Full wwPDB X-ray Structure Validation Report (i)

Jan 31, 2016 – 06:39 PM GMT

PDB ID	:	1BUC
Title	:	THREE-DIMENSIONAL STRUCTURE OF BUTYRYL-COA DEHYDROGENASE FROM MEGASPHAERA ELSDENII
Authors	:	Djordjevic, S.; Pace, C.P.; Stankovich, M.T.; Kim, J.J.P.
Deposited on	:	1994-09-06
Resolution	:	2.50 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 (i) symbol.

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

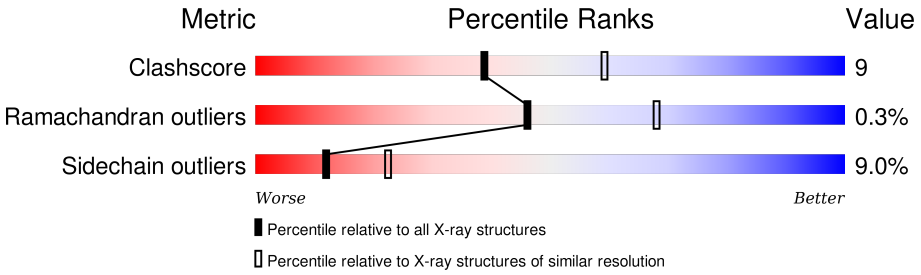
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
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 2.50 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))
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)

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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	383	74% 23% .
1	B	383	81% 17% .

2 Entry composition

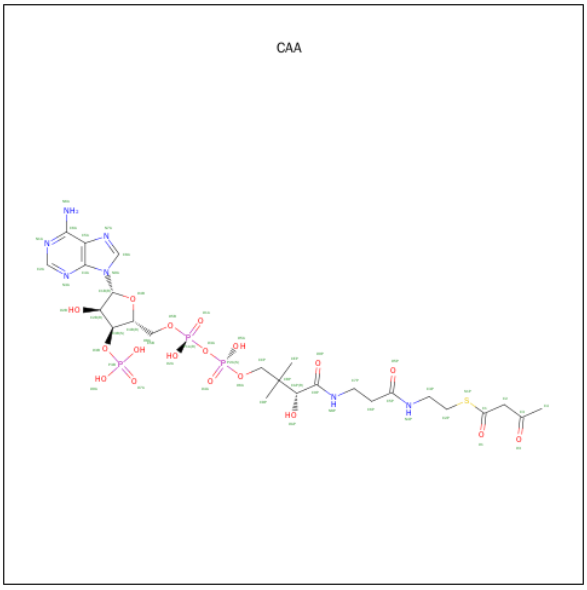
There are 3 unique types of molecules in this entry. The entry contains 6032 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 BUTYRYL-COA DEHYDROGENASE.

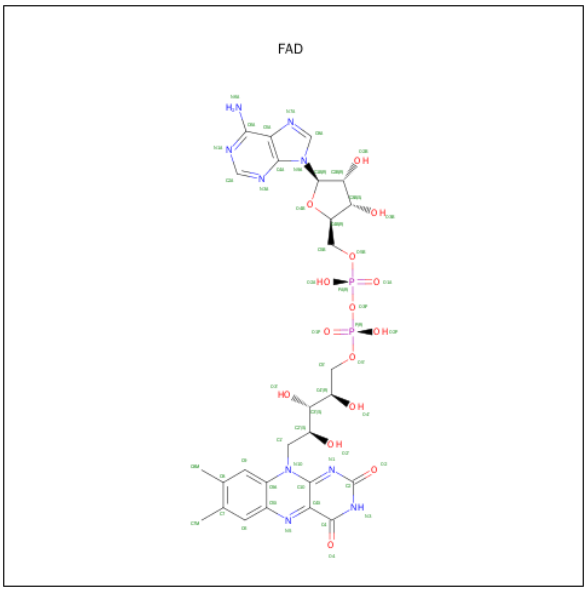
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	383	Total	C	N	O	S	0	0	0
			2909	1844	479	571	15			
1	B	383	Total	C	N	O	S	0	0	0
			2909	1844	479	571	15			

