W O R L D W I D E
wwPDB
P R O T E I N D A T A B A N K

wwPDB X-ray Structure Validation Summary Report (i)

Feb 19, 2016 – 06:39 PM GMT

PDB ID	:	3F6S
Title	:	Desulfovibrio desulfuricans (ATCC 29577) oxidized flavodoxin alternate conformers
Authors	:	Guelker, M.; Shamoo, Y.
Deposited on	:	2008-11-06
Resolution	:	2.50 Å(reported)

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

|		
MolProbity	:	4.02b-467
Mogul	:	1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026982
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)	:	rb-20026982

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.
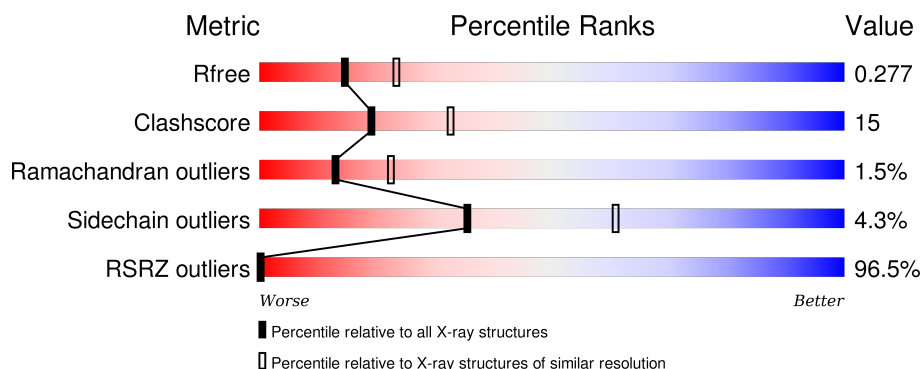
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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.

Mol	Chain	Length	Quality of chain
1	A	148	
1	B	148	
1	D	148	
1	E	148	
1	F	148	

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Mol	Chain	Length	Quality of chain
1	G	148	92% / 77% ... 18%
1	H	148	99% / 64% ... 33%
1	I	148	99% / 72% ... 26%

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
2	FMN	D	151	-	-	-	X
2	FMN	F	153	-	-	-	X
2	FMN	H	154	-	-	-	X
2	FMN	I	155	-	-	-	X

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 9299 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 Flavodoxin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	147	Total	C	N	O	S	0	0	0
			1093	683	175	230	5			
1	B	147	Total	C	N	O	S	0	0	0
			1093	683	175	230	5			
1	D	147	Total	C	N	O	S	0	0	0
			1093	683	175	230	5			
1	E	147	Total	C	N	O	S	0	0	0
			1093	683	175	230	5			
1	F	147	Total	C	N	O	S	0	0	0
			1093	683	175	230	5			
1	H	147	Total	C	N	O	S	0	0	0
			1093	683	175	230	5			
1	I	147	Total	C	N	O	S	0	0	0
			1093	683	175	230	5			
1	G	147	Total	C	N	O	S	0	0	0
			1093	683	175	230	5			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	79	ASP	ASN	ENGINEERED	UNP P26492
B	79	ASP	ASN	ENGINEERED	UNP P26492
D	79	ASP	ASN	ENGINEERED	UNP P26492
E	79	ASP	ASN	ENGINEERED	UNP P26492
F	79	ASP	ASN	ENGINEERED	UNP P26492
H	79	ASP	ASN	ENGINEERED	UNP P26492
I	79	ASP	ASN	ENGINEERED	UNP P26492
G	79	ASP	ASN	ENGINEERED	UNP P26492

- Molecule 2 is FLAVIN MONONUCLEOTIDE (three-letter code: FMN) (formula: $C_{17}H_{21}N_4O_9P$).

