Full wwPDB X-ray Structure Validation Report (i)

Feb 19, 2016 – 06:44 PM GMT

PDB ID	:	3W7A
Title	:	Crystal Structure of azoreductase AzrC fin complex with sulfone-modified azo dye Acid Red 88
Authors	:	Yu, J.; Ogata, D.; Ooi, T.; Yao, M.
Deposited on	:	2013-02-27
Resolution	:	2.10 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 (1)) were used in the production of this report:

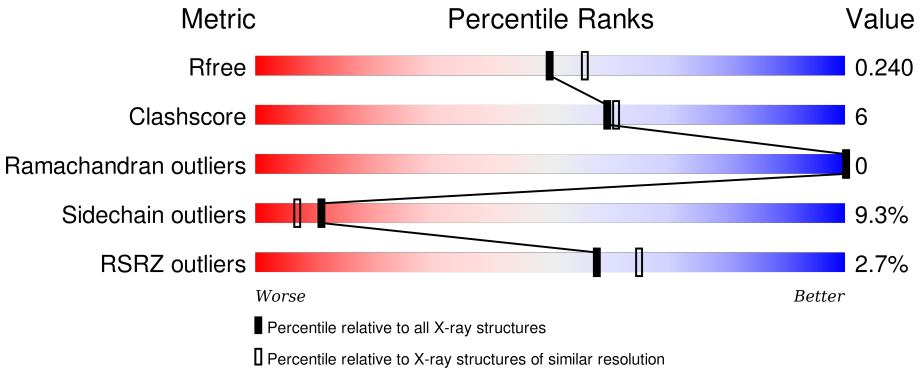
MolProbity	:	4.02b-467
Mogul	:	1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026982
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20026982

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.10 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}	91344	3939 (2.10-2.10)
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)
RSRZ outliers	91569	3948 (2.10-2.10)

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	211	4%, 82%, 14%
1	B	211	2%, 82%, 15%
1	C	211	2%, 84%, 14%
1	D	211	3%, 85%, 13%

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	RE8	A	302	-	-	-	X
3	RE8	A	303	-	-	-	X
3	RE8	C	302	-	-	-	X
3	RE8	C	303	-	-	-	X
5	K	B	302	-	-	-	X

2 Entry composition

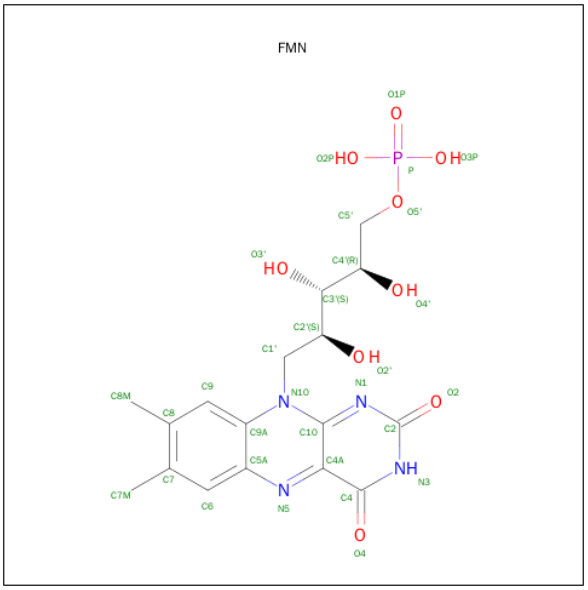
There are 6 unique types of molecules in this entry. The entry contains 6911 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 FMN-dependent NADH-azoreductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	210	Total	C	N	O	S	0	0	0
			1610	1032	264	309	5			
1	B	210	Total	C	N	O	S	0	0	0
			1610	1032	264	309	5			
1	C	210	Total	C	N	O	S	0	0	0
			1610	1032	264	309	5			
1	D	210	Total	C	N	O	S	0	0	0
			1610	1032	264	309	5			