- Molecule 2 is ACETOACETYL-COENZYME A (three-letter code: CAA) (formula: $C_{25}H_{40}N_7O_{18}P_3S$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	S	0	0
			54	25	7	18	3	1		
2	B	1	Total	C	N	O	P	S	0	0
			54	25	7	18	3	1		

- Molecule 3 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



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

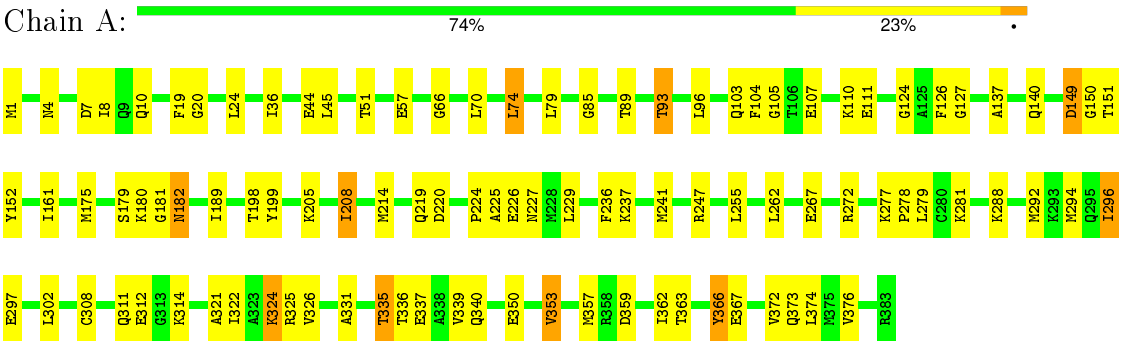
3 Residue-property plots (i)

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.

Note EDS was not executed.

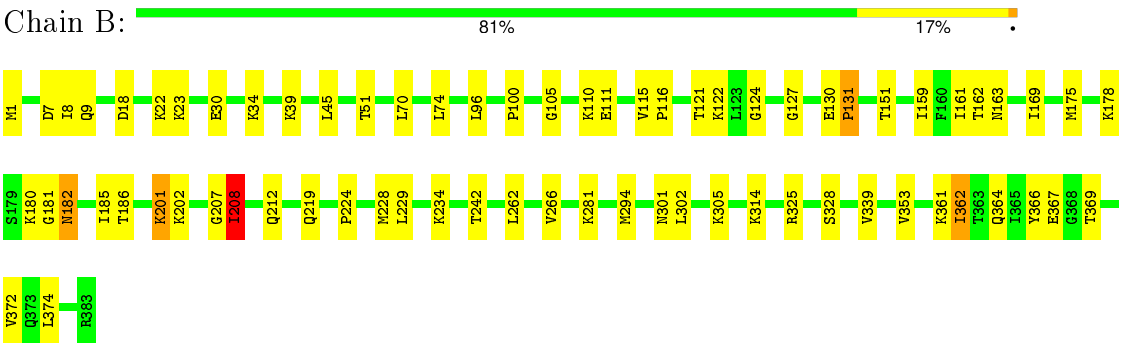
- Molecule 1: BUTYRYL-COA DEHYDROGENASE

Chain A:



- Molecule 1: BUTYRYL-COA DEHYDROGENASE

Chain B:



4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 4 2 2	Depositor
Cell constants a, b, c, α, β, γ	107.80Å 107.80Å 153.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.50	Depositor
% Data completeness (in resolution range)	80.0 (8.00-2.50)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.193 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6032	wwPDB-VP
Average B, all atoms (Å^2)	15.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CAA, 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	0.36	0/2956	0.61	1/3982 (0.0%)
1	B	0.34	0/2956	0.57	0/3982
All	All	0.35	0/5912	0.59	1/7964 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	179	SER	O-C-N	6.36	132.87	122.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2909	0	2899	63	0
1	B	2909	0	2899	48	0
2	A	54	0	36	9	0
2	B	54	0	36	7	0
3	A	53	0	31	2	0
3	B	53	0	31	0	0
All	All	6032	0	5932	108	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 9.

