



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 12:41 PM GMT

PDB ID : 3RNM
Title : The crystal structure of the subunit binding of human dihydrolipoamide transacylase (E2b) bound to human dihydrolipoamide dehydrogenase (E3)
Authors : Brautigam, C.A.; Wynn, R.M.; Chuang, J.C.; Young, B.B.; Chuang, D.T.
Deposited on : 2011-04-22
Resolution : 2.40 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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

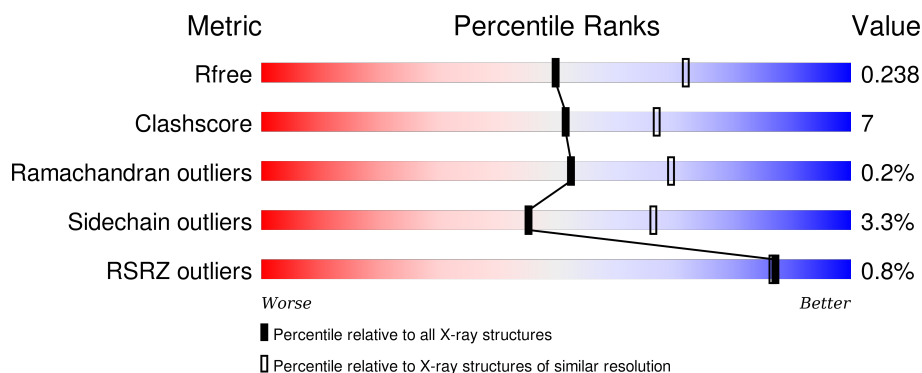
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 Å.

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




Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)

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	495	
1	B	495	
1	C	495	
1	D	495	
2	E	58	

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Mol	Chain	Length	Quality of chain
2	F	58	

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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	BME	B	500	-	-	-	X
3	BME	C	500	-	-	-	X
3	BME	D	500	-	-	-	X
5	NHE	C	475	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 15358 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 Dihydrolipoyl dehydrogenase, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	472	Total	C	N	O	S	0	0	0
			3507	2210	607	671	19			
1	B	468	Total	C	N	O	S	0	0	0
			3483	2197	602	665	19			
1	C	472	Total	C	N	O	S	0	0	0
			3507	2210	607	671	19			
1	D	468	Total	C	N	O	S	0	0	0
			3483	2197	602	665	19			

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-20	MET	-	EXPRESSION TAG	UNP P09622
A	-19	GLY	-	EXPRESSION TAG	UNP P09622
A	-18	GLY	-	EXPRESSION TAG	UNP P09622
A	-17	SER	-	EXPRESSION TAG	UNP P09622
A	-16	HIS	-	EXPRESSION TAG	UNP P09622
A	-15	HIS	-	EXPRESSION TAG	UNP P09622
A	-14	HIS	-	EXPRESSION TAG	UNP P09622
A	-13	HIS	-	EXPRESSION TAG	UNP P09622
A	-12	HIS	-	EXPRESSION TAG	UNP P09622
A	-11	HIS	-	EXPRESSION TAG	UNP P09622
A	-10	GLY	-	EXPRESSION TAG	UNP P09622
A	-9	MET	-	EXPRESSION TAG	UNP P09622
A	-8	ALA	-	EXPRESSION TAG	UNP P09622
A	-7	SER	-	EXPRESSION TAG	UNP P09622
A	-6	LEU	-	EXPRESSION TAG	UNP P09622
A	-5	GLU	-	EXPRESSION TAG	UNP P09622
A	-4	ASN	-	EXPRESSION TAG	UNP P09622
A	-3	LEU	-	EXPRESSION TAG	UNP P09622
A	-2	TYR	-	EXPRESSION TAG	UNP P09622
A	-1	PHE	-	EXPRESSION TAG	UNP P09622
A	0	GLN	-	EXPRESSION TAG	UNP P09622

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-20	MET	-	EXPRESSION TAG	UNP P09622
B	-19	GLY	-	EXPRESSION TAG	UNP P09622
B	-18	GLY	-	EXPRESSION TAG	UNP P09622
B	-17	SER	-	EXPRESSION TAG	UNP P09622
B	-16	HIS	-	EXPRESSION TAG	UNP P09622
B	-15	HIS	-	EXPRESSION TAG	UNP P09622
B	-14	HIS	-	EXPRESSION TAG	UNP P09622
B	-13	HIS	-	EXPRESSION TAG	UNP P09622
B	-12	HIS	-	EXPRESSION TAG	UNP P09622
B	-11	HIS	-	EXPRESSION TAG	UNP P09622
B	-10	GLY	-	EXPRESSION TAG	UNP P09622
B	-9	MET	-	EXPRESSION TAG	UNP P09622
B	-8	ALA	-	EXPRESSION TAG	UNP P09622
B	-7	SER	-	EXPRESSION TAG	UNP P09622
B	-6	LEU	-	EXPRESSION TAG	UNP P09622
B	-5	GLU	-	EXPRESSION TAG	UNP P09622
B	-4	ASN	-	EXPRESSION TAG	UNP P09622
B	-3	LEU	-	EXPRESSION TAG	UNP P09622
B	-2	TYR	-	EXPRESSION TAG	UNP P09622
B	-1	PHE	-	EXPRESSION TAG	UNP P09622
B	0	GLN	-	EXPRESSION TAG	UNP P09622
C	-20	MET	-	EXPRESSION TAG	UNP P09622
C	-19	GLY	-	EXPRESSION TAG	UNP P09622
C	-18	GLY	-	EXPRESSION TAG	UNP P09622
C	-17	SER	-	EXPRESSION TAG	UNP P09622
C	-16	HIS	-	EXPRESSION TAG	UNP P09622
C	-15	HIS	-	EXPRESSION TAG	UNP P09622
C	-14	HIS	-	EXPRESSION TAG	UNP P09622
C	-13	HIS	-	EXPRESSION TAG	UNP P09622
C	-12	HIS	-	EXPRESSION TAG	UNP P09622
C	-11	HIS	-	EXPRESSION TAG	UNP P09622
C	-10	GLY	-	EXPRESSION TAG	UNP P09622
C	-9	MET	-	EXPRESSION TAG	UNP P09622
C	-8	ALA	-	EXPRESSION TAG	UNP P09622
C	-7	SER	-	EXPRESSION TAG	UNP P09622
C	-6	LEU	-	EXPRESSION TAG	UNP P09622
C	-5	GLU	-	EXPRESSION TAG	UNP P09622
C	-4	ASN	-	EXPRESSION TAG	UNP P09622
C	-3	LEU	-	EXPRESSION TAG	UNP P09622
C	-2	TYR	-	EXPRESSION TAG	UNP P09622
C	-1	PHE	-	EXPRESSION TAG	UNP P09622
C	0	GLN	-	EXPRESSION TAG	UNP P09622

