



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 03:34 am GMT

PDB ID : 5EZ3
Title : Crystal structure Acyl-CoA dehydrogenase from Brucella melitensis in complex with FAD
Authors : Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on : 2015-11-26
Resolution : 2.15 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

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

A user guide is available at

<http://wwpdb.org/validation/2016/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
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : recalc28949

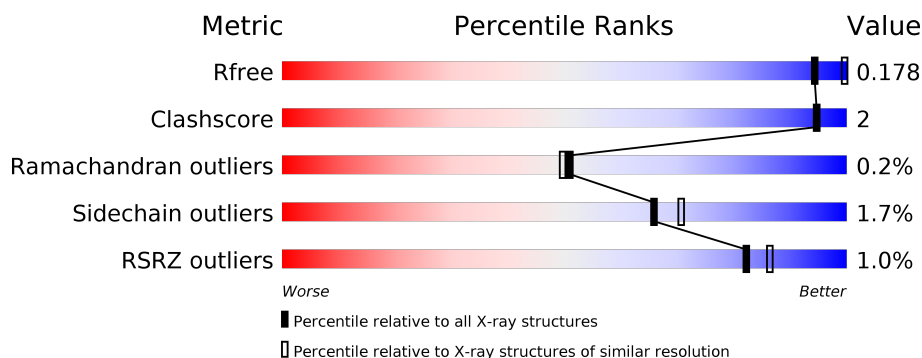
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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}	100719	1170 (2.16-2.16)
Clashscore	112137	1278 (2.16-2.16)
Ramachandran outliers	110173	1256 (2.16-2.16)
Sidechain outliers	110143	1255 (2.16-2.16)
RSRZ outliers	101464	1175 (2.16-2.16)

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 $\leq 5\%$. 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	573	<div> <div>%</div> <div> <div></div> <div>90%</div> <div>5%</div> <div>6%</div> </div> </div>
1	B	573	<div> <div>%</div> <div> <div></div> <div>90%</div> <div>5%</div> <div>6%</div> </div> </div>
1	C	573	<div> <div>%</div> <div> <div></div> <div>91%</div> <div>•</div> <div>6%</div> </div> </div>
1	D	573	<div> <div>%</div> <div> <div></div> <div>90%</div> <div>•</div> <div>6%</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	MRD	A	601	-	-	-	X
3	MRD	B	601	-	-	-	X
3	MRD	C	601	-	-	-	X
3	MRD	D	601	-	-	-	X
4	MPD	B	602	-	-	-	X
4	MPD	C	602	-	-	-	X
5	CAC	B	603	-	-	-	X
5	CAC	B	604	-	-	-	X
5	CAC	D	604	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 18169 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 Acyl-CoA dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	540	Total	C	N	O	S	0	7	0
			4151	2607	751	765	28			
1	B	541	Total	C	N	O	S	0	9	0
			4135	2596	741	769	29			
1	C	541	Total	C	N	O	S	0	6	0
			4137	2596	746	767	28			
1	D	541	Total	C	N	O	S	0	9	0
			4158	2610	752	768	28			

There are 92 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-20	MET	-	initiating methionine	UNP Q8YC61
A	-19	ALA	-	expression tag	UNP Q8YC61
A	-18	HIS	-	expression tag	UNP Q8YC61
A	-17	HIS	-	expression tag	UNP Q8YC61
A	-16	HIS	-	expression tag	UNP Q8YC61
A	-15	HIS	-	expression tag	UNP Q8YC61
A	-14	HIS	-	expression tag	UNP Q8YC61
A	-13	HIS	-	expression tag	UNP Q8YC61
A	-12	MET	-	expression tag	UNP Q8YC61
A	-11	GLY	-	expression tag	UNP Q8YC61
A	-10	THR	-	expression tag	UNP Q8YC61
A	-9	LEU	-	expression tag	UNP Q8YC61
A	-8	GLU	-	expression tag	UNP Q8YC61
A	-7	ALA	-	expression tag	UNP Q8YC61
A	-6	GLN	-	expression tag	UNP Q8YC61
A	-5	THR	-	expression tag	UNP Q8YC61
A	-4	GLN	-	expression tag	UNP Q8YC61
A	-3	GLY	-	expression tag	UNP Q8YC61
A	-2	PRO	-	expression tag	UNP Q8YC61
A	-1	GLY	-	expression tag	UNP Q8YC61
A	0	SER	-	expression tag	UNP Q8YC61