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



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		

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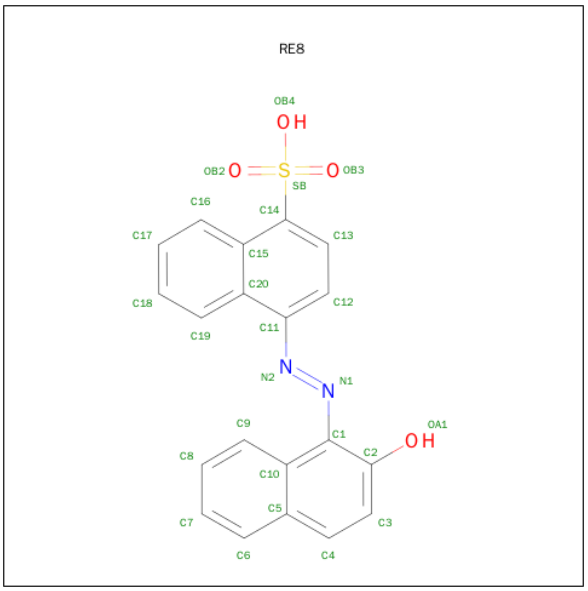
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	C	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	D	1	Total	C	N	O	P	0	0
			31	17	4	9	1		

- Molecule 3 is 4-[(E)-(2-HYDROXYNAPHTHALEN-1-YL)DIAZENYL]NAPHTHALENE-1-SULFONIC ACID (three-letter code: RE8) (formula: $C_{20}H_{14}N_2O_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			27	20	2	4	1		
3	A	1	Total	C	N	O	S	0	0
			27	20	2	4	1		
3	C	1	Total	C	N	O	S	0	0
			27	20	2	4	1		
3	C	1	Total	C	N	O	S	0	0
			27	20	2	4	1		

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Ca	0	0
			1	1		
4	C	2	Total	Ca	0	0
			2	2		

- Molecule 5 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total K 1 1	0	0
5	A	1	Total K 1 1	0	0
5	C	2	Total K 2 2	0	0

- Molecule 6 is water.

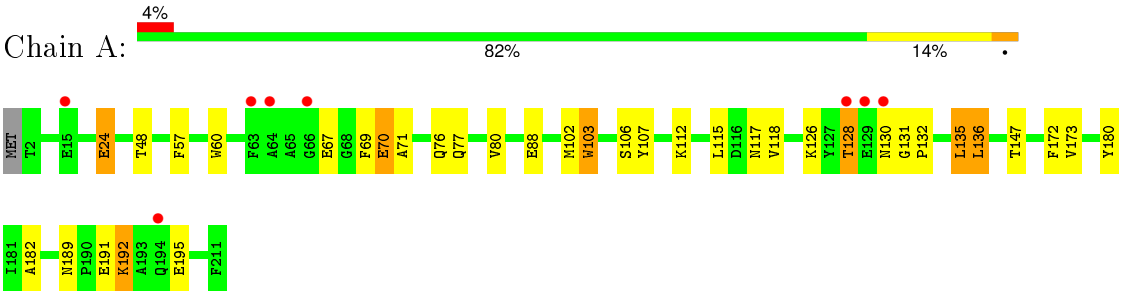
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	64	Total O 64 64	0	0
6	B	41	Total O 41 41	0	0
6	C	72	Total O 72 72	0	0
6	D	55	Total O 55 55	0	0

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.

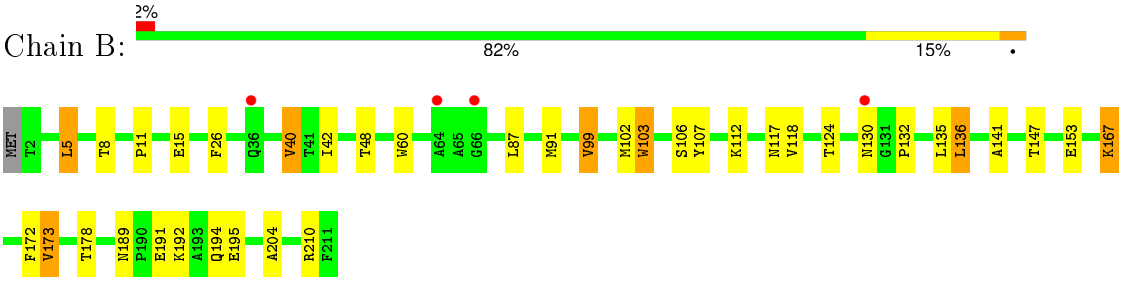
- Molecule 1: FMN-dependent NADH-azoreductase

Chain A:



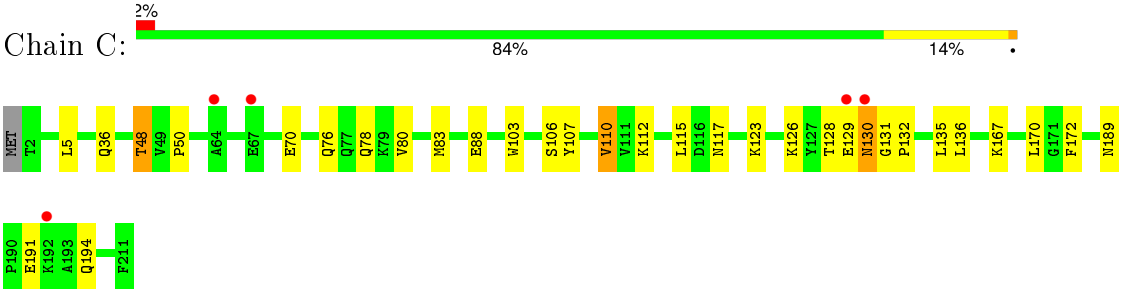
- Molecule 1: FMN-dependent NADH-azoreductase

Chain B:



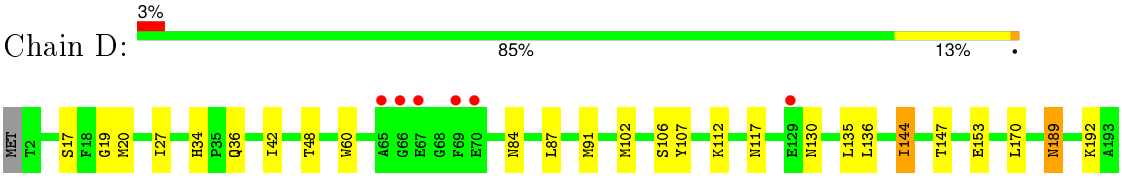
- Molecule 1: FMN-dependent NADH-azoreductase

Chain C:



- Molecule 1: FMN-dependent NADH-azoreductase

Chain D:




Q194
E195
E198
N203
F211

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	191.98Å 56.62Å 105.52Å 90.00° 115.71° 90.00°	Depositor
Resolution (Å)	50.00 – 2.10 38.28 – 2.10	Depositor EDS
% Data completeness (in resolution range)	97.2 (50.00-2.10) 97.5 (38.28-2.10)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.78 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.199 , 0.239 0.199 , 0.240	Depositor DCC
R_{free} test set	4154 reflections (7.60%)	DCC
Wilson B-factor (Å^2)	19.4	Xtriage
Anisotropy	0.875	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.41 , 50.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Outliers	0 of 58829 reflections	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	6911	wwPDB-VP
Average B, all atoms (Å^2)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.56% of the height of the origin peak. No significant pseudotranslation is detected.*

[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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FMN, K, CA, RE8

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	0.70	2/1646 (0.1%)	0.72	0/2236
1	B	0.68	2/1646 (0.1%)	0.75	0/2236
1	C	0.72	0/1646	0.78	1/2236 (0.0%)
1	D	0.69	1/1646 (0.1%)	0.71	0/2236
All	All	0.70	5/6584 (0.1%)	0.74	1/8944 (0.0%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	60	TRP	CD2-CE2	6.19	1.48	1.41
1	D	60	TRP	CD2-CE2	5.96	1.48	1.41
1	A	103	TRP	CD2-CE2	5.76	1.48	1.41
1	B	103	TRP	CD2-CE2	5.71	1.48	1.41
1	A	60	TRP	CD2-CE2	5.04	1.47	1.41

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	110	VAL	CB-CA-C	-5.18	101.55	111.40

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	1610	0	1562	27	0
1	B	1610	0	1562	18	0
1	C	1610	0	1561	14	0
1	D	1610	0	1562	16	0
2	A	31	0	19	1	0
2	B	31	0	19	1	0
2	C	31	0	19	1	0
2	D	31	0	19	1	0
3	A	54	0	28	2	0
3	C	54	0	28	2	0
4	A	1	0	0	0	0
4	C	2	0	0	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	C	2	0	0	0	0
6	A	64	0	0	2	0
6	B	41	0	0	0	0
6	C	72	0	0	1	0
6	D	55	0	0	1	0
All	All	6911	0	6379	74	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 6.