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-20	MET	-	EXPRESSION TAG	UNP P09622
D	-19	GLY	-	EXPRESSION TAG	UNP P09622
D	-18	GLY	-	EXPRESSION TAG	UNP P09622
D	-17	SER	-	EXPRESSION TAG	UNP P09622
D	-16	HIS	-	EXPRESSION TAG	UNP P09622
D	-15	HIS	-	EXPRESSION TAG	UNP P09622
D	-14	HIS	-	EXPRESSION TAG	UNP P09622
D	-13	HIS	-	EXPRESSION TAG	UNP P09622
D	-12	HIS	-	EXPRESSION TAG	UNP P09622
D	-11	HIS	-	EXPRESSION TAG	UNP P09622
D	-10	GLY	-	EXPRESSION TAG	UNP P09622
D	-9	MET	-	EXPRESSION TAG	UNP P09622
D	-8	ALA	-	EXPRESSION TAG	UNP P09622
D	-7	SER	-	EXPRESSION TAG	UNP P09622
D	-6	LEU	-	EXPRESSION TAG	UNP P09622
D	-5	GLU	-	EXPRESSION TAG	UNP P09622
D	-4	ASN	-	EXPRESSION TAG	UNP P09622
D	-3	LEU	-	EXPRESSION TAG	UNP P09622
D	-2	TYR	-	EXPRESSION TAG	UNP P09622
D	-1	PHE	-	EXPRESSION TAG	UNP P09622
D	0	GLN	-	EXPRESSION TAG	UNP P09622

- Molecule 2 is a protein called Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	51	Total	C	N	O	S	0	1	0
			419	259	82	77	1			
2	F	43	Total	C	N	O	S	0	0	0
			332	208	58	65	1			

There are 20 discrepancies between the modelled and reference sequences:

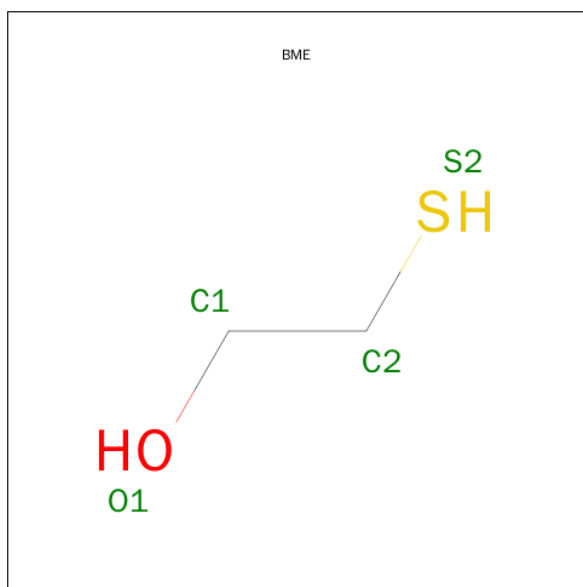
Chain	Residue	Modelled	Actual	Comment	Reference
E	103	GLY	-	EXPRESSION TAG	UNP P11182
E	118	ASN	ARG	ENGINEERED MUTATION	UNP P11182
E	153	LEU	-	EXPRESSION TAG	UNP P11182
E	154	GLU	-	EXPRESSION TAG	UNP P11182
E	155	HIS	-	EXPRESSION TAG	UNP P11182
E	156	HIS	-	EXPRESSION TAG	UNP P11182
E	157	HIS	-	EXPRESSION TAG	UNP P11182
E	158	HIS	-	EXPRESSION TAG	UNP P11182

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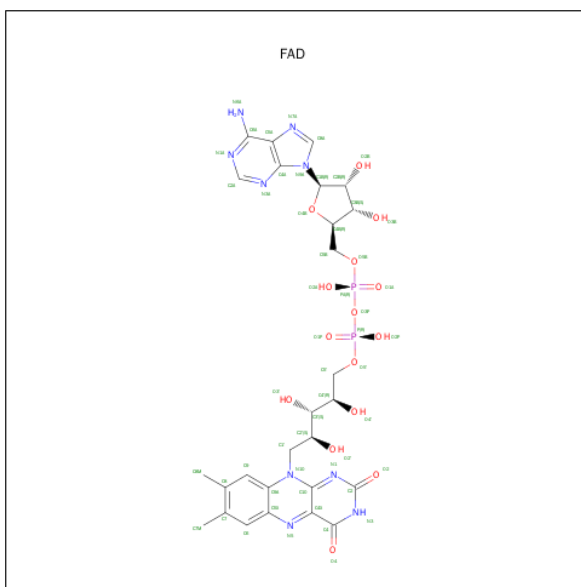
Chain	Residue	Modelled	Actual	Comment	Reference
E	159	HIS	-	EXPRESSION TAG	UNP P11182
E	160	HIS	-	EXPRESSION TAG	UNP P11182
F	103	GLY	-	EXPRESSION TAG	UNP P11182
F	118	ASN	ARG	ENGINEERED MUTATION	UNP P11182
F	153	LEU	-	EXPRESSION TAG	UNP P11182
F	154	GLU	-	EXPRESSION TAG	UNP P11182
F	155	HIS	-	EXPRESSION TAG	UNP P11182
F	156	HIS	-	EXPRESSION TAG	UNP P11182
F	157	HIS	-	EXPRESSION TAG	UNP P11182
F	158	HIS	-	EXPRESSION TAG	UNP P11182
F	159	HIS	-	EXPRESSION TAG	UNP P11182
F	160	HIS	-	EXPRESSION TAG	UNP P11182

- Molecule 3 is BETA-MERCAPTOETHANOL (three-letter code: BME) (formula: C_2H_6OS).