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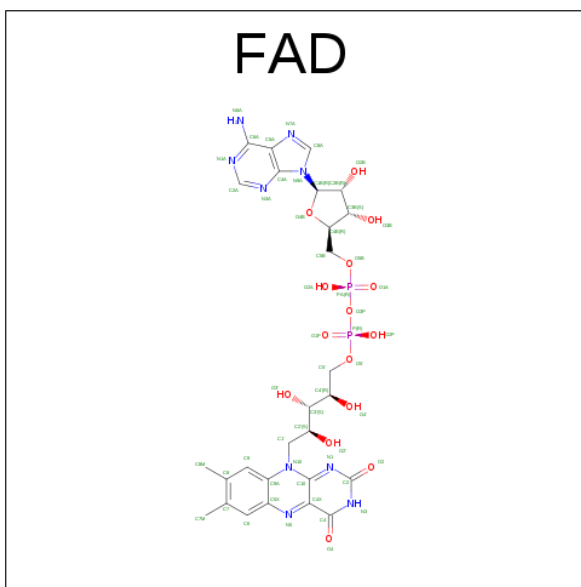
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	expression tag	UNP Q8YC61
A	2	LEU	-	expression tag	UNP Q8YC61
B	-20	MET	-	initiating methionine	UNP Q8YC61
B	-19	ALA	-	expression tag	UNP Q8YC61
B	-18	HIS	-	expression tag	UNP Q8YC61
B	-17	HIS	-	expression tag	UNP Q8YC61
B	-16	HIS	-	expression tag	UNP Q8YC61
B	-15	HIS	-	expression tag	UNP Q8YC61
B	-14	HIS	-	expression tag	UNP Q8YC61
B	-13	HIS	-	expression tag	UNP Q8YC61
B	-12	MET	-	expression tag	UNP Q8YC61
B	-11	GLY	-	expression tag	UNP Q8YC61
B	-10	THR	-	expression tag	UNP Q8YC61
B	-9	LEU	-	expression tag	UNP Q8YC61
B	-8	GLU	-	expression tag	UNP Q8YC61
B	-7	ALA	-	expression tag	UNP Q8YC61
B	-6	GLN	-	expression tag	UNP Q8YC61
B	-5	THR	-	expression tag	UNP Q8YC61
B	-4	GLN	-	expression tag	UNP Q8YC61
B	-3	GLY	-	expression tag	UNP Q8YC61
B	-2	PRO	-	expression tag	UNP Q8YC61
B	-1	GLY	-	expression tag	UNP Q8YC61
B	0	SER	-	expression tag	UNP Q8YC61
B	1	MET	-	expression tag	UNP Q8YC61
B	2	LEU	-	expression tag	UNP Q8YC61
C	-20	MET	-	initiating methionine	UNP Q8YC61
C	-19	ALA	-	expression tag	UNP Q8YC61
C	-18	HIS	-	expression tag	UNP Q8YC61
C	-17	HIS	-	expression tag	UNP Q8YC61
C	-16	HIS	-	expression tag	UNP Q8YC61
C	-15	HIS	-	expression tag	UNP Q8YC61
C	-14	HIS	-	expression tag	UNP Q8YC61
C	-13	HIS	-	expression tag	UNP Q8YC61
C	-12	MET	-	expression tag	UNP Q8YC61
C	-11	GLY	-	expression tag	UNP Q8YC61
C	-10	THR	-	expression tag	UNP Q8YC61
C	-9	LEU	-	expression tag	UNP Q8YC61
C	-8	GLU	-	expression tag	UNP Q8YC61
C	-7	ALA	-	expression tag	UNP Q8YC61
C	-6	GLN	-	expression tag	UNP Q8YC61
C	-5	THR	-	expression tag	UNP Q8YC61
C	-4	GLN	-	expression tag	UNP Q8YC61

