



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 03:39 am GMT

PDB ID : 1O96
Title : STRUCTURE OF ELECTRON TRANSFERRING FLAVOPROTEIN FOR METHYLOPHILUS METHYLOTROPHUS.
Authors : Leys, D.; Basran, J.; Talfournier, F.; Sutcliffe, M.J.; Scrutton, N.S.
Deposited on : 2002-12-11
Resolution : 3.10 Å(reported)

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

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

A user guide is available at

<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:

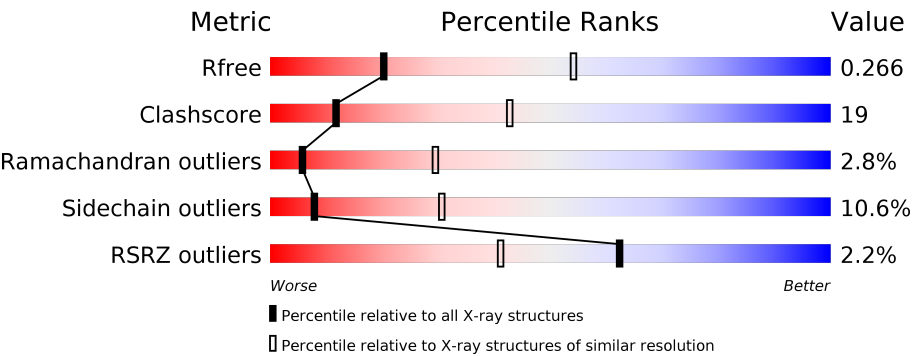
MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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	1001 (3.12-3.08)
Clashscore	112137	1099 (3.12-3.08)
Ramachandran outliers	110173	1057 (3.12-3.08)
Sidechain outliers	110143	1057 (3.12-3.08)
RSRZ outliers	101464	1006 (3.12-3.08)

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	264	<div><div></div><div>56%30%11%..</div></div>
1	C	264	<div><div></div><div>55%36%6%..</div></div>
1	E	264	<div><div></div><div>53%31%12%..</div></div>
1	Q	264	<div><div>5%</div><div>56%30%5%7%</div></div>
2	B	320	<div><div>%</div><div>61%27%8%..</div></div>
2	D	320	<div><div>%</div><div>47%38%13%..</div></div>

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Mol	Chain	Length	Quality of chain
2	F	320	<div><div></div><div>58%</div><div>30%</div><div>8%</div><div></div></div>
2	Z	320	<div><div>9%</div><div></div><div>70%</div><div>24%</div><div></div></div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 17093 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.

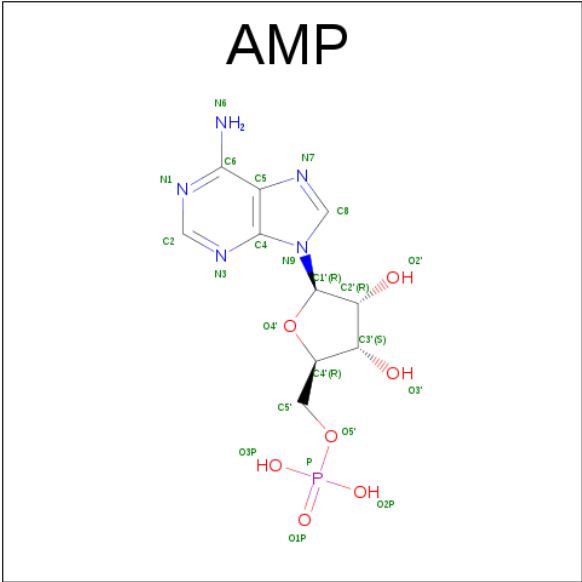
- Molecule 1 is a protein called ELECTRON TRANSFERRING FLAVOPROTEIN BETA-SUBUNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	261	Total	C	N	O	S	0	0	0
			1963	1227	336	389	11			
1	C	260	Total	C	N	O	S	0	0	0
			1942	1217	334	380	11			
1	E	260	Total	C	N	O	S	0	0	0
			1939	1216	331	381	11			
1	Q	246	Total	C	N	O	S	0	0	0
			1831	1147	311	363	10			

- Molecule 2 is a protein called ELECTRON TRANSFERRING FLAVOPROTEIN ALPHA-SUBUNIT.