All (74) 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:C:128:THR:HB	1:C:131:GLY:O	1.69	0.93
1:A:106:SER:HB3	1:B:112:LYS:HE3	1.63	0.79
1:D:34:HIS:HB3	1:D:36:GLN:HE22	1.51	0.74
1:A:191:GLU:HA	1:A:191:GLU:OE2	1.87	0.73
1:D:19:GLY:HA2	1:D:144:ILE:HD11	1.74	0.69
1:C:48:THR:HG22	6:C:429:HOH:O	1.92	0.69
1:C:76:GLN:O	1:C:80:VAL:HG12	1.93	0.68
1:B:87:LEU:O	1:B:91:MET:HG3	1.97	0.65
1:B:192:LYS:O	1:B:195:GLU:HG2	1.98	0.64
1:B:132:PRO:HB2	1:B:172:PHE:CE1	2.33	0.64
1:C:128:THR:HG22	1:C:130:ASN:H	1.64	0.63
1:C:112:LYS:HE3	1:D:106:SER:HB3	1.81	0.62
1:A:132:PRO:HB2	1:A:172:PHE:HE1	1.66	0.61
1:A:128:THR:HG22	1:A:130:ASN:H	1.66	0.60
1:C:129:GLU:H	1:C:129:GLU:CD	2.05	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:189:ASN:OD1	1:D:192:LYS:HG3	2.01	0.60
1:D:195:GLU:HA	1:D:198:GLU:HG2	1.85	0.59
1:A:128:THR:HB	1:A:131:GLY:O	2.04	0.57
3:A:303:RE8:N2	3:A:303:RE8:H9	2.19	0.57
1:A:189:ASN:ND2	1:A:192:LYS:HG3	2.20	0.56
1:D:87:LEU:O	1:D:91:MET:HG3	2.05	0.56
1:A:70:GLU:H	1:A:70:GLU:CD	2.08	0.56
1:B:136:LEU:HD22	1:B:173:VAL:HG13	1.87	0.55
3:C:303:RE8:C12	2:D:301:FMN:H1'2	2.37	0.55
1:A:67:GLU:HG2	1:A:71:ALA:CB	2.37	0.55
1:A:76:GLN:O	1:A:80:VAL:HG12	2.08	0.54
1:A:102:MET:HB2	1:A:147:THR:HG22	1.90	0.53
1:A:77:GLN:NE2	6:A:418:HOH:O	2.41	0.53
1:B:5:LEU:HD12	1:B:40:VAL:HG13	1.90	0.53
1:A:132:PRO:CB	1:A:172:PHE:HE1	2.22	0.53
1:A:112:LYS:HE3	1:B:106:SER:HB3	1.91	0.52
1:B:132:PRO:HB2	1:B:172:PHE:HE1	1.73	0.52
1:D:144:ILE:HD12	1:D:144:ILE:C	2.31	0.50
1:A:126:LYS:HD2	1:A:135:LEU:HD11	1.93	0.49
1:A:132:PRO:CB	1:A:172:PHE:CE1	2.95	0.49
1:A:132:PRO:HB2	1:A:172:PHE:CE1	2.46	0.49
1:D:102:MET:HB2	1:D:147:THR:HG22	1.94	0.49
1:D:36:GLN:CD	1:D:36:GLN:H	2.16	0.48
1:C:70:GLU:CD	1:C:70:GLU:H	2.17	0.48
1:C:191:GLU:CD	1:C:191:GLU:H	2.16	0.47
1:A:191:GLU:CA	1:A:191:GLU:OE2	2.60	0.47
1:C:106:SER:HB3	1:D:112:LYS:HE3	1.96	0.47
1:B:102:MET:HB2	1:B:147:THR:HG22	1.96	0.47
1:C:167:LYS:HE3	1:C:167:LYS:HB3	1.68	0.46
1:C:103:TRP:HA	2:C:301:FMN:C5A	2.46	0.46
1:B:167:LYS:HE3	1:B:178:THR:HG21	1.96	0.46
1:B:8:THR:HG22	1:B:99:VAL:HG13	1.98	0.46
1:D:19:GLY:CA	1:D:144:ILE:HD11	2.46	0.46
1:D:195:GLU:CD	1:D:195:GLU:H	2.18	0.45
1:C:132:PRO:HB2	1:C:172:PHE:HE1	1.80	0.45
1:A:128:THR:CG2	1:A:130:ASN:H	2.30	0.44
1:C:50:PRO:HG2	1:C:83:MET:HG3	1.98	0.44
1:A:192:LYS:O	1:A:195:GLU:HG2	2.18	0.44
1:B:167:LYS:HE2	1:B:167:LYS:HA	1.99	0.44
1:A:67:GLU:HG2	1:A:71:ALA:HB2	2.00	0.44
1:D:27:ILE:HD12	1:D:27:ILE:HA	1.87	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:84:ASN:ND2	6:D:431:HOH:O	2.51	0.43
1:A:57:PHE:CE2	1:B:11:PRO:HG2	2.53	0.43
1:B:124:THR:HB	1:B:173:VAL:HG22	1.99	0.43
1:A:103:TRP:HA	2:A:301:FMN:C5A	2.48	0.43
1:D:194:GLN:HE21	1:D:194:GLN:C	2.22	0.43
3:A:303:RE8:H6	3:A:303:RE8:OB2	2.18	0.43
3:C:303:RE8:OB2	3:C:303:RE8:H6	2.19	0.43
1:A:180:TYR:CE2	1:A:182:ALA:HB2	2.54	0.42
1:B:141:ALA:HB3	1:B:178:THR:HG22	2.02	0.41
1:A:128:THR:HG22	1:A:130:ASN:N	2.35	0.41
1:A:24:GLU:HG3	1:A:24:GLU:O	2.18	0.41
6:A:418:HOH:O	1:C:78:GLN:NE2	2.43	0.41
1:B:136:LEU:HB2	1:B:173:VAL:O	2.21	0.41
1:D:17:SER:HB3	1:D:20:MET:HB2	2.03	0.41
1:A:136:LEU:HB2	1:A:173:VAL:O	2.21	0.41
1:B:26:PHE:HB2	1:B:204:ALA:HB1	2.03	0.41
1:B:103:TRP:HA	2:B:301:FMN:C5A	2.51	0.40
1:A:69:PHE:CE2	1:A:77:GLN:HG2	2.56	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	208/211 (99%)	204 (98%)	4 (2%)	0	100	100
1	B	208/211 (99%)	204 (98%)	4 (2%)	0	100	100
1	C	208/211 (99%)	204 (98%)	4 (2%)	0	100	100
1	D	208/211 (99%)	201 (97%)	7 (3%)	0	100	100
All	All	832/844 (99%)	813 (98%)	19 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	162/163 (99%)	150 (93%)	12 (7%)	17 13
1	B	162/163 (99%)	143 (88%)	19 (12%)	7 3
1	C	162/163 (99%)	146 (90%)	16 (10%)	10 6
1	D	162/163 (99%)	149 (92%)	13 (8%)	15 11
All	All	648/652 (99%)	588 (91%)	60 (9%)	11 7