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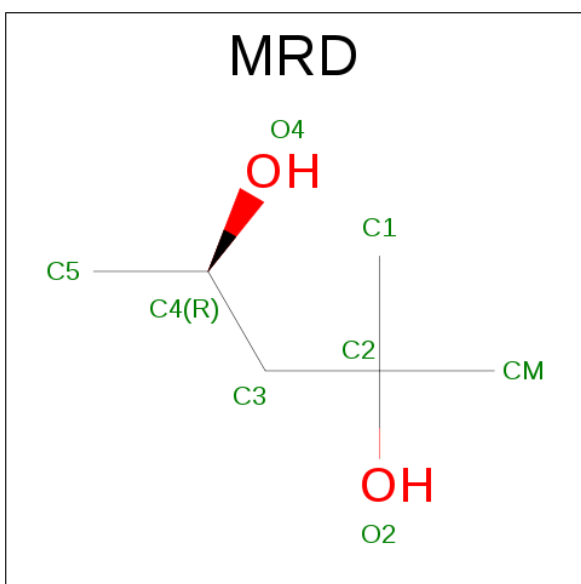
Chain	Residue	Modelled	Actual	Comment	Reference
C	-3	GLY	-	expression tag	UNP Q8YC61
C	-2	PRO	-	expression tag	UNP Q8YC61
C	-1	GLY	-	expression tag	UNP Q8YC61
C	0	SER	-	expression tag	UNP Q8YC61
C	1	MET	-	expression tag	UNP Q8YC61
C	2	LEU	-	expression tag	UNP Q8YC61
D	-20	MET	-	initiating methionine	UNP Q8YC61
D	-19	ALA	-	expression tag	UNP Q8YC61
D	-18	HIS	-	expression tag	UNP Q8YC61
D	-17	HIS	-	expression tag	UNP Q8YC61
D	-16	HIS	-	expression tag	UNP Q8YC61
D	-15	HIS	-	expression tag	UNP Q8YC61
D	-14	HIS	-	expression tag	UNP Q8YC61
D	-13	HIS	-	expression tag	UNP Q8YC61
D	-12	MET	-	expression tag	UNP Q8YC61
D	-11	GLY	-	expression tag	UNP Q8YC61
D	-10	THR	-	expression tag	UNP Q8YC61
D	-9	LEU	-	expression tag	UNP Q8YC61
D	-8	GLU	-	expression tag	UNP Q8YC61
D	-7	ALA	-	expression tag	UNP Q8YC61
D	-6	GLN	-	expression tag	UNP Q8YC61
D	-5	THR	-	expression tag	UNP Q8YC61
D	-4	GLN	-	expression tag	UNP Q8YC61
D	-3	GLY	-	expression tag	UNP Q8YC61
D	-2	PRO	-	expression tag	UNP Q8YC61
D	-1	GLY	-	expression tag	UNP Q8YC61
D	0	SER	-	expression tag	UNP Q8YC61
D	1	MET	-	expression tag	UNP Q8YC61
D	2	LEU	-	expression tag	UNP Q8YC61

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



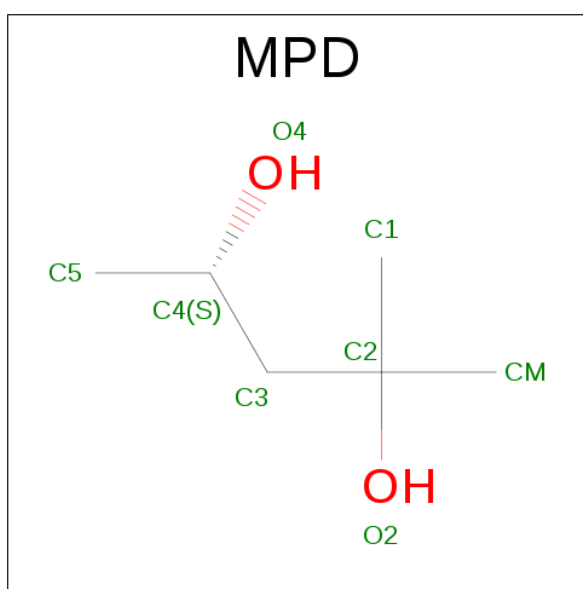
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 53	C 27	N 9	O 15	P 2	0	0
2	B	1	Total 53	C 27	N 9	O 15	P 2	0	0
2	C	1	Total 53	C 27	N 9	O 15	P 2	0	0
2	D	1	Total 53	C 27	N 9	O 15	P 2	0	0

- Molecule 3 is (4R)-2-METHYLPENTANE-2,4-DIOL (three-letter code: MRD) (formula: $\text{C}_6\text{H}_{14}\text{O}_2$).



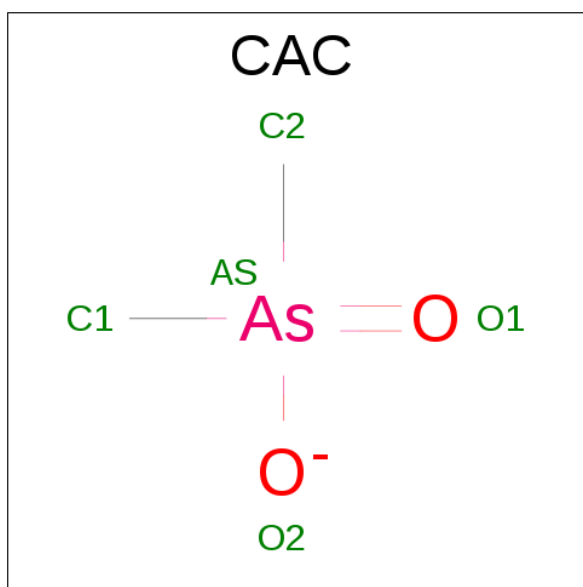
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			8	6	2		
3	B	1	Total	C	O	0	0
			8	6	2		
3	C	1	Total	C	O	0	0
			8	6	2		
3	D	1	Total	C	O	0	0
			8	6	2		