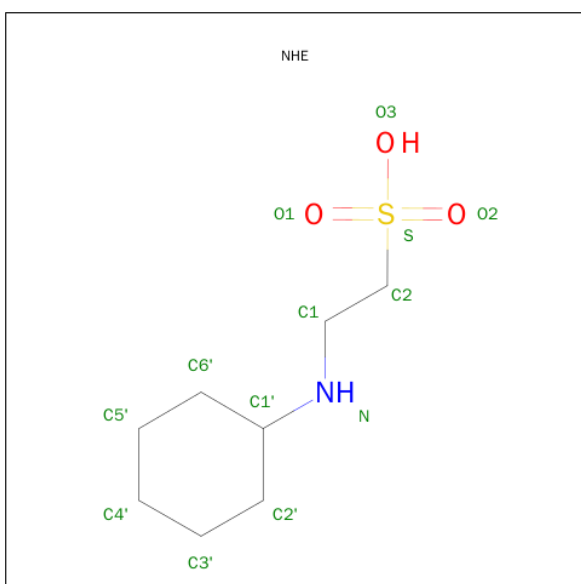
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	S	0	0
			4	2	1	1		
3	B	1	Total	C	O	S	0	0
			4	2	1	1		
3	C	1	Total	C	O	S	0	0
			4	2	1	1		
3	D	1	Total	C	O	S	0	0
			4	2	1	1		

- Molecule 4 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



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

- Molecule 5 is 2-[N-CYCLOHEXYLAMINO]ETHANE SULFONIC ACID (three-letter code: NHE) (formula: $C_8H_{17}NO_3S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	S	0	0
			13	8	1	3	1		
5	B	1	Total	C	N	O	S	0	0
			13	8	1	3	1		
5	C	1	Total	C	N	O	S	0	0
			13	8	1	3	1		
5	D	1	Total	C	N	O	S	0	0
			13	8	1	3	1		

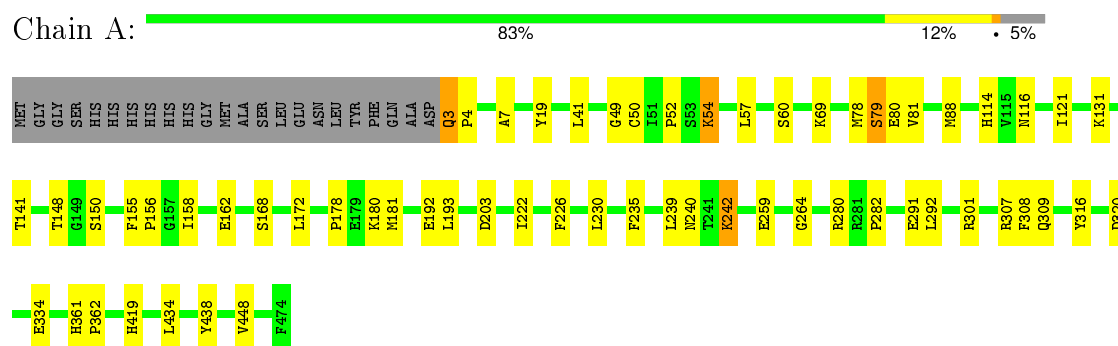
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	101	Total	O	0	0
			101	101		
6	B	34	Total	O	0	0
			34	34		
6	C	116	Total	O	0	0
			116	116		
6	D	88	Total	O	0	0
			88	88		
6	E	6	Total	O	0	0
			6	6		
6	F	2	Total	O	0	0
			2	2		

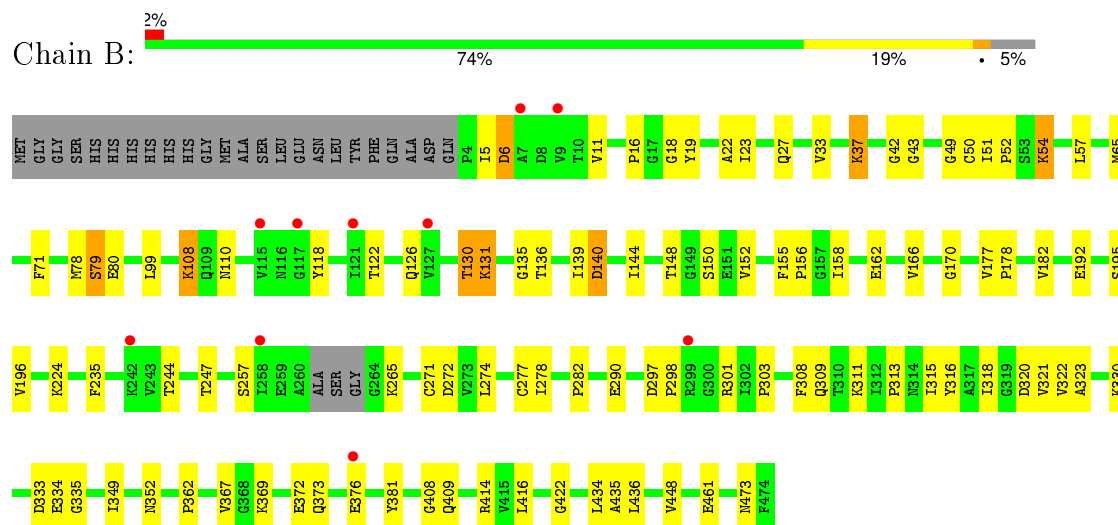
3 Residue-property plots

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

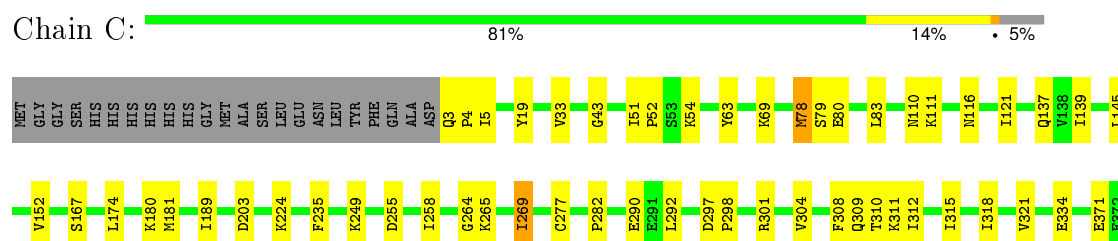
- Molecule 1: Dihydrolipoyl dehydrogenase, mitochondrial

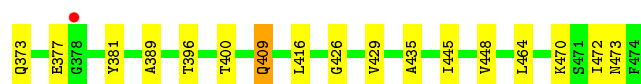


- Molecule 1: Dihydrolipoyl dehydrogenase, mitochondrial



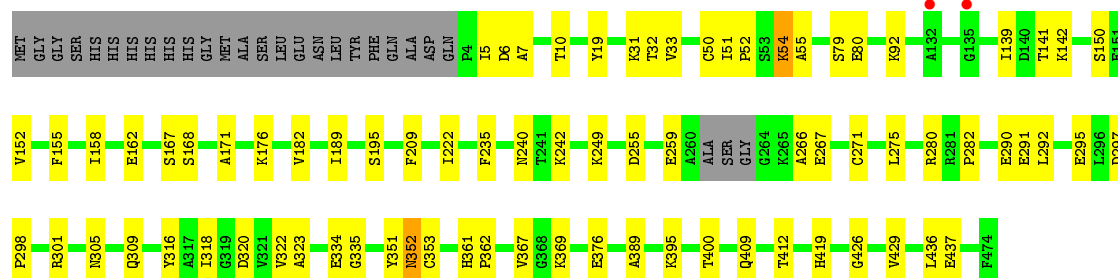
- Molecule 1: Dihydrolipoyl dehydrogenase, mitochondrial