All (60) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	GLU
1	A	48	THR
1	A	70	GLU
1	A	88	GLU
1	A	107	TYR
1	A	115	LEU
1	A	117	ASN
1	A	118	VAL
1	A	128	THR
1	A	135	LEU
1	A	136	LEU
1	A	192	LYS
1	B	5	LEU
1	B	15	GLU
1	B	40	VAL
1	B	42	ILE
1	B	48	THR
1	B	99	VAL
1	B	107	TYR
1	B	117	ASN
1	B	118	VAL
1	B	130	ASN
1	B	135	LEU
1	B	136	LEU

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Mol	Chain	Res	Type
1	B	153	GLU
1	B	167	LYS
1	B	173	VAL
1	B	189	ASN
1	B	191	GLU
1	B	194	GLN
1	B	210	ARG
1	C	5	LEU
1	C	36	GLN
1	C	48	THR
1	C	88	GLU
1	C	107	TYR
1	C	110	VAL
1	C	115	LEU
1	C	117	ASN
1	C	123	LYS
1	C	126	LYS
1	C	130	ASN
1	C	135	LEU
1	C	136	LEU
1	C	170	LEU
1	C	189	ASN
1	C	194	GLN
1	D	42	ILE
1	D	48	THR
1	D	107	TYR
1	D	117	ASN
1	D	130	ASN
1	D	135	LEU
1	D	136	LEU
1	D	144	ILE
1	D	153	GLU
1	D	170	LEU
1	D	189	ASN
1	D	194	GLN
1	D	203	ASN

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	36	GLN
1	A	77	GLN

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Mol	Chain	Res	Type
1	A	78	GLN
1	B	84	ASN
1	C	77	GLN
1	C	92	ASN
1	C	130	ASN
1	C	194	GLN
1	D	84	ASN
1	D	92	ASN
1	D	187	ASN
1	D	194	GLN
1	D	203	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

Of 15 ligands modelled in this entry, 7 are monoatomic - leaving 8 for Mogul analysis.