FMN
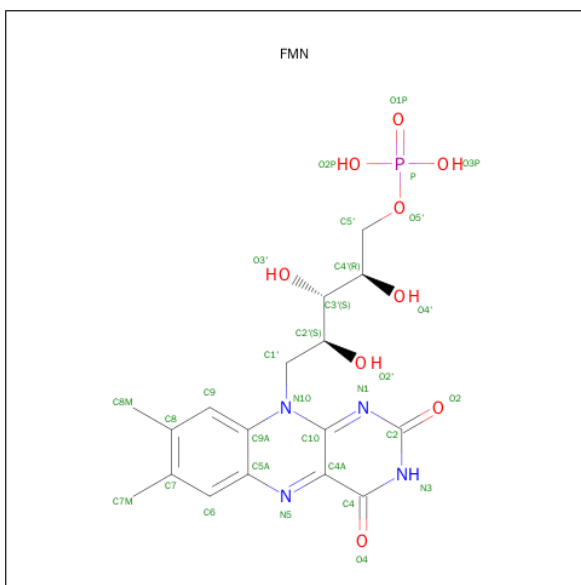
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	B	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	D	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	E	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	F	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	H	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	I	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	G	1	Total	C	N	O	P	0	0
			31	17	4	9	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	47	Total	O	0	0
			47	47		
3	B	68	Total	O	0	0
			68	68		
3	D	17	Total	O	0	0
			17	17		
3	E	43	Total	O	0	0
			43	43		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	F	26	Total 26	O 26	0	0
3	H	34	Total 34	O 34	0	0
3	I	32	Total 32	O 32	0	0
3	G	40	Total 40	O 40	0	0