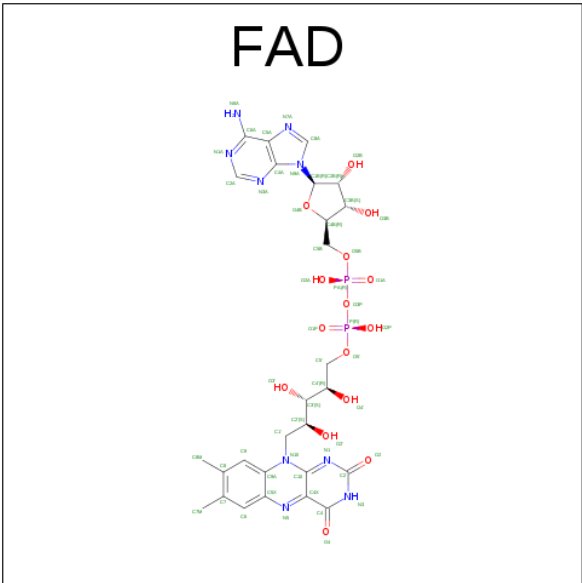
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	314	Total	C	N	O	S	0	0	0
			2287	1444	384	452	7			
2	D	314	Total	C	N	O	S	0	0	0
			2281	1440	383	451	7			
2	F	314	Total	C	N	O	S	0	0	0
			2281	1440	383	451	7			
2	Z	312	Total	C	N	O	S	0	0	0
			2265	1430	381	447	7			

- Molecule 3 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula: C₁₀H₁₄N₅O₇P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
3	C	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
3	E	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
3	Q	1	Total	C	N	O	P	0	0
			23	10	5	7	1		

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

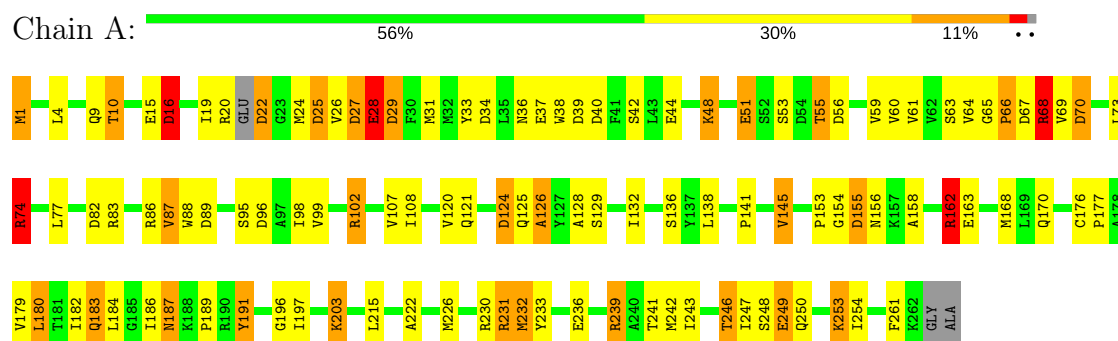


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
4	D	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
4	F	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
4	Z	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

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 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.

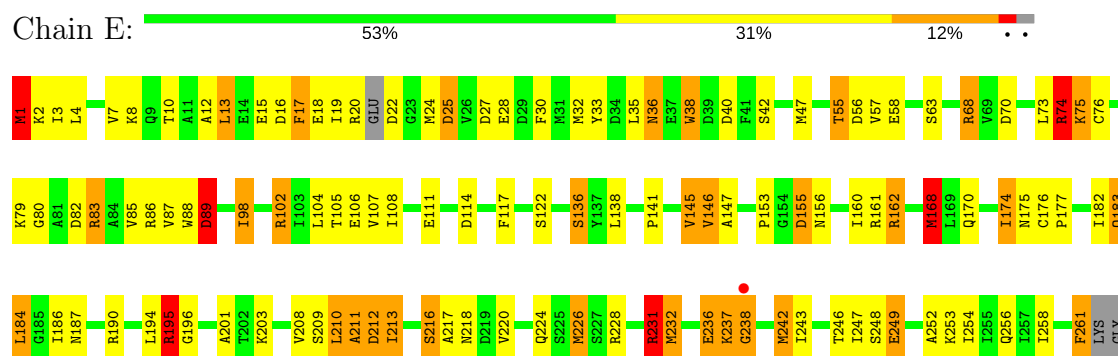
• Molecule 1: ELECTRON TRANSFERRING FLAVOPROTEIN BETA-SUBUNIT