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	301	-	32,33,33	1.53	4 (12%)	34,50,50	1.97	8 (23%)
3	RE8	A	302	-	29,30,30	3.14	9 (31%)	39,44,44	2.84	11 (28%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
3	RE8	A	303	-	29,30,30	3.21	7 (24%)	39,44,44	4.60	9 (23%)
2	FMN	B	301	-	32,33,33	1.49	4 (12%)	34,50,50	2.00	9 (26%)
2	FMN	C	301	-	32,33,33	1.29	4 (12%)	34,50,50	1.91	8 (23%)
3	RE8	C	302	-	29,30,30	3.23	8 (27%)	39,44,44	2.54	9 (23%)
3	RE8	C	303	-	29,30,30	3.23	7 (24%)	39,44,44	3.35	6 (15%)
2	FMN	D	301	-	32,33,33	1.43	4 (12%)	34,50,50	2.15	4 (11%)

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	301	-	-	0/18/18/18	0/3/3/3
3	RE8	A	302	-	-	0/11/11/11	0/4/4/4
3	RE8	A	303	-	-	2/11/11/11	0/4/4/4
2	FMN	B	301	-	-	0/18/18/18	0/3/3/3
2	FMN	C	301	-	-	0/18/18/18	0/3/3/3
3	RE8	C	302	-	-	0/11/11/11	0/4/4/4
3	RE8	C	303	-	-	0/11/11/11	0/4/4/4
2	FMN	D	301	-	-	0/18/18/18	0/3/3/3

All (47) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	303	RE8	C14-SB	-13.64	1.59	1.79
3	C	302	RE8	C14-SB	-13.17	1.60	1.79
3	A	303	RE8	C14-SB	-12.95	1.60	1.79
3	A	302	RE8	C14-SB	-11.71	1.62	1.79
3	C	302	RE8	C11-N2	-4.22	1.37	1.42
3	C	303	RE8	C11-N2	-2.40	1.39	1.42
3	A	303	RE8	C8-C9	2.09	1.41	1.36
3	A	302	RE8	C4-C3	2.27	1.41	1.36
3	A	302	RE8	C13-C14	2.28	1.40	1.37
2	B	301	FMN	C10-N1	2.35	1.39	1.35
3	A	302	RE8	C8-C9	2.39	1.42	1.36
2	C	301	FMN	C1'-N10	2.45	1.51	1.48
3	C	302	RE8	C4-C3	2.46	1.41	1.36
2	D	301	FMN	C1'-N10	2.64	1.51	1.48
2	C	301	FMN	C4-N3	2.71	1.37	1.33
2	A	301	FMN	C5A-N5	2.88	1.39	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	301	FMN	C5A-N5	2.98	1.40	1.35
3	C	302	RE8	C15-C20	3.04	1.49	1.43
2	B	301	FMN	C5A-N5	3.22	1.40	1.35
2	C	301	FMN	C5A-N5	3.29	1.40	1.35
2	A	301	FMN	C4A-N5	3.34	1.38	1.33
2	D	301	FMN	C4-N3	3.39	1.39	1.33
3	C	303	RE8	C15-C20	3.44	1.49	1.43
2	C	301	FMN	C4A-N5	3.54	1.38	1.33
3	C	302	RE8	C11-C20	3.58	1.48	1.42
2	B	301	FMN	C4-N3	3.58	1.39	1.33
3	C	303	RE8	C1-C10	3.66	1.49	1.43
3	C	302	RE8	C1-C10	3.71	1.50	1.43
3	A	303	RE8	C10-C5	3.73	1.49	1.43
2	A	301	FMN	C4-N3	3.99	1.40	1.33
3	C	303	RE8	C10-C5	4.02	1.50	1.43
2	D	301	FMN	C4A-N5	4.03	1.39	1.33
3	A	302	RE8	C15-C20	4.04	1.50	1.43
3	C	302	RE8	C10-C5	4.10	1.50	1.43
3	A	303	RE8	C15-C20	4.20	1.51	1.43
2	A	301	FMN	C1'-N10	4.29	1.53	1.48
3	A	303	RE8	C14-C15	4.36	1.49	1.43
3	A	302	RE8	C10-C5	4.40	1.51	1.43
3	C	303	RE8	C14-C15	4.48	1.50	1.43
3	C	303	RE8	C11-C20	4.57	1.50	1.42
2	B	301	FMN	C4A-N5	4.68	1.40	1.33
3	A	302	RE8	C1-C10	4.72	1.51	1.43
3	A	303	RE8	C11-C20	4.86	1.51	1.42
3	A	302	RE8	C11-C20	4.99	1.51	1.42
3	A	302	RE8	C14-C15	5.12	1.50	1.43
3	A	303	RE8	C1-C10	5.12	1.52	1.43
3	C	302	RE8	C14-C15	5.32	1.51	1.43