# 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.
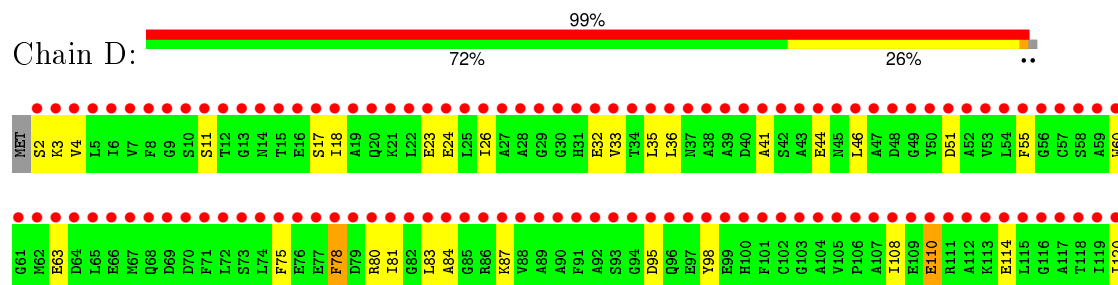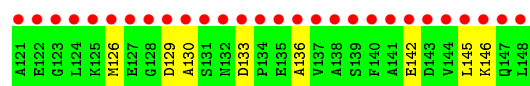
- Molecule 1: Flavodoxin
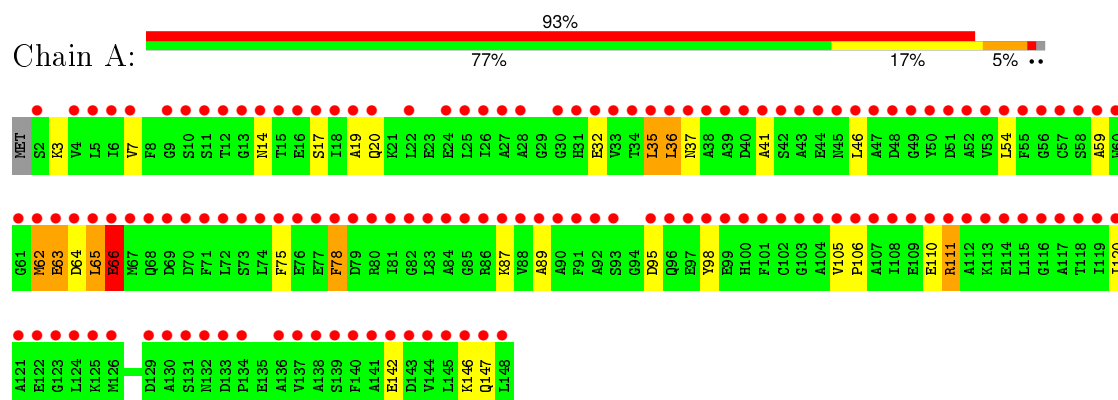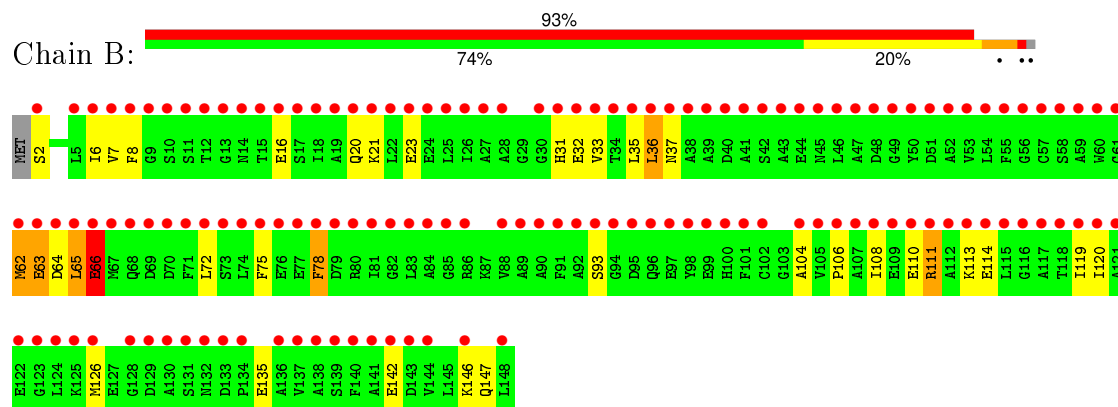
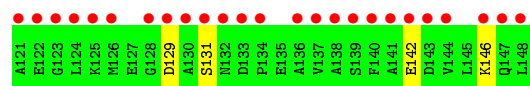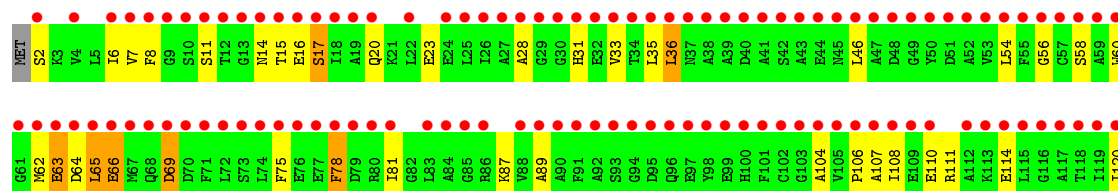- Molecule 1: Flavodoxin
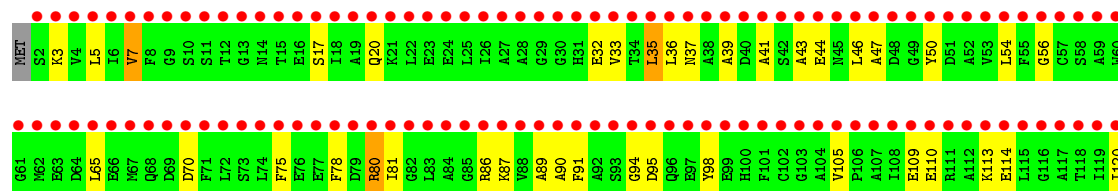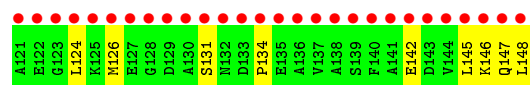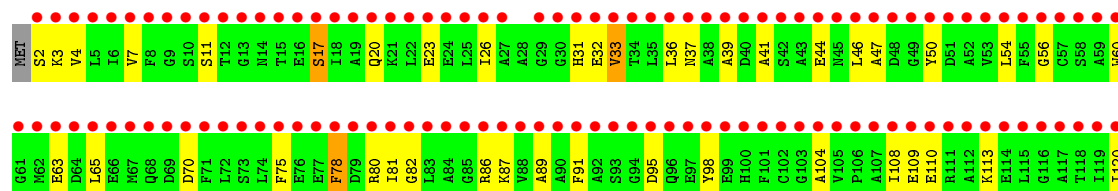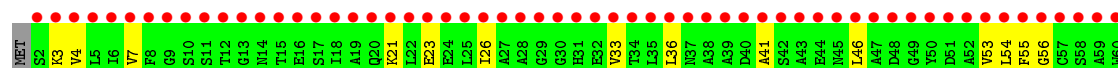