• Molecule 1: ELECTRON TRANSFERRING FLAVOPROTEIN BETA-SUBUNIT

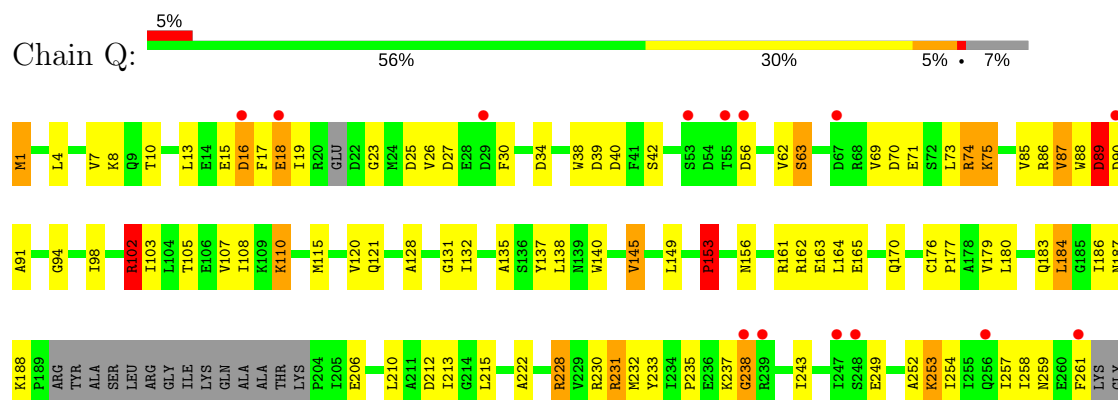


• Molecule 1: ELECTRON TRANSFERRING FLAVOPROTEIN BETA-SUBUNIT



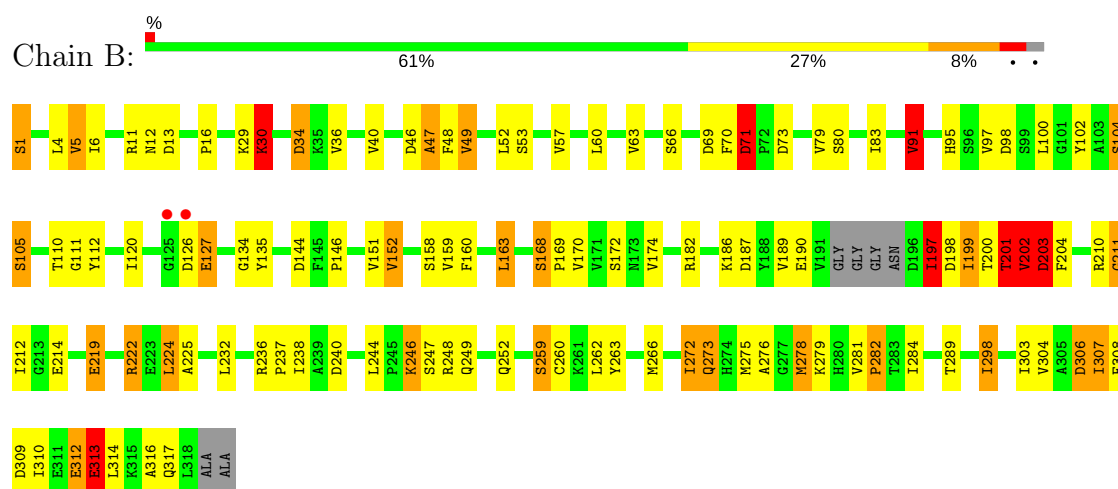
ALA

• Molecule 1: ELECTRON TRANSFERRING FLAVOPROTEIN BETA-SUBUNIT