- Molecule 4 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: $C_6H_{14}O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			8	6	2		
4	B	1	Total	C	O	0	0
			8	6	2		
4	C	1	Total	C	O	0	0
			8	6	2		
4	D	1	Total	C	O	0	0
			8	6	2		

- Molecule 5 is CACODYLATE ION (three-letter code: CAC) (formula: $C_2H_6AsO_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	As	C	O	0	0
			5	1	2	2		
5	B	1	Total	As	C	O	0	0
			5	1	2	2		
5	B	1	Total	As	C	O	0	0
			5	1	2	2		
5	C	1	Total	As	C	O	0	0
			5	1	2	2		
5	C	1	Total	As	C	O	0	0
			5	1	2	2		
5	D	1	Total	As	C	O	0	0
			4	1	2	1		
5	D	1	Total	As	C	O	0	0
			5	1	2	2		

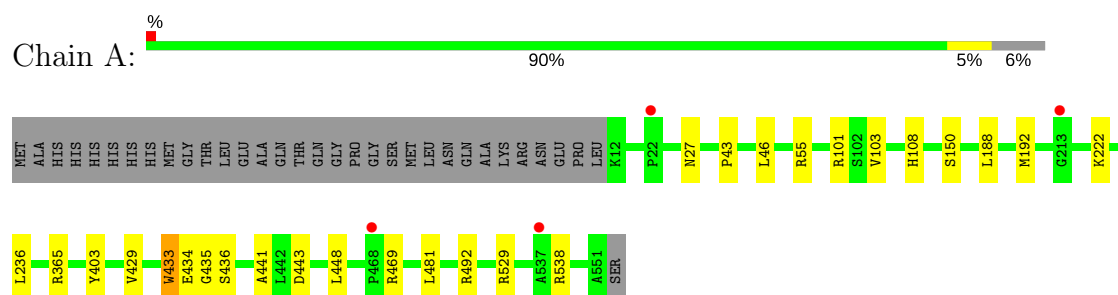
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	352	Total	O	0	0
			352	352		
6	B	267	Total	O	0	0
			267	267		
6	C	329	Total	O	0	0
			329	329		
6	D	329	Total	O	0	1
			330	330		

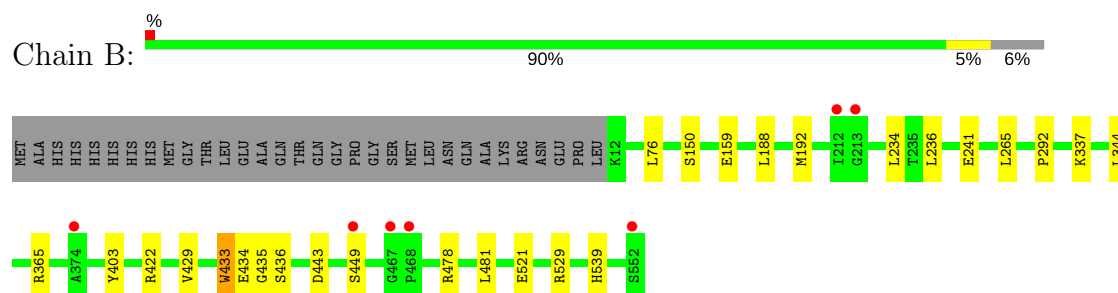
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

