Full wwPDB X-ray Structure Validation Report (i)

Jun 9, 2016 – 02:51 PM EDT

PDB ID	:	5FJN
Title	:	Structure of L-Amino acid deaminase from Proteus myxofaciens in complex with anthranilate
Authors	:	Motta, P.; Molla, G.; Pollegioni, L.; Nardini, M.
Deposited on	:	2015-10-11
Resolution	:	1.75 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:

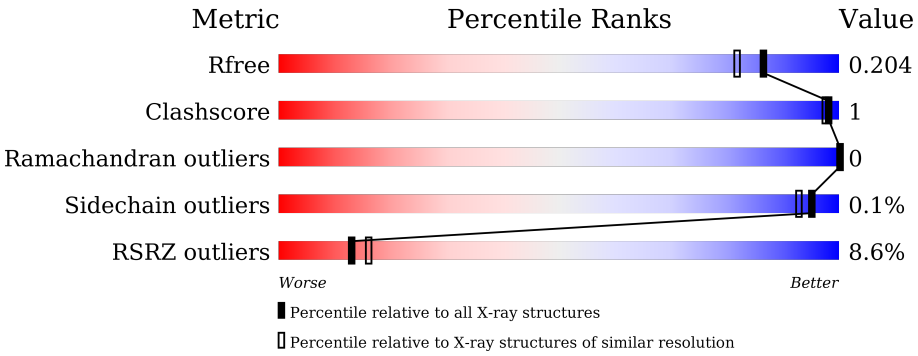
MolProbity	:	4.02b-467
Mogul	:	1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20027674
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20027674

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 1.75 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	1609 (1.76-1.76)
Clashscore	102246	1730 (1.76-1.76)
Ramachandran outliers	100387	1711 (1.76-1.76)
Sidechain outliers	100360	1711 (1.76-1.76)
RSRZ outliers	91569	1610 (1.76-1.76)

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	456	9% 96%
1	B	456	8% 96%

2 Entry composition

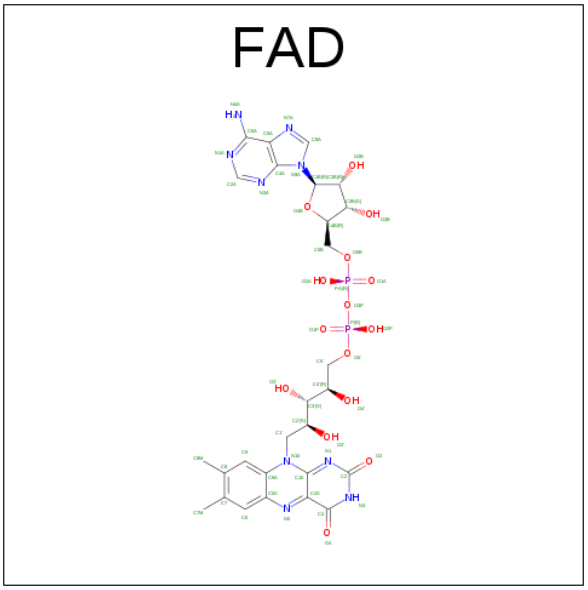
There are 4 unique types of molecules in this entry. The entry contains 7620 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 L-AMINO ACID DEAMINASE.

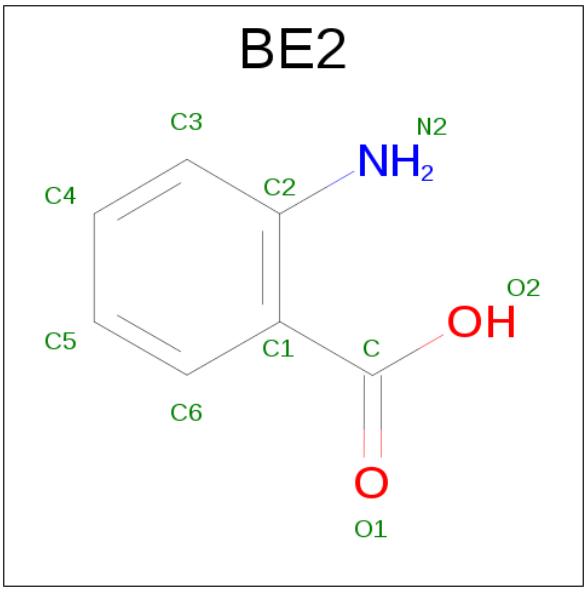
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	447	Total	C	N	O	S	0	4	0
			3464	2202	592	659	11			
1	B	447	Total	C	N	O	S	0	7	0
			3480	2214	592	663	11			