- Molecule 1: Flavodoxin

• Molecule 1: Flavodoxin

Chain E:

• Molecule 1: Flavodoxin

Chain F:

• Molecule 1: Flavodoxin

Chain H:

• Molecule 1: Flavodoxin

Chain I:

• Molecule 1: Flavodoxin

Chain G:
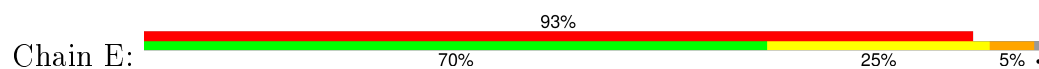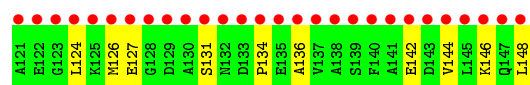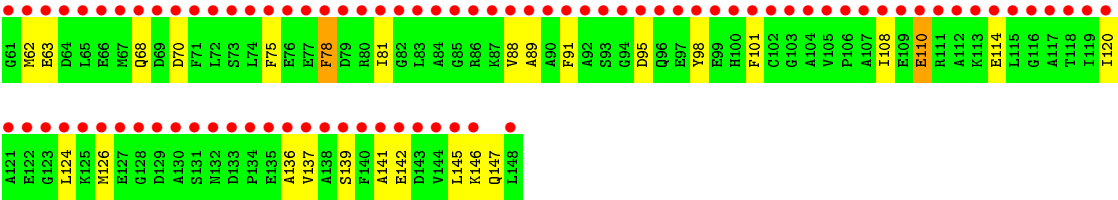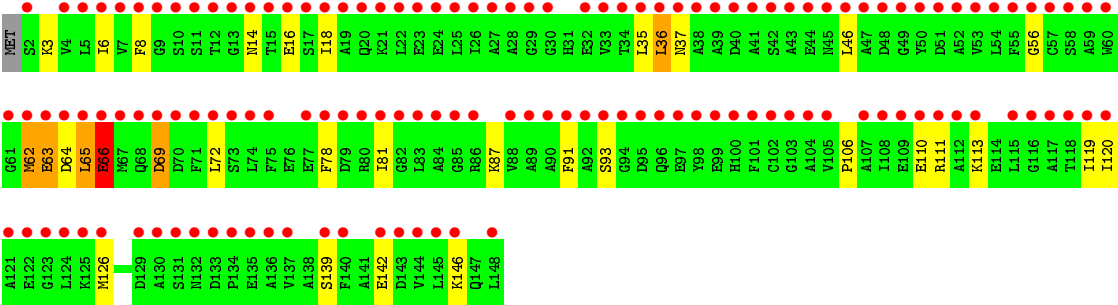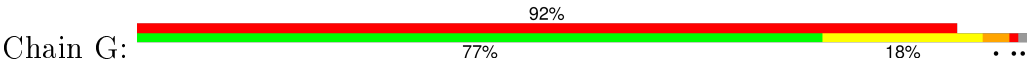
4   Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α, β, γ	94.89Å 94.89Å 238.10Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.89 – 2.50 19.89 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.8 (19.89-2.50) 99.8 (19.89-2.50)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	6.10 (at 2.50Å)	Xtriage
Refinement program	CNS, PHENIX (phenix.refine)	Depositor
R, R_{free}	0.220 , 0.279 0.221 , 0.277	Depositor DCC
R_{free} test set	4386 reflections (10.06%)	DCC
Wilson B-factor (Å^2)	10.6	Xtriage
Anisotropy	0.659	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 71.7	EDS
Estimated twinning fraction	0.071 for H, K, L 0.929 for -H, -K, L 0.053 for -h,-k,l	Xtriage
Reported twinning fraction	0.071 for H, K, L 0.929 for -H, -K, L	Depositor
L-test for twinning[2]	$< |L| > = 0.46, < L^2 > = 0.29$	Xtriage
Outliers	13 of 43606 reflections (0.030%)	Xtriage
F_o,F_c correlation	0.50	EDS
Total number of atoms	9299	wwPDB-VP
Average B, all atoms (Å^2)	67.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 70.32 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 3.1875e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: FMN