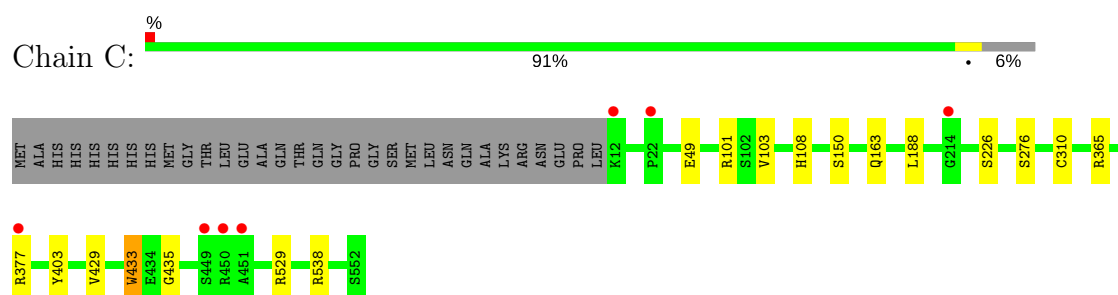
- Molecule 1: Acyl-CoA dehydrogenase



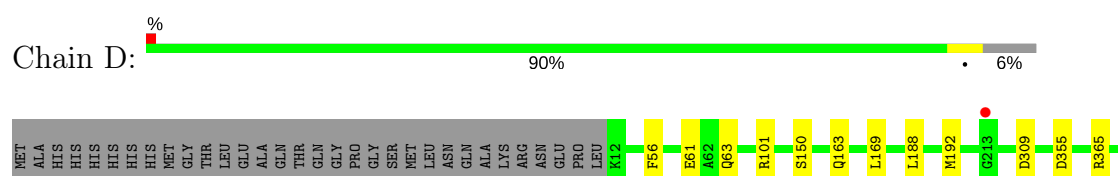
- Molecule 1: Acyl-CoA dehydrogenase

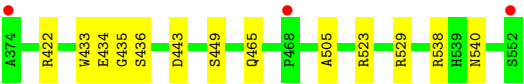


- Molecule 1: Acyl-CoA dehydrogenase



- Molecule 1: Acyl-CoA dehydrogenase





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	96.92Å 141.25Å 193.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.75 – 2.15 19.75 – 2.15	Depositor EDS
% Data completeness (in resolution range)	99.2 (19.75-2.15) 99.2 (19.75-2.15)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.99 (at 2.15Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.145 , 0.178 0.144 , 0.178	Depositor DCC
R_{free} test set	2002 reflections (1.40%)	DCC
Wilson B-factor (Å ²)	26.8	Xtriage
Anisotropy	0.248	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 47.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	18169	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.45% of the height of the origin peak. No significant pseudotranslation is detected.*

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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CAC, MRD, MPD, 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	0.40	0/4250	0.56	0/5760
1	B	0.38	0/4240	0.54	0/5752
1	C	0.41	0/4233	0.56	0/5738
1	D	0.41	0/4263	0.57	0/5778
All	All	0.40	0/16986	0.56	0/23028