All (108) 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:100:PRO:HB3	1:B:242:THR:HG21	1.47	0.94
1:A:237:LYS:HE3	1:A:241:MET:SD	2.19	0.83
1:A:367:GLU:HG2	2:A:384:CAA:H2'2	1.60	0.81
1:B:186:THR:HG21	1:B:228:MET:HE2	1.63	0.79
1:A:93:THR:HG23	1:A:124:GLY:H	1.48	0.78
1:A:331:ALA:O	1:A:335:THR:HB	1.85	0.76
1:A:321:ALA:HA	1:A:373:GLN:HE21	1.53	0.74
1:A:278:PRO:HG2	1:A:281:LYS:HG3	1.69	0.73
1:A:335:THR:CG2	1:A:357:MET:HA	2.22	0.69
1:A:182:ASN:HD21	2:A:384:CAA:H51A	1.57	0.68
1:A:182:ASN:HD21	2:A:384:CAA:C5B	2.09	0.66
1:B:202:LYS:HE2	1:B:212:GLN:HG3	1.78	0.64
1:B:207:GLY:O	1:B:208:ILE:HG22	1.97	0.64
1:B:8:ILE:H	1:B:8:ILE:HD12	1.64	0.63
1:A:140:GLN:HB2	1:A:175:MET:HE1	1.82	0.62
1:A:4:ASN:HD21	1:B:314:LYS:HE2	1.66	0.61
1:A:335:THR:HG23	1:A:357:MET:HA	1.82	0.60
1:A:8:ILE:HD13	1:A:66:GLY:HA3	1.83	0.60
1:A:205:LYS:HE2	1:A:208:ILE:CG2	2.31	0.60
1:A:247:ARG:HD3	1:A:373:GLN:HE22	1.66	0.60
1:A:367:GLU:HG2	2:A:384:CAA:C2	2.31	0.60
1:B:208:ILE:O	1:B:208:ILE:HG23	2.02	0.59
1:A:127:GLY:HA2	1:A:161:ILE:HD12	1.85	0.58
1:A:224:PRO:HB2	1:A:226:GLU:OE2	2.03	0.58
1:A:339:VAL:HG22	1:A:353:VAL:HG13	1.86	0.57
1:A:182:ASN:C	1:A:182:ASN:OD1	2.43	0.57
1:A:294:MET:SD	1:B:325:ARG:HD3	2.44	0.57
1:A:150:GLY:O	1:A:225:ALA:HB2	2.05	0.56
1:A:70:LEU:HG	1:A:74:LEU:HD22	1.87	0.56
1:B:18:ASP:O	1:B:22:LYS:HG2	2.07	0.55
1:A:93:THR:HG23	1:A:124:GLY:N	2.20	0.55
1:B:127:GLY:HA2	1:B:161:ILE:HD12	1.90	0.54
1:B:367:GLU:HG2	2:B:384:CAA:H2'2	1.90	0.54
1:A:104:PHE:HE1	1:A:237:LYS:HE2	1.73	0.54
1:B:339:VAL:HA	1:B:353:VAL:HG11	1.90	0.53
1:A:208:ILE:O	1:A:208:ILE:HG23	2.08	0.53
1:A:335:THR:HG21	1:A:357:MET:HA	1.88	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:34:LYS:HB3	1:B:34:LYS:NZ	2.24	0.53
1:B:105:GLY:O	1:B:110:LYS:HE3	2.09	0.52
1:B:115:VAL:CG2	1:B:116:PRO:HD3	2.40	0.52
1:A:288:LYS:HD3	1:A:337:GLU:HG3	1.93	0.51
1:A:182:ASN:ND2	2:A:384:CAA:C5B	2.74	0.51
1:A:198:THR:HG22	1:A:199:TYR:N	2.26	0.51
1:A:359:ASP:O	1:A:362:ILE:HG22	2.10	0.51
1:B:339:VAL:HA	1:B:353:VAL:CG1	2.41	0.51
1:B:367:GLU:HG2	2:B:384:CAA:C2	2.41	0.51
1:B:115:VAL:HG22	1:B:116:PRO:HD3	1.92	0.50
1:A:96:LEU:HB3	1:A:126:PHE:HB2	1.94	0.50
1:A:325:ARG:HD3	1:B:294:MET:SD	2.51	0.50
1:B:301:ASN:O	1:B:305:LYS:HB2	2.12	0.50
1:B:208:ILE:HD13	1:B:362:ILE:HD11	1.94	0.49
1:A:205:LYS:HE2	1:A:208:ILE:HG23	1.94	0.49
1:A:335:THR:HG22	1:A:336:THR:N	2.27	0.49
1:B:130:GLU:HA	1:B:159:ILE:HG22	1.95	0.49
1:A:321:ALA:HA	1:A:373:GLN:NE2	2.26	0.49
2:A:384:CAA:S1P	3:A:385:FAD:C2	3.01	0.48