- Molecule 1: Dihydrolipoyl dehydrogenase, mitochondrial

Chain D: 79% 16% 5%



- Molecule 2: Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial

Chain E: 81% 5% 12%



- Molecule 2: Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial

Chain F: 3% 60% 12% 26%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	84.14Å 112.31Å 122.55Å 90.00° 91.40° 90.00°	Depositor
Resolution (Å)	44.87 – 2.40 44.87 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.3 (44.87-2.40) 99.3 (44.87-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.31 (at 2.39Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7_650)	Depositor
R, R_{free}	0.181 , 0.239 0.180 , 0.238	Depositor DCC
R_{free} test set	4446 reflections (5.28%)	DCC
Wilson B-factor (Å ²)	39.5	Xtriage
Anisotropy	0.499	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 41.5	EDS
Estimated twinning fraction	0.022 for h,-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 88659 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	15358	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.49% 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, 0.375 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: NHE, FAD, BME

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	0/3562	0.56	0/4810
1	B	0.36	0/3537	0.52	0/4774
1	C	0.43	0/3562	0.57	0/4810
1	D	0.41	0/3537	0.55	0/4774
2	E	0.33	0/426	0.49	0/573
2	F	0.28	0/333	0.43	0/447
All	All	0.40	0/14957	0.55	0/20188

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	3507	0	3561	44	0
1	B	3483	0	3540	69	0
1	C	3507	0	3561	45	0
1	D	3483	0	3540	48	0
2	E	419	0	418	3	0
2	F	332	0	351	6	0
3	A	4	0	5	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	4	0	5	1	0
3	C	4	0	5	2	0
3	D	4	0	5	3	0
4	A	53	0	31	1	0
4	B	53	0	31	5	0
4	C	53	0	31	1	0
4	D	53	0	31	1	0
5	A	13	0	16	0	0
5	B	13	0	16	0	0
5	C	13	0	16	0	0
5	D	13	0	17	0	0
6	A	101	0	0	1	0
6	B	34	0	0	0	0
6	C	116	0	0	1	0
6	D	88	0	0	1	0
6	E	6	0	0	0	0
6	F	2	0	0	0	0
All	All	15358	0	15180	204	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 7.