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



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

- Molecule 3 is 2-AMINOBENZOIC ACID (three-letter code: BE2) (formula: $C_7H_7NO_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O 10 7 1 2	0	0
3	B	1	Total C N O 10 7 1 2	0	0

- Molecule 4 is water.

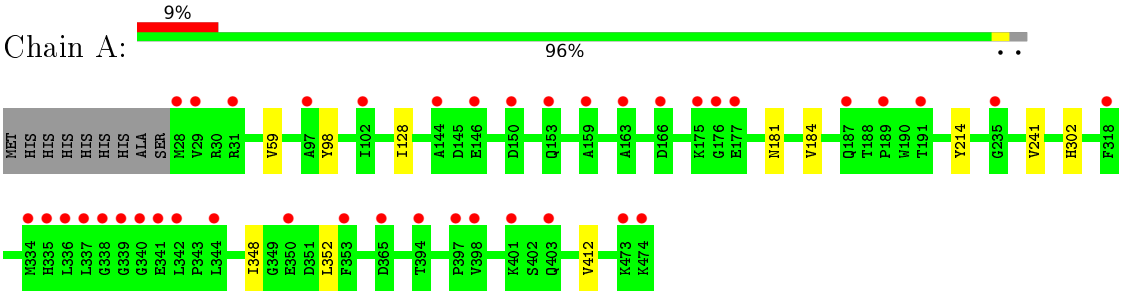
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	263	Total O 267 267	0	4
4	B	279	Total O 283 283	0	4

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.

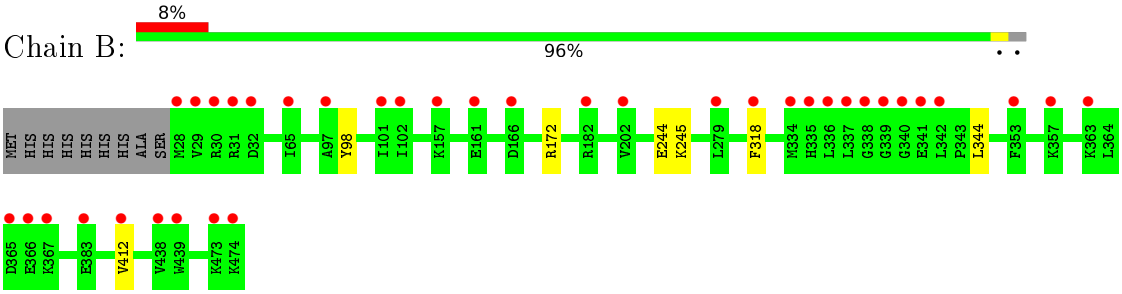
- Molecule 1: L-AMINO ACID DEAMINASE

Chain A:



- Molecule 1: L-AMINO ACID DEAMINASE

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	72.81Å 93.32Å 75.07Å 90.00° 103.22° 90.00°	Depositor
Resolution (Å)	41.19 – 1.75 39.33 – 1.75	Depositor EDS
% Data completeness (in resolution range)	97.9 (41.19-1.75) 97.9 (39.33-1.75)	Depositor EDS
R_{merge}	0.03	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.88 (at 1.75Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.156 , 0.197 0.166 , 0.204	Depositor DCC
R_{free} test set	4818 reflections (5.26%)	DCC
Wilson B-factor (Å^2)	31.6	Xtriage
Anisotropy	0.060	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 41.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.022 for l,-k,h	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	7620	wwPDB-VP
Average B, all atoms (Å^2)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.30% 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: BE2, 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	0.29	0/3550	0.52	0/4811
1	B	0.30	0/3575	0.54	0/4845
All	All	0.30	0/7125	0.53	0/9656

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

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	3464	0	3473	8	0
1	B	3480	0	3494	6	0
2	A	53	0	31	4	0
2	B	53	0	31	3	0
3	A	10	0	6	0	0
3	B	10	0	6	0	0
4	A	267	0	0	0	0
4	B	283	0	0	1	0
All	All	7620	0	7041	14	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 1.