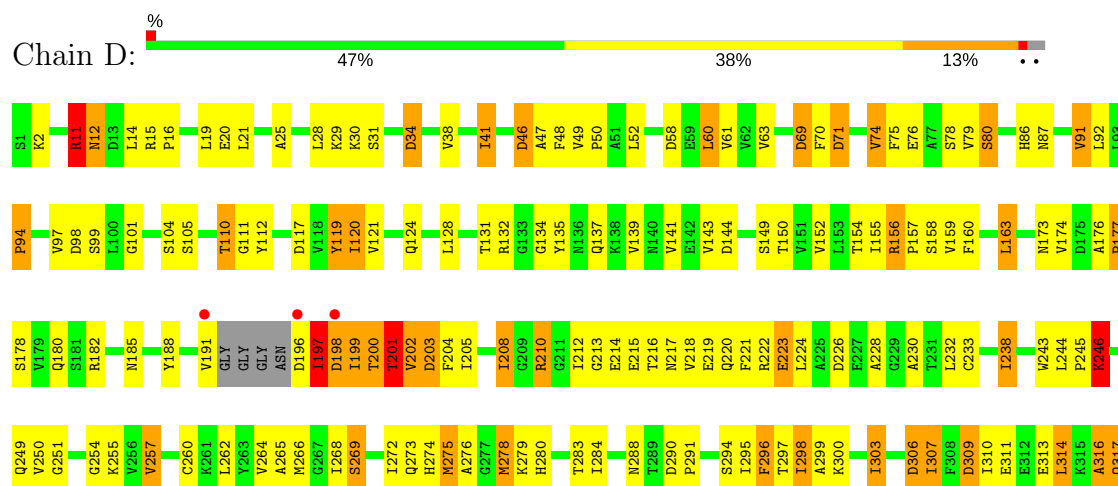


ALA

• Molecule 2: ELECTRON TRANSFERRING FLAVOPROTEIN ALPHA-SUBUNIT



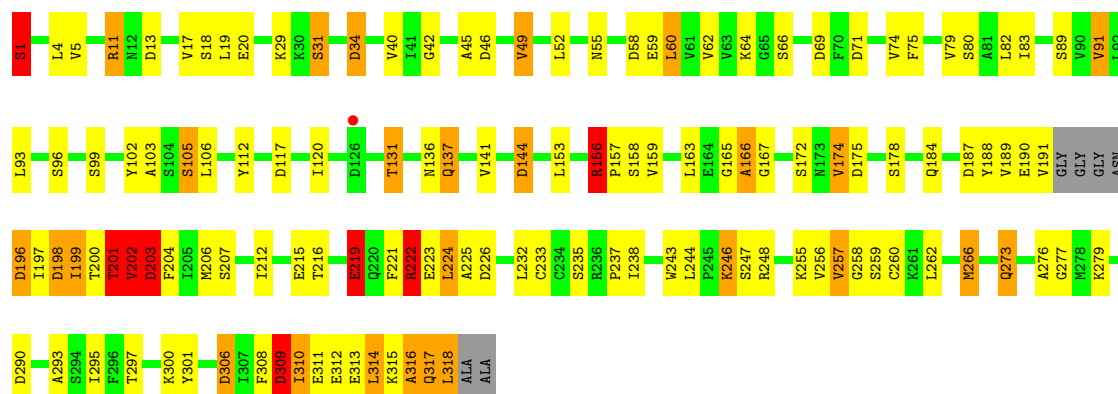
• Molecule 2: ELECTRON TRANSFERRING FLAVOPROTEIN ALPHA-SUBUNIT