All (204) 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)
2:F:125:ILE:HD11	2:F:148:LEU:HG	1.69	0.74
1:A:3:GLN:N	1:A:4:PRO:HD3	2.06	0.69
1:A:155:PHE:CD1	1:A:158:ILE:HD12	2.28	0.69
1:B:322:VAL:HG12	1:B:323:ALA:N	2.07	0.68
1:B:362:PRO:HB2	1:B:422:GLY:HA2	1.76	0.68
1:B:6:ASP:HB2	1:B:140:ASP:O	1.95	0.67
1:A:3:GLN:HE21	1:A:3:GLN:N	1.91	0.67
1:D:353:CYS:HB3	6:D:535:HOH:O	1.93	0.67
1:A:79:SER:HB3	1:B:79:SER:HB2	1.77	0.66
1:D:155:PHE:CD1	1:D:158:ILE:HD12	2.32	0.65
1:C:264:GLY:O	1:C:265:LYS:HB2	1.94	0.65
1:B:308:PHE:CZ	1:B:334:GLU:HG2	2.32	0.65
1:C:3:GLN:N	1:C:4:PRO:CD	2.60	0.64
1:C:33:VAL:HG11	1:C:139:ILE:HD13	1.79	0.64
1:A:81:VAL:HG22	1:B:78:MET:HG2	1.80	0.62
1:B:322:VAL:CG1	1:B:323:ALA:N	2.62	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:182:VAL:HG23	1:B:271:CYS:HB3	1.82	0.62
1:B:155:PHE:HD2	1:B:278:ILE:HG21	1.63	0.61
1:B:130:THR:HG23	1:B:136:THR:HG22	1.82	0.61
1:B:162:GLU:HA	1:B:166:VAL:HG12	1.81	0.61
1:B:192:GLU:O	1:B:196:VAL:HG23	2.01	0.61
1:A:280:ARG:HG3	3:A:500:BME:H11	1.82	0.61
2:F:112:ALA:HB2	2:F:139:ILE:CG2	2.31	0.61
2:F:125:ILE:HD13	2:F:147:TYR:HD2	1.66	0.60
1:D:7:ALA:O	1:D:141:THR:HA	2.02	0.59
1:D:352:ASN:OD1	1:D:369:LYS:HE3	2.02	0.59
1:B:369:LYS:HA	1:B:373:GLN:OE1	2.02	0.58
1:C:121:ILE:HG21	1:C:292:LEU:HD11	1.83	0.58
1:B:155:PHE:HD1	1:B:158:ILE:HG13	1.69	0.58
1:D:280:ARG:HG3	3:D:500:BME:H11	1.84	0.58
1:B:330:LYS:HE2	1:B:334:GLU:OE2	2.03	0.58
1:B:282:PRO:HB3	1:B:321:VAL:HA	1.86	0.58
1:D:33:VAL:HG11	1:D:139:ILE:HG21	1.86	0.58
2:E:125:ILE:HD11	2:E:148:LEU:HD13	1.84	0.58
1:C:464:LEU:HG	1:C:470:LYS:O	2.03	0.57
1:B:297:ASP:HB2	1:B:298:PRO:HD2	1.85	0.57
1:B:155:PHE:CD2	1:B:278:ILE:HG21	2.39	0.57
1:A:49:GLY:O	1:A:52:PRO:HD2	2.06	0.56
1:D:171:ALA:HB2	1:D:275:LEU:HD13	1.88	0.56
1:B:5:ILE:O	1:B:139:ILE:HA	2.05	0.56
1:B:318:ILE:HD13	1:B:335:GLY:HA2	1.88	0.55
1:D:52:PRO:HB3	1:D:92:LYS:HD2	1.88	0.55
1:A:80:GLU:HG2	1:B:79:SER:HB2	1.87	0.55
1:D:280:ARG:CG	3:D:500:BME:H11	2.37	0.55
1:D:367:VAL:HG13	1:D:436:LEU:HD11	1.88	0.55
2:F:111:LEU:O	2:F:139:ILE:HG22	2.08	0.54
3:C:500:BME:H21	6:C:503:HOH:O	2.07	0.54
1:D:182:VAL:HG23	1:D:271:CYS:HB3	1.90	0.53
1:C:409:GLN:HG2	1:C:416:LEU:HD11	1.91	0.53
1:A:434:LEU:HD21	1:B:435:ALA:HB2	1.90	0.53
1:C:78:MET:HE2	1:C:78:MET:N	2.23	0.53
1:A:79:SER:HB3	1:B:79:SER:CB	2.38	0.53
1:B:322:VAL:CG1	1:B:323:ALA:H	2.21	0.53
1:C:3:GLN:N	1:C:4:PRO:HD3	2.24	0.53
1:C:79:SER:OG	1:D:79:SER:HB2	2.09	0.52
1:D:297:ASP:HB2	1:D:298:PRO:CD	2.39	0.52
1:B:297:ASP:HB2	1:B:298:PRO:CD	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3:GLN:N	1:A:4:PRO:CD	2.73	0.52
1:B:290:GLU:CD	1:B:290:GLU:H	2.13	0.52
1:B:409:GLN:HB2	1:B:416:LEU:HD11	1.92	0.52
1:A:180:LYS:HD2	1:A:203:ASP:O	2.09	0.52
1:D:10:THR:HA	1:D:33:VAL:HG13	1.92	0.52
1:A:309:GLN:HG2	1:A:316:TYR:CE2	2.45	0.52
1:D:209:PHE:O	1:D:240:ASN:HA	2.09	0.51
1:C:152:VAL:HG21	1:C:167:SER:HB2	1.91	0.51
1:C:80:GLU:HB2	1:D:79:SER:OG	2.09	0.51
1:B:152:VAL:HG22	3:B:500:BME:H11	1.91	0.51
1:D:297:ASP:HB2	1:D:298:PRO:HD2	1.93	0.51
1:C:371:GLU:HG2	1:C:381:TYR:OH	2.10	0.51
1:D:305:ASN:HD21	1:D:309:GLN:CG	2.24	0.51
1:A:60:SER:N	1:A:88:MET:HE3	2.26	0.50
1:A:434:LEU:HD13	1:B:448:VAL:HG21	1.95	0.49
1:D:54:LYS:N	1:D:54:LYS:HE3	2.28	0.49
1:C:249:LYS:HD2	1:C:255:ASP:OD2	2.13	0.49
1:A:121:ILE:HG21	1:A:292:LEU:HD11	1.94	0.49
1:C:290:GLU:CD	1:C:290:GLU:H	2.16	0.49
1:C:78:MET:HE3	1:C:78:MET:HB2	1.71	0.49
1:D:290:GLU:C	1:D:292:LEU:H	2.15	0.48
1:A:307:ARG:HG3	6:A:564:HOH:O	2.13	0.48
1:A:259:GLU:HB2	1:A:264:GLY:O	2.13	0.48
1:C:145:LEU:HD11	1:C:318:ILE:HG23	1.95	0.48
1:C:396:THR:HG23	1:D:55:ALA:HB2	1.96	0.48
1:A:282:PRO:HG2	1:A:301:ARG:HG3	1.94	0.48
1:C:249:LYS:HD2	1:C:255:ASP:CG	2.33	0.47
1:B:372:GLU:CD	1:B:372:GLU:H	2.17	0.47
1:C:110:ASN:O	1:C:111:LYS:HB2	2.14	0.47
1:A:7:ALA:O	1:A:141:THR:HA	2.14	0.47
1:C:426:GLY:O	1:C:429:VAL:HG12	2.14	0.47
1:A:307:ARG:HB2	1:A:307:ARG:NH1	2.29	0.47
1:C:304:VAL:HA	1:C:309:GLN:O	2.15	0.47
1:B:166:VAL:HB	1:B:170:GLY:HA3	1.97	0.47
1:D:168:SER:HB3	3:D:500:BME:S2	2.55	0.47
1:B:16:PRO:HD3	1:B:42:GLY:O	2.14	0.47
1:B:57:LEU:HD11	1:B:192:GLU:HB3	1.97	0.47
1:A:361:HIS:HA	1:A:362:PRO:C	2.36	0.47
1:C:310:THR:HG23	1:C:315:ILE:O	2.14	0.47
1:A:168:SER:HB3	3:A:500:BME:S2	2.55	0.47
1:C:472:ILE:HG22	1:C:473:ASN:ND2	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:244:THR:HB	1:B:257:SER:HB2	1.97	0.46
1:B:65:MET:HE2	1:B:71:PHE:HE1	1.80	0.46
1:C:435:ALA:HB1	1:C:445:ILE:HD11	1.97	0.46
1:B:461:GLU:OE2	1:B:473:ASN:HB2	2.16	0.46