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	0/1108	0.57	0/1494
1	B	0.40	0/1108	0.55	0/1494
1	D	0.30	0/1108	0.44	0/1494
1	E	0.41	0/1108	0.56	0/1494
1	F	0.32	0/1108	0.44	0/1494
1	G	0.39	0/1108	0.55	0/1494
1	H	0.31	0/1108	0.44	0/1494
1	I	0.31	0/1108	0.45	0/1494
All	All	0.36	0/8864	0.50	0/11952

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	1093	0	1038	31	0
1	B	1093	0	1038	31	0
1	D	1093	0	1038	31	0
1	E	1093	0	1038	36	0
1	F	1093	0	1038	41	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	G	1093	0	1038	28	0
1	H	1093	0	1038	39	0
1	I	1093	0	1038	35	0
2	A	31	0	19	3	0
2	B	31	0	19	0	0
2	D	31	0	19	1	0
2	E	31	0	19	2	0
2	F	31	0	19	0	0
2	G	31	0	19	0	0
2	H	31	0	19	0	0
2	I	31	0	19	2	0
3	A	47	0	0	1	0
3	B	68	0	0	2	0
3	D	17	0	0	0	0
3	E	43	0	0	1	0
3	F	26	0	0	0	0
3	G	40	0	0	2	0
3	H	34	0	0	0	0
3	I	32	0	0	0	0
All	All	9299	0	8456	265	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 15.

The worst 5 of 265 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:124:LEU:HD21	1:H:126:MET:HE3	1.46	0.96
1:D:4:VAL:HB	1:D:33:VAL:HG12	1.49	0.93
1:E:142:GLU:HG2	1:E:146:LYS:HE3	1.52	0.92
1:H:124:LEU:HD11	1:H:126:MET:HE2	1.54	0.86
1:D:126:MET:HE2	1:D:133:ASP:HB3	1.56	0.86

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	145/148 (98%)	138 (95%)	3 (2%)	4 (3%)	6	9
1	B	145/148 (98%)	139 (96%)	2 (1%)	4 (3%)	6	9
1	D	145/148 (98%)	137 (94%)	8 (6%)	0	100	100
1	E	145/148 (98%)	140 (97%)	1 (1%)	4 (3%)	6	9
1	F	145/148 (98%)	138 (95%)	7 (5%)	0	100	100
1	G	145/148 (98%)	138 (95%)	2 (1%)	5 (3%)	5	6
1	H	145/148 (98%)	141 (97%)	4 (3%)	0	100	100
1	I	145/148 (98%)	139 (96%)	6 (4%)	0	100	100
All	All	1160/1184 (98%)	1110 (96%)	33 (3%)	17 (2%)	13	22

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	63	GLU
1	A	65	LEU
1	A	66	GLU
1	B	63	GLU
1	B	65	LEU

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	110/111 (99%)	104 (94%)	6 (6%)	27	48

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	110/111 (99%)	104 (94%)	6 (6%)	27	48
1	D	110/111 (99%)	107 (97%)	3 (3%)	52	79
1	E	110/111 (99%)	104 (94%)	6 (6%)	27	48
1	F	110/111 (99%)	106 (96%)	4 (4%)	42	69
1	G	110/111 (99%)	105 (96%)	5 (4%)	34	59
1	H	110/111 (99%)	105 (96%)	5 (4%)	34	59
1	I	110/111 (99%)	107 (97%)	3 (3%)	52	79
All	All	880/888 (99%)	842 (96%)	38 (4%)	35	61

5 of 38 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	36	LEU
1	F	7	VAL
1	G	69	ASP
1	E	78	PHE
1	F	33	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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)