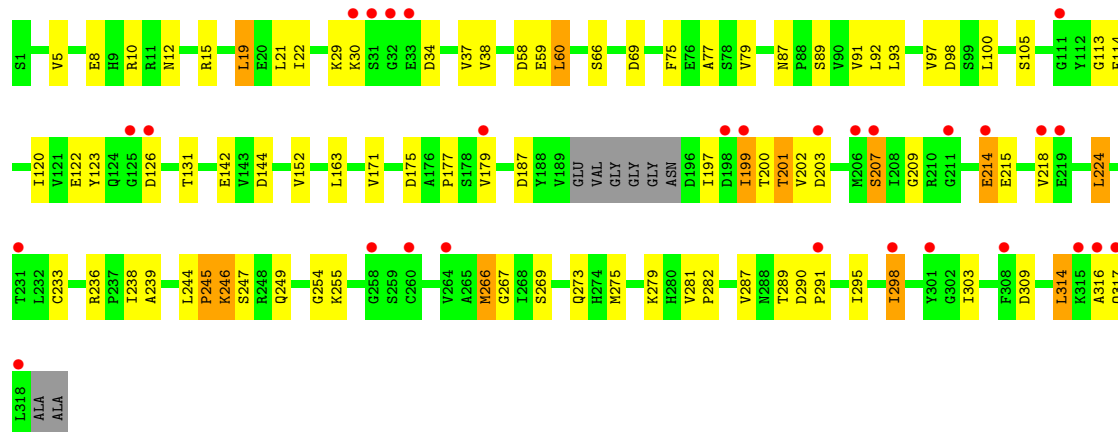
• Molecule 2: ELECTRON TRANSFERRING FLAVOPROTEIN ALPHA-SUBUNIT

Chain F: 58% 30% 8%



• Molecule 2: ELECTRON TRANSFERRING FLAVOPROTEIN ALPHA-SUBUNIT

Chain Z: 9% 70% 24%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	117.52Å 126.88Å 221.39Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.92 – 3.10 19.93 – 3.10	Depositor EDS
% Data completeness (in resolution range)	100.0 (19.92-3.10) 97.8 (19.93-3.10)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.11 (at 3.09Å)	Xtriage
Refinement program	REFMAC 5.1.08	Depositor
R, R_{free}	0.212 , 0.278 0.207 , 0.266	Depositor DCC
R_{free} test set	2989 reflections (5.32%)	DCC
Wilson B-factor (Å ²)	61.9	Xtriage
Anisotropy	0.422	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 56.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	17093	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.18% 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: AMP, 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	1.69	17/1986 (0.9%)	1.59	26/2688 (1.0%)
1	C	1.72	20/1965 (1.0%)	1.53	24/2660 (0.9%)
1	E	1.55	19/1962 (1.0%)	1.51	31/2657 (1.2%)
1	Q	1.28	10/1851 (0.5%)	1.25	10/2507 (0.4%)
2	B	1.49	20/2324 (0.9%)	1.48	28/3167 (0.9%)
2	D	1.53	21/2318 (0.9%)	1.54	34/3159 (1.1%)
2	F	1.57	24/2318 (1.0%)	1.53	31/3159 (1.0%)
2	Z	1.06	6/2302 (0.3%)	1.17	11/3137 (0.4%)
All	All	1.50	137/17026 (0.8%)	1.46	195/23134 (0.8%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	E	0	1
1	Q	0	1
2	B	0	3
2	D	0	2
2	F	0	2
All	All	0	10

The worst 5 of 137 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	28	GLU	CD-OE2	30.98	1.59	1.25
1	C	249	GLU	CD-OE1	22.16	1.50	1.25
1	A	74	ARG	CZ-NH2	15.41	1.53	1.33
1	A	28	GLU	CD-OE2	13.61	1.40	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	222	ARG	NE-CZ	13.57	1.50	1.33

The worst 5 of 195 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	74	ARG	NE-CZ-NH2	-12.17	114.22	120.30
2	D	198	ASP	CB-CG-OD2	11.85	128.97	118.30
1	C	56	ASP	CB-CG-OD2	11.16	128.35	118.30
1	Q	16	ASP	CB-CG-OD2	10.98	128.18	118.30
1	A	68	ARG	NE-CZ-NH1	10.87	125.73	120.30