All (14) 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:181:ASN:O	1:A:184:VAL:HG13	1.90	0.71
1:B:412:VAL:HG13	2:B:500:FAD:C8M	2.31	0.60
1:A:412:VAL:HG13	2:A:500:FAD:C8M	2.33	0.59
1:A:128[A]:ILE:HG13	1:A:214:TYR:CG	2.40	0.57
1:A:98:TYR:H	2:A:500:FAD:C6	2.20	0.53
1:B:412:VAL:HG13	2:B:500:FAD:HM83	1.90	0.53
1:A:59:VAL:HG11	1:A:241:VAL:HG21	1.92	0.51
1:B:98:TYR:H	2:B:500:FAD:C6	2.26	0.49
1:A:412:VAL:HG13	2:A:500:FAD:HM81	1.96	0.47
1:B:172:ARG:HD2	4:B:2148:HOH:O	2.17	0.44
1:B:318:PHE:HB2	1:B:344:LEU:HD12	2.00	0.43
1:A:412:VAL:HG13	2:A:500:FAD:HM83	2.00	0.43
1:A:348:ILE:HD11	1:A:352:LEU:HD22	2.03	0.40
1:B:244:GLU:HG3	1:B:245:LYS:HG3	2.02	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	449/456 (98%)	434 (97%)	15 (3%)	0	100	100
1	B	452/456 (99%)	436 (96%)	16 (4%)	0	100	100
All	All	901/912 (99%)	870 (97%)	31 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	373/377 (99%)	372 (100%)	1 (0%)	94 92
1	B	376/377 (100%)	376 (100%)	0	100 100
All	All	749/754 (99%)	748 (100%)	1 (0%)	95 93

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	302	HIS

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

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	$\#\|Z\| > 2$
3	BE2	A	1476	-	7,10,10	2.34	1 (14%)	8,13,13	0.39	0
2	FAD	A	500	-	52,58,58	1.32	7 (13%)	52,89,89	2.25	11 (21%)
3	BE2	B	1476	-	7,10,10	2.34	1 (14%)	8,13,13	0.36	0
2	FAD	B	500	-	52,58,58	1.33	7 (13%)	52,89,89	2.29	11 (21%)

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	BE2	A	1476	-	-	0/0/4/4	0/1/1/1
2	FAD	A	500	-	-	0/30/50/50	0/6/6/6
3	BE2	B	1476	-	-	0/0/4/4	0/1/1/1
2	FAD	B	500	-	-	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)
2	A	500	FAD	C1'-N10	-2.26	1.46	1.48
2	B	500	FAD	C4X-N5	2.51	1.37	1.33
2	B	500	FAD	C9A-N10	2.54	1.42	1.38
2	A	500	FAD	C9A-N10	2.62	1.42	1.38
2	B	500	FAD	C8-C7	2.76	1.48	1.41
2	B	500	FAD	C5A-C4A	2.79	1.46	1.40
2	A	500	FAD	C8-C7	2.89	1.48	1.41
2	A	500	FAD	C5A-C4A	2.93	1.47	1.40
2	A	500	FAD	C4-C4X	2.99	1.47	1.41
2	B	500	FAD	C9A-C5X	3.26	1.49	1.42
2	A	500	FAD	C9A-C5X	3.40	1.49	1.42
2	B	500	FAD	C4-C4X	3.56	1.48	1.41
2	A	500	FAD	C4X-C10	3.65	1.47	1.40
2	B	500	FAD	C4X-C10	3.84	1.47	1.40
3	B	1476	BE2	C1-C2	6.12	1.49	1.41
3	A	1476	BE2	C1-C2	6.12	1.49	1.41