8 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#|Z| > 2$	Counts	RMSZ	$\#|Z| > 2$
2	FMN	A	149	-	32,33,33	1.18	3 (9%)	34,50,50	1.76	5 (14%)
2	FMN	B	150	-	32,33,33	1.18	3 (9%)	34,50,50	1.77	5 (14%)
2	FMN	D	151	-	32,33,33	1.19	3 (9%)	34,50,50	1.73	5 (14%)
2	FMN	E	152	-	32,33,33	1.24	4 (12%)	34,50,50	1.69	7 (20%)
2	FMN	F	153	-	32,33,33	1.20	3 (9%)	34,50,50	1.76	5 (14%)
2	FMN	G	156	-	32,33,33	1.20	4 (12%)	34,50,50	1.91	7 (20%)
2	FMN	H	154	-	32,33,33	1.17	3 (9%)	34,50,50	1.62	5 (14%)
2	FMN	I	155	-	32,33,33	1.19	3 (9%)	34,50,50	1.85	5 (14%)

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	FMN	A	149	-	-	0/18/18/18	0/3/3/3
2	FMN	B	150	-	-	0/18/18/18	0/3/3/3
2	FMN	D	151	-	-	0/18/18/18	0/3/3/3
2	FMN	E	152	-	-	0/18/18/18	0/3/3/3
2	FMN	F	153	-	-	0/18/18/18	0/3/3/3
2	FMN	G	156	-	-	0/18/18/18	0/3/3/3
2	FMN	H	154	-	-	0/18/18/18	0/3/3/3
2	FMN	I	155	-	-	0/18/18/18	0/3/3/3

The worst 5 of 26 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	151	FMN	C5A-N5	2.00	1.38	1.35
2	I	155	FMN	C5A-N5	2.02	1.38	1.35
2	E	152	FMN	C1'-N10	2.06	1.50	1.48
2	G	156	FMN	C1'-N10	2.09	1.50	1.48
2	G	156	FMN	C5A-N5	2.13	1.38	1.35

The worst 5 of 44 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	I	155	FMN	N3-C2-N1	-4.75	119.70	127.69
2	F	153	FMN	N3-C2-N1	-4.63	119.89	127.69
2	D	151	FMN	N3-C2-N1	-4.54	120.04	127.69
2	H	154	FMN	N3-C2-N1	-4.45	120.19	127.69
2	G	156	FMN	N3-C2-N1	-4.44	120.22	127.69

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	149	FMN	3	0
2	D	151	FMN	1	0
2	E	152	FMN	2	0
2	I	155	FMN	2	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	147/148 (99%)	4.43	138 (93%)	0	0	45, 56, 75, 107	0
1	B	147/148 (99%)	4.05	138 (93%)	0	0	45, 57, 74, 107	0
1	D	147/148 (99%)	7.84	147 (100%)	0	0	59, 71, 93, 114	0
1	E	147/148 (99%)	4.10	137 (93%)	0	0	45, 56, 74, 107	0
1	F	147/148 (99%)	7.68	147 (100%)	0	0	59, 70, 92, 114	0
1	G	147/148 (99%)	4.08	136 (92%)	0	0	46, 56, 74, 107	0
1	H	147/148 (99%)	7.79	146 (99%)	0	0	60, 70, 92, 114	0
1	I	147/148 (99%)	7.73	146 (99%)	0	0	59, 71, 92, 115	0
All	All	1176/1184 (99%)	5.96	1135 (96%)	0	0	45, 65, 89, 115	0

The worst 5 of 1135 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	47	ALA	21.4
1	H	103	GLY	19.7
1	H	97	GLU	19.3
1	F	103	GLY	19.2
1	F	42	SER	17.3

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
2	FMN	F	153	31/31	0.24	0.71	0.43	69,74,76,80	0
2	FMN	H	154	31/31	0.29	0.69	0.23	66,75,77,80	0
2	FMN	I	155	31/31	0.40	0.69	-0.06	74,84,86,88	0
2	FMN	D	151	31/31	0.37	0.69	-0.07	73,82,86,87	0
2	FMN	G	156	31/31	0.71	0.36	-0.50	54,58,63,70	0
2	FMN	E	152	31/31	0.76	0.36	-0.60	56,60,63,71	0
2	FMN	A	149	31/31	0.72	0.36	-0.60	56,60,63,71	0
2	FMN	B	150	31/31	0.75	0.34	-0.98	55,58,63,69	0

6.5 Other polymers (i)

There are no such residues in this entry.