1:D:409:GLN:HG3	1:D:412:THR:H	1.81	0.46
1:D:176:LYS:HB3	1:D:176:LYS:NZ	2.30	0.46
1:D:259:GLU:HG2	1:D:266:ALA:HB2	1.96	0.46
1:D:282:PRO:HG2	1:D:301:ARG:HG3	1.97	0.46
1:A:178:PRO:HG2	1:A:181:MET:CE	2.44	0.46
1:A:308:PHE:CZ	1:A:334:GLU:HG2	2.51	0.46
2:F:112:ALA:HB2	2:F:139:ILE:HG22	1.97	0.46
1:A:162:GLU:HA	1:A:162:GLU:OE1	2.16	0.46
1:D:150:SER:HB3	1:D:320:ASP:HB3	1.97	0.46
1:D:139:ILE:N	1:D:139:ILE:HD12	2.30	0.45
1:B:23:ILE:O	1:B:27:GLN:HG3	2.16	0.45
1:A:148:THR:O	4:A:480:FAD:H8A	2.16	0.45
1:C:43:GLY:HA2	4:C:480:FAD:O3B	2.16	0.45
1:B:301:ARG:HD2	1:B:323:ALA:HA	1.99	0.45
1:B:309:GLN:HB3	1:B:316:TYR:CE2	2.52	0.45
1:B:11:VAL:HG11	1:B:22:ALA:HB2	1.97	0.45
2:F:121:MET:CE	2:F:121:MET:HA	2.47	0.45
1:A:150:SER:HB3	1:A:320:ASP:HB3	1.98	0.45
1:D:309:GLN:HB3	1:D:316:TYR:CE2	2.52	0.44
1:B:49:GLY:HA2	4:B:480:FAD:C7	2.47	0.44
1:B:54:LYS:HE3	1:B:54:LYS:N	2.33	0.44
1:C:180:LYS:HG3	1:C:203:ASP:HB3	1.99	0.44
1:A:226:PHE:CZ	1:A:230:LEU:HD11	2.53	0.44
1:D:389:ALA:HA	1:D:400:THR:HB	1.99	0.44
1:A:57:LEU:HD11	1:A:192:GLU:HB3	1.98	0.44
1:C:292:LEU:HB3	1:C:312:ILE:CD1	2.48	0.44
1:A:222:ILE:HG13	1:A:419:HIS:HB3	2.00	0.44
1:B:349:ILE:O	1:B:349:ILE:HG23	2.17	0.44
1:A:116:ASN:O	1:A:131:LYS:HG2	2.17	0.44
1:B:362:PRO:CB	1:B:422:GLY:HA2	2.44	0.44
1:D:5:ILE:O	1:D:139:ILE:HA	2.17	0.44
1:A:280:ARG:CG	3:A:500:BME:H11	2.46	0.43
1:B:23:ILE:HG23	1:B:110:ASN:ND2	2.33	0.43
1:B:311:LYS:O	1:B:313:PRO:HD3	2.18	0.43
1:B:367:VAL:HG13	1:B:436:LEU:HD11	2.00	0.43
1:C:78:MET:HA	1:D:80:GLU:O	2.17	0.43
1:A:41:LEU:HD21	1:A:114:HIS:CE1	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:189:ILE:HD13	4:D:480:FAD:C7	2.48	0.43
1:C:311:LYS:HB3	1:C:311:LYS:HE2	1.64	0.43
1:B:155:PHE:CD1	1:B:158:ILE:HG13	2.52	0.43
1:D:334:GLU:OE2	1:D:351:TYR:OH	2.32	0.43
1:B:37:LYS:HD3	4:B:480:FAD:C4A	2.49	0.43
1:B:148:THR:O	4:B:480:FAD:H8A	2.19	0.43
1:D:322:VAL:CG1	1:D:323:ALA:N	2.81	0.43
1:B:37:LYS:HG2	4:B:480:FAD:N3A	2.34	0.43
1:A:3:GLN:NE2	1:A:3:GLN:N	2.65	0.43
1:B:162:GLU:CA	1:B:166:VAL:HG12	2.48	0.43
1:B:11:VAL:HG21	1:B:18:GLY:HA2	2.00	0.43
1:C:258:ILE:HD13	1:C:269:ILE:HD13	2.00	0.43
1:A:155:PHE:HA	1:A:156:PRO:HD3	1.93	0.42
1:B:43:GLY:HA2	4:B:480:FAD:O3B	2.19	0.42
1:A:239:LEU:O	1:A:240:ASN:C	2.56	0.42
1:B:381:TYR:HB2	1:B:408:GLY:O	2.20	0.42
1:B:150:SER:HB3	1:B:320:ASP:HB3	2.01	0.42
1:B:51:ILE:HB	1:B:52:PRO:HD3	2.01	0.42
1:B:376:GLU:O	1:B:376:GLU:HG3	2.19	0.42
1:A:448:VAL:HG21	1:B:434:LEU:CD1	2.49	0.42
1:A:178:PRO:HG2	1:A:181:MET:HE2	2.01	0.42
1:B:177:VAL:HA	1:B:178:PRO:HD3	1.90	0.42
1:D:361:HIS:HA	1:D:362:PRO:C	2.40	0.42
2:E:148:LEU:HD12	2:E:148:LEU:HA	1.81	0.42
1:B:122:THR:OG1	1:B:126:GLN:HG2	2.19	0.42
1:D:318:ILE:HD13	1:D:335:GLY:HA2	2.01	0.42
1:A:307:ARG:HB2	1:A:307:ARG:HH11	1.84	0.42
1:C:448:VAL:HG22	1:D:437:GLU:HG2	2.01	0.42
1:D:162:GLU:HA	1:D:162:GLU:OE1	2.19	0.42
1:D:222:ILE:HG13	1:D:419:HIS:HB3	2.02	0.42
1:B:182:VAL:O	1:B:274:LEU:HD12	2.19	0.42
1:A:50:CYS:O	1:A:54:LYS:HD2	2.20	0.42
1:D:295:GLU:HG2	1:D:295:GLU:H	1.70	0.42
1:C:63:TYR:CE1	1:C:83:LEU:HB2	2.55	0.42
1:C:174:LEU:HD11	1:C:181:MET:HE1	2.02	0.41
1:D:142:LYS:HG2	1:D:142:LYS:H	1.71	0.41
1:C:189:ILE:HG21	3:C:500:BME:H22	2.01	0.41
1:A:242:LYS:HB3	1:A:242:LYS:HE3	1.67	0.41
1:D:242:LYS:HB3	1:D:242:LYS:HE2	1.80	0.41
1:B:301:ARG:O	1:B:303:PRO:HD3	2.20	0.41
1:D:51:ILE:HB	1:D:52:PRO:HD3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:434:LEU:HD11	1:A:438:TYR:HE1	1.86	0.41
1:D:426:GLY:O	1:D:429:VAL:HG12	2.20	0.41
1:C:389:ALA:HA	1:C:400:THR:HB	2.02	0.41
1:B:362:PRO:HB2	1:B:422:GLY:CA	2.47	0.41
1:C:282:PRO:HG3	1:C:301:ARG:HG2	2.02	0.41
1:B:144:ILE:HB	1:B:315:ILE:HG12	2.02	0.41
1:C:78:MET:H	1:C:78:MET:HE2	1.85	0.41
1:C:5:ILE:HG13	1:C:137:GLN:NE2	2.36	0.41
1:C:308:PHE:CZ	1:C:334:GLU:HG2	2.55	0.41
1:C:292:LEU:HB3	1:C:312:ILE:HD11	2.03	0.41
1:C:51:ILE:HB	1:C:52:PRO:HD3	2.02	0.41
1:D:31:LYS:HD3	1:D:32:THR:N	2.36	0.40
1:B:108:LYS:HE3	1:B:108:LYS:HB2	1.80	0.40
1:C:224:LYS:HD3	1:C:224:LYS:HA	1.92	0.40
1:D:152:VAL:HG21	1:D:167:SER:HB2	2.04	0.40
1:C:297:ASP:HB2	1:C:298:PRO:CD	2.51	0.40
1:C:373:GLN:O	1:C:377:GLU:HG3	2.21	0.40
2:E:117:ARG:HG2	2:E:127:LEU:HD11	2.03	0.40
1:C:371:GLU:HG2	1:C:381:TYR:CZ	2.57	0.40
1:D:249:LYS:HE2	1:D:255:ASP:OD1	2.22	0.40
1:B:99:LEU:HD23	1:B:99:LEU:HA	1.85	0.40
1:B:131:LYS:HG3	1:B:135:GLY:O	2.20	0.40
1:B:224:LYS:HA	1:B:224:LYS:HD3	1.85	0.40
1:A:172:LEU:HD21	1:A:193:LEU:HD21	2.04	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	470/495 (95%)	445 (95%)	24 (5%)	1 (0%)	52 69