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	4151	0	4099	15	0
1	B	4135	0	4041	16	0
1	C	4137	0	4059	7	0
1	D	4158	0	4097	14	0
2	A	53	0	31	2	0
2	B	53	0	31	1	0
2	C	53	0	31	0	0
2	D	53	0	31	1	0
3	A	8	0	14	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	8	0	14	1	0
3	C	8	0	14	1	0
3	D	8	0	14	2	0
4	A	8	0	14	0	0
4	B	8	0	14	1	0
4	C	8	0	14	0	0
4	D	8	0	14	0	0
5	A	5	0	0	0	0
5	B	10	0	0	0	0
5	C	10	0	0	1	0
5	D	9	0	0	1	0
6	A	352	0	0	2	0
6	B	267	0	0	1	0
6	C	329	0	0	1	0
6	D	330	0	0	2	0
All	All	18169	0	16532	51	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 (51) 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:B:436:SER:HG	2:B:600:FAD:HO2A	1.23	0.82
1:A:436:SER:HG	2:A:600:FAD:HO2A	1.40	0.70
1:A:436:SER:OG	2:A:600:FAD:O2B	2.15	0.65
1:A:192[B]:MET:HG3	1:A:236:LEU:HD12	1.82	0.61
1:C:101:ARG:NH1	6:C:703:HOH:O	2.34	0.60
1:A:101:ARG:NH1	6:A:702:HOH:O	2.33	0.58
1:D:163:GLN:HG2	5:D:604:CAC:C2	2.33	0.58
1:B:429:VAL:O	1:B:433[B]:TRP:HB3	2.03	0.57
1:C:163:GLN:HG2	5:C:604:CAC:C2	2.37	0.55
1:A:27:ASN:ND2	1:A:55:ARG:HG3	2.24	0.53
1:D:436:SER:HG	2:D:600:FAD:HO2A	1.57	0.53
1:A:492:ARG:HG3	1:B:344:LEU:HD11	1.92	0.52
1:D:433[B]:TRP:CD1	1:D:434[B]:GLU:N	2.79	0.51
1:A:43:PRO:HD2	1:A:46:LEU:HD22	1.93	0.51
1:D:433[B]:TRP:CE2	3:D:601:MRD:H5C2	2.46	0.50
1:C:310:CYS:HA	3:C:601:MRD:HMC2	1.93	0.50
1:D:150[A]:SER:OG	1:D:188:LEU:HD12	2.11	0.49
1:D:169:LEU:O	6:D:702:HOH:O	2.19	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:103:VAL:HG13	1:C:108:HIS:CE1	2.48	0.49
1:D:56:PHE:CZ	1:D:101[B]:ARG:HD3	2.48	0.48
1:B:192[B]:MET:HG3	1:B:236:LEU:HD12	1.96	0.48
1:C:429:VAL:O	1:C:433[B]:TRP:HB3	2.14	0.48
1:A:441:ALA:HB3	1:B:344:LEU:HD21	1.96	0.47
1:B:433[B]:TRP:CE2	3:B:601:MRD:H5C2	2.50	0.47
1:B:150:SER:HB2	1:B:234:LEU:HD23	1.97	0.47
1:B:478:ARG:HA	1:B:481:LEU:HD12	1.97	0.46
1:D:309:ASP:HB3	3:D:601:MRD:HMC1	1.97	0.45
1:C:226:SER:HA	1:C:276:SER:HA	1.99	0.45
1:B:433[B]:TRP:CD1	1:B:434[B]:GLU:N	2.85	0.44
1:A:448:LEU:HD13	1:A:481:LEU:HD22	1.98	0.44
1:D:56:PHE:CZ	1:D:101[A]:ARG:HD3	2.52	0.44
1:A:103:VAL:HG13	1:A:108:HIS:CE1	2.53	0.44
1:B:422[B]:ARG:NE	6:B:710:HOH:O	2.48	0.44
1:A:27:ASN:HD22	1:A:55:ARG:HG3	1.83	0.44
1:B:241:GLU:HG3	1:B:292:PRO:HB2	2.00	0.44
1:B:150:SER:OG	1:B:188:LEU:HD12	2.19	0.43
1:D:61:GLU:H	1:D:61:GLU:CD	2.21	0.43
1:A:433[B]:TRP:CD1	1:A:434[B]:GLU:N	2.87	0.43
1:D:355:ASP:CG	1:D:523:ARG:HH21	2.22	0.43
1:A:150:SER:OG	1:A:188:LEU:HD12	2.19	0.42
1:D:56:PHE:CE2	1:D:101[A]:ARG:HD3	2.54	0.42
1:C:150:SER:OG	1:C:188:LEU:HD12	2.20	0.41
1:B:521:GLU:CD	1:B:539:HIS:HE2	2.23	0.41
1:B:150:SER:HB2	1:B:234:LEU:CD2	2.51	0.41
1:D:422[A]:ARG:NH2	6:D:708:HOH:O	2.49	0.41
1:D:465:GLN:HB2	1:D:505:ALA:HB1	2.02	0.41
1:A:429:VAL:O	1:A:433[B]:TRP:HB3	2.20	0.41
4:B:602:MPD:H12	4:B:602:MPD:H4	1.88	0.41
1:A:222:LYS:HB3	6:A:704:HOH:O	2.21	0.40
1:B:76:LEU:HB2	1:B:265:LEU:HG	2.02	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	545/573 (95%)	531 (97%)	13 (2%)	1 (0%)	51	50
1	B	548/573 (96%)	536 (98%)	11 (2%)	1 (0%)	51	50
1	C	545/573 (95%)	533 (98%)	11 (2%)	1 (0%)	51	50
1	D	548/573 (96%)	535 (98%)	11 (2%)	2 (0%)	38	32
All	All	2186/2292 (95%)	2135 (98%)	46 (2%)	5 (0%)	51	50

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	435	GLY
1	B	435	GLY
1	C	435	GLY
1	D	435	GLY
1	D	540	ASN

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	416/446 (93%)	408 (98%)	8 (2%)	62	66
1	B	411/446 (92%)	403 (98%)	8 (2%)	62	66
1	C	412/446 (92%)	404 (98%)	8 (2%)	62	66
1	D	416/446 (93%)	408 (98%)	8 (2%)	62	66
All	All	1655/1784 (93%)	1623 (98%)	32 (2%)	66	66

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	365	ARG

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Mol	Chain	Res	Type
1	A	403	TYR
1	A	433[A]	TRP
1	A	433[B]	TRP
1	A	443	ASP
1	A	469	ARG
1	A	529	ARG
1	A	538	ARG
1	B	337	LYS
1	B	365	ARG
1	B	403	TYR
1	B	433[A]	TRP
1	B	433[B]	TRP
1	B	443	ASP
1	B	449	SER
1	B	529	ARG
1	C	49	GLU
1	C	365	ARG
1	C	377	ARG
1	C	403	TYR
1	C	433[A]	TRP
1	C	433[B]	TRP
1	C	529	ARG
1	C	538	ARG
1	D	63	GLN
1	D	192[A]	MET
1	D	192[B]	MET
1	D	365	ARG
1	D	443	ASP
1	D	449	SER
1	D	529	ARG
1	D	538	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	204	ASN
1	C	52	GLN
1	D	539	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 ⓘ