All (64) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	303	RE8	C12-C11-N2	-8.74	111.56	124.33
3	C	303	RE8	C12-C11-N2	-6.67	114.58	124.33
3	C	302	RE8	C12-C11-N2	-5.38	116.47	124.33
2	D	301	FMN	N3-C2-N1	-5.33	118.71	127.69
2	C	301	FMN	N3-C2-N1	-4.55	120.02	127.69
2	A	301	FMN	N3-C2-N1	-4.30	120.45	127.69
2	B	301	FMN	N3-C2-N1	-4.26	120.52	127.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	301	FMN	C4A-C4-N3	-3.66	118.73	123.52
3	A	302	RE8	C13-C14-C15	-3.66	117.56	121.00
2	A	301	FMN	C4A-C4-N3	-3.46	119.00	123.52
2	B	301	FMN	C4A-C4-N3	-3.37	119.12	123.52
3	A	302	RE8	C12-C11-N2	-3.25	119.58	124.33
2	C	301	FMN	C4A-C4-N3	-3.01	119.59	123.52
3	C	302	RE8	C11-C20-C15	-2.96	116.58	118.73
3	A	302	RE8	C12-C11-C20	-2.61	116.77	119.75
2	B	301	FMN	O4'-C4'-C5'	-2.35	104.97	110.09
2	B	301	FMN	O5'-P-O1P	-2.24	101.47	107.08
3	A	303	RE8	C13-C14-C15	-2.06	119.06	121.00
3	A	302	RE8	C4-C3-C2	2.01	122.40	120.31
3	C	302	RE8	C19-C20-C15	2.07	121.08	118.50
2	C	301	FMN	C4-C4A-N5	2.14	121.30	118.70
2	A	301	FMN	C4-C4A-N5	2.14	121.30	118.70
2	B	301	FMN	C5A-C9A-N10	2.15	119.19	117.58
2	C	301	FMN	O2'-C2'-C1'	2.21	115.38	109.93
3	C	302	RE8	C10-C1-N1	2.31	121.71	115.63
2	C	301	FMN	C6-C5A-N5	2.31	121.80	118.92
3	C	302	RE8	C4-C3-C2	2.33	122.72	120.31
3	A	303	RE8	C13-C12-C11	2.43	123.72	121.92
3	C	303	RE8	C10-C1-N1	2.44	122.05	115.63
3	A	302	RE8	C10-C1-N1	2.53	122.30	115.63
2	A	301	FMN	C5A-C9A-N10	2.56	119.50	117.58
3	A	303	RE8	C4-C3-C2	2.65	123.06	120.31
2	A	301	FMN	O3P-P-O1P	2.69	119.41	110.63
3	C	303	RE8	OB3-SB-C14	2.83	109.41	106.20
2	C	301	FMN	C5A-C9A-N10	2.92	119.77	117.58
2	B	301	FMN	O2P-P-O5'	2.95	115.33	106.72
2	B	301	FMN	C4-C4A-N5	3.13	122.51	118.70
2	A	301	FMN	C4A-N5-C5A	3.14	120.43	116.72
3	C	302	RE8	C15-C14-SB	3.18	124.57	121.21
2	C	301	FMN	C4A-N5-C5A	3.23	120.53	116.72
3	A	302	RE8	C13-C12-C11	3.30	124.37	121.92
2	A	301	FMN	C1'-N10-C9A	3.32	122.68	118.83
3	A	302	RE8	OB2-SB-C14	3.36	110.01	106.20
3	A	302	RE8	OB3-SB-C14	3.44	110.10	106.20
2	D	301	FMN	C1'-N10-C9A	3.52	122.91	118.83
3	A	303	RE8	C10-C1-N1	3.60	125.11	115.63
2	B	301	FMN	C4A-N5-C5A	3.61	120.97	116.72
3	C	302	RE8	OB3-SB-C14	3.80	110.51	106.20
3	A	303	RE8	C15-C14-SB	3.96	125.40	121.21

