1	B	91	ALA	2.2
1	E	191	ASP	2.2
1	B	191	ASP	2.2
1	E	181	GLU	2.2
1	G	6	ASN	2.2
1	D	8	GLN	2.1
1	E	217	GLU	2.1
1	C	155	TYR	2.1
1	F	131	GLN	2.0
1	E	57	ALA	2.0
1	A	148	ASP	2.0
1	D	151	ILE	2.0
1	F	146	ASP	2.0
1	H	180	LYS	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	400	53/53	0.94	0.16	0.43	15,22,29,30	0
2	FAD	G	400	53/53	0.93	0.18	0.22	22,25,35,36	0
2	FAD	D	400	53/53	0.94	0.16	0.16	14,22,31,33	0
2	FAD	F	400	53/53	0.94	0.17	0.11	17,25,34,36	0
2	FAD	H	400	53/53	0.93	0.16	0.08	16,25,35,36	0
2	FAD	B	400	53/53	0.95	0.16	0.01	13,19,33,33	0
2	FAD	C	400	53/53	0.95	0.15	-0.06	15,20,29,30	0
2	FAD	E	400	53/53	0.95	0.14	-0.33	19,22,31,32	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.