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	464/495 (94%)	430 (93%)	32 (7%)	2 (0%)	39	56
1	C	470/495 (95%)	457 (97%)	13 (3%)	0	100	100
1	D	464/495 (94%)	447 (96%)	16 (3%)	1 (0%)	52	69
2	E	50/58 (86%)	48 (96%)	2 (4%)	0	100	100
2	F	41/58 (71%)	38 (93%)	3 (7%)	0	100	100
All	All	1959/2096 (94%)	1865 (95%)	90 (5%)	4 (0%)	52	69

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	291	GLU
1	A	79	SER
1	B	131	LYS
1	B	156	PRO

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	372/390 (95%)	364 (98%)	8 (2%)	60	79
1	B	370/390 (95%)	349 (94%)	21 (6%)	25	40
1	C	372/390 (95%)	362 (97%)	10 (3%)	52	73
1	D	370/390 (95%)	360 (97%)	10 (3%)	52	73
2	E	46/50 (92%)	45 (98%)	1 (2%)	60	79
2	F	37/50 (74%)	35 (95%)	2 (5%)	27	43
All	All	1567/1660 (94%)	1515 (97%)	52 (3%)	45	66

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	GLN
1	A	19	TYR

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Mol	Chain	Res	Type
1	A	54	LYS
1	A	69	LYS
1	A	78	MET
1	A	235	PHE
1	A	242	LYS
1	A	291	GLU
1	B	6	ASP
1	B	19	TYR
1	B	33	VAL
1	B	37	LYS
1	B	50	CYS
1	B	54	LYS
1	B	79	SER
1	B	80	GLU
1	B	108	LYS
1	B	118	TYR
1	B	130	THR
1	B	140	ASP
1	B	195	SER
1	B	235	PHE
1	B	247	THR
1	B	265	LYS
1	B	272	ASP
1	B	277	CYS
1	B	333	ASP
1	B	352	ASN
1	B	414	ARG
1	C	19	TYR
1	C	54	LYS
1	C	69	LYS
1	C	78	MET
1	C	116	ASN
1	C	235	PHE
1	C	269	ILE
1	C	277	CYS
1	C	321	VAL
1	C	409	GLN
1	D	6	ASP
1	D	19	TYR
1	D	50	CYS
1	D	54	LYS
1	D	195	SER

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Mol	Chain	Res	Type
1	D	235	PHE
1	D	267	GLU
1	D	352	ASN
1	D	376	GLU
1	D	395	LYS
2	E	148	LEU
2	F	121	MET
2	F	151	GLN

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	38	ASN
1	C	116	ASN
1	C	137	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

12 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
5	NHE	A	475	-	12,13,13	1.24	1 (8%)	15,17,17	1.72	3 (20%)
4	FAD	A	480	-	48,58,58	1.20	4 (8%)	54,89,89	2.10	8 (14%)
3	BME	A	500	1	3,3,3	0.41	0	2,2,2	0.31	0
5	NHE	B	475	-	12,13,13	1.23	1 (8%)	15,17,17	1.40	2 (13%)
4	FAD	B	480	-	48,58,58	1.17	4 (8%)	54,89,89	2.14	7 (12%)
3	BME	B	500	1	3,3,3	0.37	0	2,2,2	0.48	0
5	NHE	C	475	-	12,13,13	1.29	1 (8%)	15,17,17	1.66	4 (26%)
4	FAD	C	480	-	48,58,58	1.21	5 (10%)	54,89,89	2.15	8 (14%)
3	BME	C	500	1	3,3,3	0.26	0	2,2,2	0.62	0
5	NHE	D	475	-	12,13,13	1.28	1 (8%)	15,17,17	1.68	4 (26%)
4	FAD	D	480	-	48,58,58	1.19	5 (10%)	54,89,89	1.98	7 (12%)
3	BME	D	500	1	3,3,3	0.46	0	2,2,2	0.59	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NHE	A	475	-	-	0/7/15/15	0/1/1/1
4	FAD	A	480	-	-	0/30/50/50	0/6/6/6
3	BME	A	500	1	-	0/1/1/1	0/0/0/0
5	NHE	B	475	-	-	0/7/15/15	0/1/1/1
4	FAD	B	480	-	-	0/30/50/50	0/6/6/6
3	BME	B	500	1	-	0/1/1/1	0/0/0/0
5	NHE	C	475	-	-	0/7/15/15	0/1/1/1
4	FAD	C	480	-	-	0/30/50/50	0/6/6/6
3	BME	C	500	1	-	0/1/1/1	0/0/0/0
5	NHE	D	475	-	-	0/7/15/15	0/1/1/1
4	FAD	D	480	-	-	0/30/50/50	0/6/6/6
3	BME	D	500	1	-	0/1/1/1	0/0/0/0

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	475	NHE	C1-C2	-2.35	1.36	1.50
5	A	475	NHE	C1-C2	-2.31	1.37	1.50
5	C	475	NHE	C1-C2	-2.30	1.37	1.50
5	D	475	NHE	C1-C2	-2.24	1.37	1.50
4	D	480	FAD	C5X-N5	2.05	1.38	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	480	FAD	C10-N1	2.07	1.39	1.35
4	A	480	FAD	C2A-N1A	2.25	1.38	1.33
4	C	480	FAD	C2A-N1A	2.32	1.38	1.33
4	D	480	FAD	C4-N3	2.41	1.37	1.33
4	B	480	FAD	C2A-N1A	2.47	1.38	1.33
4	C	480	FAD	C4-N3	2.50	1.37	1.33
4	B	480	FAD	C4-N3	2.55	1.37	1.33
4	A	480	FAD	C4X-N5	2.83	1.37	1.33
4	A	480	FAD	C4-N3	2.97	1.38	1.33
4	D	480	FAD	C4X-N5	2.99	1.38	1.33
4	D	480	FAD	C2A-N1A	3.00	1.39	1.33
4	B	480	FAD	C4X-N5	3.10	1.38	1.33
4	C	480	FAD	C4X-N5	3.41	1.38	1.33
4	C	480	FAD	C2A-N3A	3.56	1.38	1.32
4	B	480	FAD	C2A-N3A	3.58	1.38	1.32
4	A	480	FAD	C2A-N3A	3.64	1.38	1.32
4	D	480	FAD	C2A-N3A	3.69	1.38	1.32