1:B:175:MET:CE	1:B:181:GLY:HA2	2.44	0.48
1:A:85:GLY:O	1:A:89:THR:HG23	2.13	0.48
1:B:175:MET:SD	1:B:185:ILE:HG12	2.54	0.48
1:A:308:CYS:HA	1:A:311:GLN:HG2	1.95	0.47
1:A:105:GLY:O	1:A:110:LYS:HE3	2.14	0.47
1:A:372:VAL:O	1:A:376:VAL:HG23	2.15	0.47
1:B:100:PRO:HB3	1:B:242:THR:CG2	2.32	0.47
1:B:151:THR:HG22	1:B:224:PRO:HA	1.95	0.47
1:B:162:THR:O	1:B:163:ASN:HB2	2.14	0.47
1:B:262:LEU:O	1:B:266:VAL:HG23	2.15	0.47
1:A:205:LYS:HE2	1:A:208:ILE:HG22	1.97	0.46
1:B:182:ASN:HD21	2:B:384:CAA:H52A	1.80	0.46
1:A:292:MET:O	1:A:296:ILE:HG23	2.15	0.46
1:B:339:VAL:HG22	1:B:353:VAL:HG13	1.98	0.46
1:B:369:THR:O	1:B:372:VAL:HG22	2.16	0.46
1:A:312:GLU:OE1	1:A:314:LYS:HE2	2.16	0.45
1:A:198:THR:HG22	1:A:199:TYR:H	1.82	0.45
1:A:296:ILE:HG13	1:A:297:GLU:N	2.30	0.45
1:B:121:THR:HG22	1:B:122:LYS:HG3	1.99	0.44
1:A:137:ALA:HB3	1:A:236:PHE:HE1	1.82	0.44
1:B:328:SER:HB2	1:B:364:GLN:HG2	1.98	0.44
1:A:85:GLY:HA2	1:A:208:ILE:HG13	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:22:LYS:HG3	1:B:23:LYS:HG2	2.00	0.44
1:B:182:ASN:ND2	2:B:384:CAA:H52A	2.32	0.44
1:A:288:LYS:HD3	1:A:337:GLU:CG	2.48	0.44
1:B:201:LYS:HD2	1:B:202:LYS:N	2.32	0.44
1:B:96:LEU:HD12	2:B:384:CAA:H4'3	1.99	0.44
1:A:20:GLY:HA2	1:A:24:LEU:HD12	2.00	0.44
1:B:201:LYS:HD2	1:B:202:LYS:H	1.83	0.43
1:A:182:ASN:ND2	2:A:384:CAA:H52A	2.33	0.43
1:A:1:MET:HG3	1:B:70:LEU:HD21	2.00	0.43
1:A:140:GLN:HB2	1:A:175:MET:CE	2.49	0.43
1:A:149:ASP:HB2	1:A:151:THR:OG1	2.19	0.43
1:A:324:LYS:HE3	1:A:363:THR:O	2.19	0.43
1:A:1:MET:HG3	1:B:70:LEU:CD2	2.49	0.43
1:A:324:LYS:NZ	1:A:366:TYR:O	2.52	0.43
1:A:322:ILE:O	1:A:326:VAL:HG23	2.18	0.43
1:A:107:GLU:O	1:A:111:GLU:HG3	2.19	0.42
1:A:151:THR:HG22	1:A:152:TYR:N	2.34	0.42
1:A:70:LEU:HG	1:A:74:LEU:CD2	2.48	0.42
1:A:189:ILE:HD11	1:A:229:LEU:HD13	2.02	0.42
1:B:124:GLY:HA2	1:B:169:ILE:O	2.20	0.42
1:B:96:LEU:CD1	2:B:384:CAA:H4'3	2.49	0.42
1:A:19:PHE:HE1	1:A:44:GLU:HB3	1.84	0.42
2:A:384:CAA:H31	3:A:385:FAD:O2'	2.20	0.42
1:B:9:GLN:NE2	1:B:70:LEU:HD23	2.35	0.42
1:B:182:ASN:HD21	2:B:384:CAA:C5B	2.33	0.41
1:B:130:GLU:HB2	1:B:131:PRO:HD2	2.02	0.41
1:A:367:GLU:CG	2:A:384:CAA:H2'2	2.41	0.41
1:B:175:MET:HE3	1:B:181:GLY:HA2	2.03	0.41
1:B:39:LYS:HB3	1:B:39:LYS:HE2	1.84	0.40
1:B:361:LYS:HA	1:B:361:LYS:HD2	1.81	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	381/383 (100%)	364 (96%)	16 (4%)	1 (0%)	46 68
1	B	381/383 (100%)	367 (96%)	13 (3%)	1 (0%)	46 68
All	All	762/766 (100%)	731 (96%)	29 (4%)	2 (0%)	46 68