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	22	ASP	Peptide
2	B	201	THR	Peptide
2	B	312	GLU	Peptide
2	B	313	GLU	Peptide
2	D	197	ILE	Peptide

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	1963	0	1916	87	1
1	C	1942	0	1901	99	0
1	E	1939	0	1891	107	0
1	Q	1831	0	1768	68	0
2	B	2287	0	2250	81	0
2	D	2281	0	2237	125	0
2	F	2281	0	2237	85	1
2	Z	2265	0	2222	52	0
3	A	23	0	12	0	0
3	C	23	0	12	3	0
3	E	23	0	12	2	0
3	Q	23	0	12	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	53	0	31	1	0
4	D	53	0	31	8	0
4	F	53	0	31	0	0
4	Z	53	0	31	4	0
All	All	17093	0	16594	655	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 19.

The worst 5 of 655 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:A:74:ARG:CG	1:A:74:ARG:CD	1.75	1.56
2:B:30:LYS:NZ	2:B:30:LYS:CE	1.68	1.54
1:Q:115:MET:CE	1:Q:115:MET:SD	2.03	1.46
1:Q:232:MET:SD	1:Q:232:MET:CE	2.05	1.44
2:Z:266:MET:CE	2:Z:266:MET:SD	2.07	1.42

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:191:TYR:OH	2:F:216:THR:CG2[4_456]	2.19	0.01

5.3 Torsion angles

5.3.1 Protein backbone

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	257/264 (97%)	228 (89%)	22 (9%)	7 (3%)	6	30
1	C	256/264 (97%)	221 (86%)	29 (11%)	6 (2%)	7	33

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	256/264 (97%)	227 (89%)	20 (8%)	9 (4%)	4	23
1	Q	240/264 (91%)	221 (92%)	15 (6%)	4 (2%)	11	42
2	B	310/320 (97%)	269 (87%)	33 (11%)	8 (3%)	6	31
2	D	310/320 (97%)	272 (88%)	26 (8%)	12 (4%)	3	21
2	F	310/320 (97%)	272 (88%)	25 (8%)	13 (4%)	3	19
2	Z	308/320 (96%)	279 (91%)	24 (8%)	5 (2%)	11	43
All	All	2247/2336 (96%)	1989 (88%)	194 (9%)	64 (3%)	6	29

5 of 64 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	155	ASP
2	B	211	GLY
1	C	247	ILE
2	D	197	ILE
2	D	201	THR

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	200/216 (93%)	173 (86%)	27 (14%)	4	19
1	C	196/216 (91%)	181 (92%)	15 (8%)	15	48
1	E	195/216 (90%)	176 (90%)	19 (10%)	9	35
1	Q	184/216 (85%)	166 (90%)	18 (10%)	9	35
2	B	245/258 (95%)	220 (90%)	25 (10%)	8	32
2	D	243/258 (94%)	209 (86%)	34 (14%)	4	18
2	F	243/258 (94%)	213 (88%)	30 (12%)	5	23
2	Z	241/258 (93%)	223 (92%)	18 (8%)	16	49
All	All	1747/1896 (92%)	1561 (89%)	186 (11%)	8	30

5 of 186 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	212	ILE
1	E	55	THR
2	Z	66	SER
2	D	216	THR
2	D	295	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 48 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	273	GLN
1	E	183	GLN
2	Z	173	ASN
2	D	317	GLN
1	E	170	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
3	AMP	A	1263	-	22,25,25	1.89	5 (22%)	24,38,38	2.16	9 (37%)
4	FAD	B	1319	-	51,58,58	1.98	12 (23%)	54,89,89	2.23	8 (14%)
3	AMP	C	1262	-	22,25,25	1.48	4 (18%)	24,38,38	3.16	8 (33%)
4	FAD	D	1319	-	51,58,58	2.47	18 (35%)	54,89,89	1.93	11 (20%)
3	AMP	E	1262	-	22,25,25	1.73	3 (13%)	24,38,38	3.25	8 (33%)
4	FAD	F	1319	-	51,58,58	1.98	17 (33%)	54,89,89	1.94	14 (25%)
3	AMP	Q	1262	-	22,25,25	1.52	4 (18%)	24,38,38	3.88	6 (25%)
4	FAD	Z	1319	-	51,58,58	1.65	10 (19%)	54,89,89	2.38	11 (20%)