19 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	600	-	51,58,58	1.04	4 (7%)	54,89,89	2.21	5 (9%)
3	MRD	A	601	-	7,7,7	0.34	0	9,10,10	0.30	0
4	MPD	A	602	-	7,7,7	0.24	0	9,10,10	0.17	0
5	CAC	A	603	-	0,4,4	0.00	-	0,6,6	0.00	-
2	FAD	B	600	-	51,58,58	1.14	5 (9%)	54,89,89	2.20	5 (9%)
3	MRD	B	601	-	7,7,7	0.30	0	9,10,10	0.36	0
4	MPD	B	602	-	7,7,7	0.25	0	9,10,10	0.17	0
5	CAC	B	603	-	0,4,4	0.00	-	0,6,6	0.00	-
5	CAC	B	604	-	0,4,4	0.00	-	0,6,6	0.00	-
2	FAD	C	600	-	51,58,58	1.05	4 (7%)	54,89,89	2.21	5 (9%)
3	MRD	C	601	-	7,7,7	0.35	0	9,10,10	0.33	0
4	MPD	C	602	-	7,7,7	0.27	0	9,10,10	0.26	0
5	CAC	C	603	-	0,4,4	0.00	-	0,6,6	0.00	-
5	CAC	C	604	-	0,4,4	0.00	-	0,6,6	0.00	-
2	FAD	D	600	-	51,58,58	1.21	5 (9%)	54,89,89	2.25	5 (9%)
3	MRD	D	601	-	7,7,7	0.32	0	9,10,10	0.34	0
4	MPD	D	602	-	7,7,7	0.28	0	9,10,10	0.37	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	CAC	D	603	-	0,3,4	0.00	-	0,3,6	0.00	-
5	CAC	D	604	-	0,4,4	0.00	-	0,6,6	0.00	-

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	FAD	A	600	-	-	0/28/50/50	0/6/6/6
3	MRD	A	601	-	-	0/5/5/5	0/0/0/0
4	MPD	A	602	-	-	0/5/5/5	0/0/0/0
5	CAC	A	603	-	-	0/0/0/0	0/0/0/0
2	FAD	B	600	-	-	0/28/50/50	0/6/6/6
3	MRD	B	601	-	-	0/5/5/5	0/0/0/0
4	MPD	B	602	-	-	0/5/5/5	0/0/0/0
5	CAC	B	603	-	-	0/0/0/0	0/0/0/0
5	CAC	B	604	-	-	0/0/0/0	0/0/0/0
2	FAD	C	600	-	-	0/28/50/50	0/6/6/6
3	MRD	C	601	-	-	0/5/5/5	0/0/0/0
4	MPD	C	602	-	-	0/5/5/5	0/0/0/0
5	CAC	C	603	-	-	0/0/0/0	0/0/0/0
5	CAC	C	604	-	-	0/0/0/0	0/0/0/0
2	FAD	D	600	-	-	0/28/50/50	0/6/6/6
3	MRD	D	601	-	-	0/5/5/5	0/0/0/0
4	MPD	D	602	-	-	0/5/5/5	0/0/0/0
5	CAC	D	603	-	-	0/0/0/0	0/0/0/0
5	CAC	D	604	-	-	0/0/0/0	0/0/0/0

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	600	FAD	C9A-N10	2.04	1.41	1.38
2	C	600	FAD	C9A-N10	2.09	1.41	1.38
2	A	600	FAD	C4X-C10	2.16	1.44	1.41
2	D	600	FAD	C4X-C10	2.40	1.45	1.41
2	B	600	FAD	C9A-N10	2.63	1.42	1.38
2	A	600	FAD	C4-C4X	2.72	1.46	1.41
2	C	600	FAD	C4X-C10	2.77	1.45	1.41
2	A	600	FAD	C5X-N5	2.87	1.39	1.35
2	B	600	FAD	C5X-N5	2.94	1.39	1.35
2	B	600	FAD	C4X-C10	2.97	1.46	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	600	FAD	C5X-N5	3.08	1.40	1.35
2	A	600	FAD	C4-N3	3.25	1.38	1.33
2	B	600	FAD	C4-N3	3.29	1.39	1.33
2	D	600	FAD	C4-N3	3.38	1.39	1.33
2	B	600	FAD	C4-C4X	3.56	1.48	1.41
2	C	600	FAD	C4-N3	3.57	1.39	1.33
2	D	600	FAD	C5X-N5	3.57	1.40	1.35
2	D	600	FAD	C4-C4X	4.67	1.50	1.41