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	181	GLY
1	B	208	ILE

5.3.2 Protein sidechains (i)

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	300/300 (100%)	267 (89%)	33 (11%)	8 14
1	B	300/300 (100%)	279 (93%)	21 (7%)	19 34
All	All	600/600 (100%)	546 (91%)	54 (9%)	12 22

All (54) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	ASP
1	A	10	GLN
1	A	36	ILE
1	A	45	LEU
1	A	51	THR
1	A	57	GLU
1	A	74	LEU
1	A	79	LEU
1	A	93	THR
1	A	103	GLN
1	A	149	ASP

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Mol	Chain	Res	Type
1	A	180	LYS
1	A	182	ASN
1	A	208	ILE
1	A	214	MET
1	A	219	GLN
1	A	220	ASP
1	A	227	ASN
1	A	255	LEU
1	A	262	LEU
1	A	267	GLU
1	A	272	ARG
1	A	277	LYS
1	A	279	LEU
1	A	296	ILE
1	A	302	LEU
1	A	324	LYS
1	A	335	THR
1	A	340	GLN
1	A	350	GLU
1	A	353	VAL
1	A	366	TYR
1	A	374	LEU
1	B	1	MET
1	B	7	ASP
1	B	30	GLU
1	B	45	LEU
1	B	51	THR
1	B	74	LEU
1	B	111	GLU
1	B	131	PRO
1	B	178	LYS
1	B	180	LYS
1	B	182	ASN
1	B	201	LYS
1	B	208	ILE
1	B	219	GLN
1	B	229	LEU
1	B	234	LYS
1	B	281	LYS
1	B	302	LEU
1	B	362	ILE
1	B	366	TYR

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Mol	Chain	Res	Type
1	B	374	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	4	ASN
1	A	99	ASN
1	A	182	ASN
1	A	227	ASN
1	A	295	GLN
1	A	340	GLN
1	A	356	HIS
1	A	370	ASN
1	A	373	GLN
1	B	140	GLN
1	B	155	ASN
1	B	356	HIS
1	B	370	ASN

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

4 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	CAA	A	384	-	45,56,56	1.02	4 (8%)	58,83,83	1.92	6 (10%)
3	FAD	A	385	-	48,58,58	1.13	4 (8%)	54,89,89	2.77	10 (18%)
2	CAA	B	384	-	45,56,56	1.01	3 (6%)	58,83,83	2.15	9 (15%)
3	FAD	B	385	-	48,58,58	1.16	5 (10%)	54,89,89	2.75	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	CAA	A	384	-	-	0/50/71/71	0/3/3/3
3	FAD	A	385	-	-	0/30/50/50	0/6/6/6
2	CAA	B	384	-	-	0/50/71/71	0/3/3/3
3	FAD	B	385	-	-	0/30/50/50	0/6/6/6