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
3	AMP	A	1263	-	-	0/6/26/26	0/3/3/3
4	FAD	B	1319	-	-	0/28/50/50	0/6/6/6
3	AMP	C	1262	-	-	0/6/26/26	0/3/3/3
4	FAD	D	1319	-	-	0/28/50/50	0/6/6/6
3	AMP	E	1262	-	-	0/6/26/26	0/3/3/3
4	FAD	F	1319	-	-	0/28/50/50	0/6/6/6
3	AMP	Q	1262	-	-	0/6/26/26	0/3/3/3
4	FAD	Z	1319	-	-	0/28/50/50	0/6/6/6

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	1319	FAD	C6-C5X	-3.07	1.37	1.41
3	A	1263	AMP	C2'-C1'	-3.06	1.48	1.53
4	Z	1319	FAD	C9A-C5X	-2.44	1.37	1.42
4	F	1319	FAD	C2B-C1B	-2.39	1.49	1.53
3	C	1262	AMP	O4'-C4'	-2.31	1.39	1.45

The worst 5 of 75 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	Q	1262	AMP	N3-C2-N1	-16.46	114.52	128.86
3	E	1262	AMP	N3-C2-N1	-12.48	117.99	128.86
3	C	1262	AMP	N3-C2-N1	-11.54	118.81	128.86
4	Z	1319	FAD	N3A-C2A-N1A	-11.29	119.03	128.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1319	FAD	N3A-C2A-N1A	-10.17	120.00	128.86

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 20 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	1319	FAD	1	0
3	C	1262	AMP	3	0
4	D	1319	FAD	8	0
3	E	1262	AMP	2	0
3	Q	1262	AMP	2	0
4	Z	1319	FAD	4	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 [i](#)

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	261/264 (98%)	-0.74	0 100 100	20, 43, 65, 83	0
1	C	260/264 (98%)	-0.60	0 100 100	29, 52, 90, 112	0
1	E	260/264 (98%)	-0.60	1 (0%) 92 84	27, 52, 77, 88	0
1	Q	246/264 (93%)	0.08	14 (5%) 24 11	41, 76, 93, 102	27 (10%)
2	B	314/320 (98%)	-0.65	2 (0%) 89 77	25, 47, 68, 86	0
2	D	314/320 (98%)	-0.58	3 (0%) 82 67	2, 50, 83, 98	0
2	F	314/320 (98%)	-0.65	1 (0%) 93 86	31, 49, 70, 88	0
2	Z	312/320 (97%)	0.44	29 (9%) 9 3	46, 77, 95, 114	123 (39%)
All	All	2281/2336 (97%)	-0.41	50 (2%) 62 41	2, 54, 86, 114	150 (6%)

The worst 5 of 50 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	Z	198	ASP	7.9
2	Z	203	ASP	5.1
2	Z	315	LYS	5.1
2	Z	316	ALA	4.8
2	Z	219	GLU	4.6

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

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
4	FAD	B	1319	53/53	0.96	0.14	0.26	17,24,31,33	0
4	FAD	D	1319	53/53	0.95	0.15	0.02	21,28,38,42	0
4	FAD	F	1319	53/53	0.97	0.12	-0.27	17,24,29,35	0
3	AMP	A	1263	23/23	0.98	0.12	-0.46	23,28,34,37	0
4	FAD	Z	1319	53/53	0.89	0.22	-0.59	17,28,36,42	53
3	AMP	C	1262	23/23	0.99	0.12	-0.61	30,46,52,52	0
3	AMP	E	1262	23/23	0.98	0.11	-0.80	25,33,38,39	0
3	AMP	Q	1262	23/23	0.96	0.13	-1.02	57,62,69,74	0

6.5 Other polymers

There are no such residues in this entry.