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	480	FAD	N3A-C2A-N1A	-11.77	119.88	128.89
4	B	480	FAD	N3A-C2A-N1A	-11.57	120.03	128.89
4	A	480	FAD	N3A-C2A-N1A	-11.44	120.14	128.89
4	D	480	FAD	N3A-C2A-N1A	-10.64	120.75	128.89
4	B	480	FAD	C4X-C4-N3	-3.37	118.98	123.59
4	B	480	FAD	P-O3P-PA	-3.05	124.17	132.73
4	C	480	FAD	C4X-C4-N3	-3.04	119.43	123.59
4	A	480	FAD	C4X-C4-N3	-2.89	119.63	123.59
4	D	480	FAD	C4X-C4-N3	-2.83	119.72	123.59
4	A	480	FAD	C9A-C5X-N5	-2.41	118.79	122.36
4	A	480	FAD	P-O3P-PA	-2.13	126.74	132.73
4	C	480	FAD	P-O3P-PA	-2.12	126.78	132.73
4	D	480	FAD	C1B-N9A-C4A	-2.08	123.80	126.94
4	C	480	FAD	C4X-C10-N10	-2.01	119.33	120.52
4	B	480	FAD	C4A-C5A-N7A	-2.01	107.63	109.48
5	A	475	NHE	C6'-C1'-N	2.02	119.48	111.10
5	D	475	NHE	C2'-C1'-N	2.04	119.57	111.10
5	D	475	NHE	C2-C1-N	2.09	117.50	111.32
4	D	480	FAD	C2B-C1B-N9A	2.13	117.55	114.29
4	B	480	FAD	C5X-C9A-N10	2.34	119.40	117.62
5	B	475	NHE	C2-C1-N	2.35	118.25	111.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	475	NHE	O1-S-C2	2.39	108.94	106.91
4	A	480	FAD	C1'-N10-C9A	2.52	121.69	118.86
5	C	475	NHE	C2-C1-N	2.60	119.00	111.32
5	C	475	NHE	C1-C2-S	2.60	120.75	113.73
5	B	475	NHE	C1-C2-S	2.61	120.77	113.73
4	C	480	FAD	C2B-C1B-N9A	2.72	118.44	114.29
5	C	475	NHE	O2-S-C2	2.80	109.30	106.91
4	D	480	FAD	C5X-C9A-N10	2.80	119.75	117.62
4	C	480	FAD	C5X-C9A-N10	2.90	119.83	117.62
5	D	475	NHE	C1-C2-S	3.06	121.98	113.73
4	D	480	FAD	C4X-N5-C5X	3.07	120.29	116.76
4	C	480	FAD	C4X-N5-C5X	3.18	120.43	116.76
5	D	475	NHE	O1-S-C2	3.31	109.73	106.91
5	A	475	NHE	C2-C1-N	3.50	121.67	111.32
4	A	480	FAD	C4X-N5-C5X	3.54	120.83	116.76
5	A	475	NHE	O2-S-C2	3.63	110.00	106.91
4	B	480	FAD	C4X-N5-C5X	3.94	121.30	116.76
4	A	480	FAD	C5X-C9A-N10	3.98	120.64	117.62
4	A	480	FAD	C4-N3-C2	4.89	119.47	115.25
4	B	480	FAD	C4-N3-C2	6.12	120.53	115.25
4	D	480	FAD	C4-N3-C2	6.22	120.63	115.25
4	C	480	FAD	C4-N3-C2	6.59	120.94	115.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

8 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	480	FAD	1	0
3	A	500	BME	3	0
4	B	480	FAD	5	0
3	B	500	BME	1	0
4	C	480	FAD	1	0
3	C	500	BME	2	0
4	D	480	FAD	1	0
3	D	500	BME	3	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, 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	472/495 (95%)	-0.50	0 100 100	20, 39, 70, 97	0
1	B	468/495 (94%)	-0.09	10 (2%) 67 66	21, 56, 92, 114	0
1	C	472/495 (95%)	-0.52	1 (0%) 95 95	19, 36, 64, 90	0
1	D	468/495 (94%)	-0.49	2 (0%) 93 93	22, 42, 70, 101	0
2	E	51/58 (87%)	-0.29	0 100 100	35, 53, 78, 81	0
2	F	43/58 (74%)	0.38	2 (4%) 35 36	59, 75, 101, 107	0
All	All	1974/2096 (94%)	-0.38	15 (0%) 87 87	19, 43, 82, 114	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	121	ILE	3.1
2	F	153	LEU	2.8
1	B	7	ALA	2.8
1	B	376	GLU	2.7
1	B	127	VAL	2.7
1	B	117	GLY	2.6
1	D	132	ALA	2.5
2	F	146	ASN	2.3
1	D	135	GLY	2.3
1	B	115	VAL	2.2
1	B	9	VAL	2.2
1	B	299	ARG	2.1
1	B	258	ILE	2.1
1	C	378	GLY	2.1
1	B	242	LYS	2.1

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
5	NHE	C	475	13/13	0.86	0.23	5.12	63,89,148,152	0
3	BME	C	500	4/4	0.85	0.26	4.21	70,75,78,80	0
3	BME	B	500	4/4	0.78	0.22	2.83	55,74,75,110	0
3	BME	D	500	4/4	0.90	0.13	2.21	38,47,52,78	0
5	NHE	B	475	13/13	0.96	0.14	1.97	29,54,65,69	0
3	BME	A	500	4/4	0.92	0.13	1.73	34,57,62,72	0
5	NHE	A	475	13/13	0.95	0.15	1.47	55,67,77,78	0
4	FAD	C	480	53/53	0.97	0.15	0.56	18,27,36,40	0
4	FAD	A	480	53/53	0.98	0.12	0.16	16,28,40,47	0
5	NHE	D	475	13/13	0.96	0.13	-0.26	47,62,90,94	0
4	FAD	D	480	53/53	0.98	0.11	-0.30	22,32,46,52	0
4	FAD	B	480	53/53	0.94	0.14	-0.37	31,45,69,73	0

6.5 Other polymers [i](#)

There are no such residues in this entry.