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	385	FAD	C1'-N10	-3.25	1.45	1.48
3	A	385	FAD	C1'-N10	-2.19	1.46	1.48
2	A	384	CAA	C8A-N7A	-2.05	1.30	1.34
3	B	385	FAD	C9A-N10	2.05	1.41	1.38
3	A	385	FAD	C4X-N5	2.16	1.36	1.33
2	B	384	CAA	C9P-N8P	2.39	1.38	1.33
2	B	384	CAA	O4B-C1B	2.39	1.44	1.41
3	B	385	FAD	C4X-N5	2.40	1.37	1.33
2	A	384	CAA	C5P-N4P	2.56	1.39	1.33
2	A	384	CAA	C9P-N8P	2.62	1.39	1.33
2	B	384	CAA	C5P-N4P	2.71	1.39	1.33
2	A	384	CAA	O4B-C1B	2.74	1.44	1.41
3	B	385	FAD	C10-N10	2.78	1.42	1.39
3	B	385	FAD	C4-N3	2.82	1.38	1.33
3	A	385	FAD	C4-N3	2.87	1.38	1.33
3	A	385	FAD	C10-N10	3.19	1.42	1.39

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	384	CAA	O1-C1-S1P	-11.80	113.47	122.83
2	A	384	CAA	O1-C1-S1P	-11.01	114.10	122.83
3	B	385	FAD	C4X-C10-N10	-8.20	115.69	120.52
3	A	385	FAD	C4X-C10-N10	-7.12	116.32	120.52
2	B	384	CAA	C2-C1-S1P	-6.96	106.55	113.50
3	A	385	FAD	C4X-C4-N3	-6.44	114.78	123.59
3	B	385	FAD	C4X-C4-N3	-6.01	115.36	123.59
3	B	385	FAD	C4-C4X-C10	-5.36	116.51	119.94
3	A	385	FAD	C4-C4X-C10	-4.75	116.90	119.94
2	A	384	CAA	C2B-C1B-N9A	-4.31	107.70	114.29
3	A	385	FAD	C4X-N5-C5X	-4.08	112.07	116.76
3	B	385	FAD	C4X-N5-C5X	-3.92	112.25	116.76
2	B	384	CAA	C2B-C1B-N9A	-3.75	108.56	114.29
3	B	385	FAD	P-O3P-PA	-3.62	122.57	132.73
2	A	384	CAA	C6P-C7P-N8P	-3.13	105.01	111.88
3	B	385	FAD	C4-C4X-N5	-2.90	115.20	118.72
3	A	385	FAD	C4-C4X-N5	-2.85	115.26	118.72
3	A	385	FAD	C6-C5X-N5	-2.85	115.30	118.96
3	B	385	FAD	C6-C5X-N5	-2.58	115.64	118.96
3	A	385	FAD	P-O3P-PA	-2.49	125.73	132.73
2	B	384	CAA	C2B-C3B-C4B	-2.45	98.69	103.29
2	A	384	CAA	C2-C1-S1P	-2.32	111.18	113.50
2	A	384	CAA	C2B-C3B-C4B	-2.18	99.19	103.29
2	B	384	CAA	C3P-N4P-C5P	-2.11	118.64	122.79
2	B	384	CAA	C4B-O4B-C1B	-2.02	107.50	109.72
2	B	384	CAA	O4B-C1B-N9A	2.03	112.34	108.10
2	B	384	CAA	O6A-CCP-CBP	2.11	113.93	110.55
2	B	384	CAA	C6P-C5P-N4P	2.18	120.24	116.46
2	A	384	CAA	O4B-C1B-N9A	2.26	112.82	108.10
3	A	385	FAD	O2'-C2'-C1'	2.41	115.86	109.94
3	B	385	FAD	C9A-C5X-N5	3.35	127.31	122.36
3	A	385	FAD	C9A-C5X-N5	3.61	127.69	122.36
3	B	385	FAD	C4-N3-C2	13.77	127.15	115.25
3	A	385	FAD	C4-N3-C2	14.31	127.62	115.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	384	CAA	9	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	385	FAD	2	0
2	B	384	CAA	7	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

EDS was not executed - this section will therefore be empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates

EDS was not executed - this section will therefore be empty.

6.4 Ligands

EDS was not executed - this section will therefore be empty.

6.5 Other polymers

EDS was not executed - this section will therefore be empty.