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	C	303	RE8	OB2-SB-C14	4.01	110.74	106.20
3	A	303	RE8	OB2-SB-C14	4.36	111.14	106.20
3	C	302	RE8	C20-C11-N2	6.38	121.00	115.91
2	B	301	FMN	C4-N3-C2	6.42	120.51	115.16
2	A	301	FMN	C4-N3-C2	6.44	120.53	115.16
2	C	301	FMN	C4-N3-C2	6.75	120.79	115.16
3	A	302	RE8	C1-N1-N2	8.00	129.07	116.10
3	A	302	RE8	C11-N2-N1	8.10	120.93	114.32
2	D	301	FMN	C4-N3-C2	8.58	122.31	115.16
3	A	302	RE8	C20-C11-N2	9.51	123.50	115.91
3	C	302	RE8	C11-N2-N1	10.53	122.92	114.32
3	C	303	RE8	C20-C11-N2	10.99	124.68	115.91
3	C	303	RE8	C11-N2-N1	14.63	126.26	114.32
3	A	303	RE8	C20-C11-N2	17.45	129.83	115.91
3	A	303	RE8	C11-N2-N1	18.80	129.66	114.32

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	303	RE8	C12-C11-N2-N1
3	A	303	RE8	C20-C11-N2-N1

There are no ring outliers.

6 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	FMN	1	0
3	A	303	RE8	2	0
2	B	301	FMN	1	0
2	C	301	FMN	1	0
3	C	303	RE8	2	0
2	D	301	FMN	1	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, 95^{th} 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	210/211 (99%)	-0.03	8 (3%)	44	53	12, 21, 48, 73	0
1	B	210/211 (99%)	-0.01	4 (1%)	70	75	14, 23, 41, 70	0
1	C	210/211 (99%)	-0.07	5 (2%)	62	68	11, 20, 43, 69	0
1	D	210/211 (99%)	-0.03	6 (2%)	55	63	12, 22, 45, 66	0
All	All	840/844 (99%)	-0.04	23 (2%)	58	65	11, 22, 45, 73	0

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	130	ASN	5.7
1	B	66	GLY	4.7
1	C	129	GLU	4.7
1	B	130	ASN	4.0
1	C	67	GLU	3.7
1	A	64	ALA	3.6
1	A	129	GLU	3.5
1	D	70	GLU	3.4
1	D	66	GLY	3.2
1	A	66	GLY	3.0
1	B	36	GLN	2.5
1	C	64	ALA	2.5
1	C	130	ASN	2.4
1	A	15	GLU	2.4
1	D	69	PHE	2.3
1	A	194	GLN	2.3
1	D	65	ALA	2.3
1	D	67	GLU	2.3
1	A	63	PHE	2.2
1	B	64	ALA	2.2
1	C	192	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	D	129	GLU	2.1
1	A	128	THR	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, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
3	RE8	A	303	27/27	0.78	0.26	5.64	52,59,77,78	0
3	RE8	A	302	27/27	0.74	0.25	4.34	41,47,56,59	0
3	RE8	C	303	27/27	0.73	0.27	4.20	53,63,75,77	0
5	K	B	302	1/1	0.94	0.17	4.15	56,56,56,56	0
3	RE8	C	302	27/27	0.87	0.19	4.14	39,46,59,61	0
5	K	C	305	1/1	0.98	0.11	0.70	47,47,47,47	0
2	FMN	A	301	31/31	0.97	0.10	0.44	15,17,20,20	0
2	FMN	C	301	31/31	0.97	0.10	-0.14	15,17,20,21	0
2	FMN	D	301	31/31	0.97	0.10	-0.14	17,19,21,21	0
2	FMN	B	301	31/31	0.97	0.09	-0.59	17,20,22,23	0
5	K	A	305	1/1	0.99	0.05	-	43,43,43,43	0
4	CA	A	304	1/1	0.88	0.12	-	66,66,66,66	0
5	K	C	307	1/1	0.93	0.07	-	43,43,43,43	0
4	CA	C	304	1/1	0.98	0.04	-	47,47,47,47	0
4	CA	C	306	1/1	0.95	0.05	-	49,49,49,49	0

6.5 Other polymers (i)

There are no such residues in this entry.