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	600	FAD	C4X-C4-N3	-7.41	112.92	123.48
2	A	600	FAD	C4X-C4-N3	-7.15	113.30	123.48
2	B	600	FAD	C4X-C4-N3	-6.96	113.58	123.48
2	C	600	FAD	C4X-C4-N3	-6.72	113.91	123.48
2	C	600	FAD	C4X-C10-N10	-5.02	117.03	120.52
2	B	600	FAD	C4X-C10-N10	-4.96	117.08	120.52
2	D	600	FAD	C4X-C10-N10	-4.59	117.33	120.52
2	A	600	FAD	C4X-C10-N10	-4.15	117.64	120.52
2	C	600	FAD	C4-C4X-C10	-3.22	117.36	119.96
2	D	600	FAD	C4-C4X-C10	-3.22	117.36	119.96
2	A	600	FAD	C4-C4X-C10	-3.12	117.44	119.96
2	B	600	FAD	C4-C4X-C10	-3.11	117.44	119.96
2	D	600	FAD	C10-C4X-N5	3.08	124.14	120.59
2	A	600	FAD	C10-C4X-N5	3.08	124.14	120.59
2	B	600	FAD	C10-C4X-N5	3.21	124.28	120.59
2	C	600	FAD	C10-C4X-N5	3.26	124.35	120.59
2	A	600	FAD	C4-N3-C2	12.37	125.98	115.16
2	C	600	FAD	C4-N3-C2	12.39	126.00	115.16
2	B	600	FAD	C4-N3-C2	12.40	126.00	115.16
2	D	600	FAD	C4-N3-C2	12.54	126.13	115.16

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

9 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	600	FAD	2	0
2	B	600	FAD	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	601	MRD	1	0
4	B	602	MPD	1	0
3	C	601	MRD	1	0
5	C	604	CAC	1	0
2	D	600	FAD	1	0
3	D	601	MRD	2	0
5	D	604	CAC	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	540/573 (94%)	-0.56	4 (0%) 87 90	15, 27, 49, 75	0
1	B	541/573 (94%)	-0.45	7 (1%) 77 82	16, 35, 61, 83	0
1	C	541/573 (94%)	-0.63	7 (1%) 77 82	15, 27, 52, 78	0
1	D	541/573 (94%)	-0.57	4 (0%) 87 90	15, 26, 47, 82	0
All	All	2163/2292 (94%)	-0.55	22 (1%) 82 86	15, 29, 54, 83	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	468	PRO	4.0
1	D	552	SER	3.7
1	C	377	ARG	3.5
1	B	374	ALA	3.3
1	B	212	ILE	3.3
1	B	449	SER	3.1
1	B	213	GLY	3.1
1	C	450	ARG	3.0
1	A	537	ALA	2.9
1	C	449	SER	2.9
1	D	374	ALA	2.8
1	B	467	GLY	2.8
1	D	213	GLY	2.8
1	B	552	SER	2.7
1	C	12	LYS	2.7
1	A	22	PRO	2.7
1	C	214	GLY	2.4
1	A	468	PRO	2.3
1	D	468	PRO	2.3
1	C	22	PRO	2.2
1	A	213	GLY	2.1
1	C	451	ALA	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, 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	LLDF	B-factors(Å ²)	Q<0.9
3	MRD	C	601	8/8	0.93	0.18	4.29	53,55,60,66	0
5	CAC	B	603	5/5	0.96	0.14	3.77	96,97,98,99	5
4	MPD	C	602	8/8	0.92	0.18	3.32	38,48,57,61	0
5	CAC	D	604	5/5	0.88	0.22	2.98	89,91,92,93	5
3	MRD	B	601	8/8	0.92	0.18	2.58	54,56,62,62	0
4	MPD	B	602	8/8	0.92	0.16	2.48	63,68,73,77	0
3	MRD	D	601	8/8	0.90	0.19	2.47	54,64,70,74	0
5	CAC	B	604	5/5	0.95	0.23	2.32	95,96,98,100	5
3	MRD	A	601	8/8	0.90	0.14	2.26	49,57,63,65	0
5	CAC	A	603	5/5	0.95	0.13	1.65	94,98,99,99	5
5	CAC	C	604	5/5	0.94	0.17	1.52	82,82,88,90	5
5	CAC	C	603	5/5	0.96	0.12	1.11	84,84,87,88	5
4	MPD	D	602	8/8	0.94	0.12	1.08	39,48,57,58	0
5	CAC	D	603	4/5	0.97	0.10	0.94	94,95,99,100	4
4	MPD	A	602	8/8	0.96	0.09	0.52	60,63,65,66	0
2	FAD	B	600	53/53	0.95	0.10	-0.16	27,36,45,46	0
2	FAD	D	600	53/53	0.96	0.09	-0.34	21,35,43,49	0
2	FAD	C	600	53/53	0.98	0.06	-0.80	18,25,30,44	0
2	FAD	A	600	53/53	0.98	0.06	-1.01	15,23,29,40	0

6.5 Other polymers [i](#)

There are no such residues in this entry.