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	500	FAD	N3A-C2A-N1A	-7.62	122.89	128.87
2	B	500	FAD	N3A-C2A-N1A	-7.45	123.02	128.87
2	B	500	FAD	C4-C4X-C10	-6.72	115.64	119.94
2	A	500	FAD	C4-C4X-C10	-6.40	115.84	119.94
2	B	500	FAD	C4X-C4-N3	-3.26	119.26	123.52
2	A	500	FAD	C4X-C4-N3	-3.21	119.32	123.52
2	B	500	FAD	N3-C2-N1	-3.13	122.43	127.69
2	A	500	FAD	N3-C2-N1	-3.13	122.43	127.69
2	B	500	FAD	C4X-C10-N10	-2.90	118.41	120.52
2	B	500	FAD	C1B-N9A-C4A	-2.77	123.71	126.81
2	A	500	FAD	C4X-C10-N10	-2.34	118.82	120.52
2	A	500	FAD	C1B-N9A-C4A	-2.33	124.21	126.81
2	A	500	FAD	C5X-C9A-N10	2.15	119.19	117.58
2	B	500	FAD	N6A-C6A-N1A	2.25	122.30	118.52
2	A	500	FAD	C4-C4X-N5	2.61	121.88	118.70
2	B	500	FAD	C1'-N10-C9A	2.90	122.20	118.83
2	A	500	FAD	C4X-N5-C5X	3.06	120.33	116.72
2	B	500	FAD	C4-C4X-N5	3.40	122.83	118.70
2	B	500	FAD	C4X-N5-C5X	3.52	120.87	116.72
2	A	500	FAD	C1'-N10-C9A	3.73	123.16	118.83
2	A	500	FAD	C4-N3-C2	8.01	121.84	115.16
2	B	500	FAD	C4-N3-C2	8.19	121.99	115.16

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	500	FAD	4	0
2	B	500	FAD	3	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

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	447/456 (98%)	0.36	40 (8%)	12 14	22, 35, 61, 113	0
1	B	447/456 (98%)	0.44	37 (8%)	14 17	20, 31, 55, 113	0
All	All	894/912 (98%)	0.40	77 (8%)	13 16	20, 33, 60, 113	0

All (77) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	337	LEU	20.4
1	B	337	LEU	14.7
1	B	28	MET	14.6
1	B	342	LEU	11.2
1	B	338	GLY	10.9
1	A	341	GLU	9.5
1	A	342	LEU	9.3
1	A	338	GLY	8.6
1	B	474	LYS	8.6
1	B	341	GLU	8.5
1	A	474	LYS	7.8
1	B	340	GLY	7.4
1	A	235	GLY	7.1
1	A	29	VAL	6.6
1	B	29	VAL	6.4
1	B	31	ARG	5.8
1	B	32	ASP	5.6
1	A	28	MET	5.6
1	A	339	GLY	5.5
1	A	340	GLY	5.2
1	B	336	LEU	4.9
1	A	336	LEU	4.8
1	B	353	PHE	4.2
1	A	353	PHE	3.9

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Mol	Chain	Res	Type	RSRZ
1	A	176	GLY	3.8
1	A	318	PHE	3.7
1	B	97	ALA	3.5
1	B	363	LYS	3.5
1	A	189	PRO	3.5
1	A	398	VAL	3.5
1	B	318	PHE	3.5
1	B	365	ASP	3.4
1	A	146	GLU	3.3
1	A	144	ALA	3.2
1	B	202	VAL	3.1
1	A	150	ASP	3.0
1	B	30	ARG	3.0
1	A	344	LEU	3.0
1	A	473	LYS	2.9
1	B	339	GLY	2.9
1	B	473	LYS	2.9
1	A	177	GLU	2.9
1	A	403	GLN	2.7
1	B	65[A]	ILE	2.7
1	B	161	GLU	2.7
1	B	367	LYS	2.7
1	B	366	GLU	2.6
1	B	335	HIS	2.6
1	A	394	THR	2.6
1	B	334	MET	2.6
1	A	175	LYS	2.5
1	A	166	ASP	2.5
1	A	97	ALA	2.5
1	A	397	PRO	2.5
1	B	412	VAL	2.4
1	B	102	ILE	2.4
1	A	334	MET	2.4
1	B	101	ILE	2.4
1	A	102	ILE	2.3
1	B	438	VAL	2.3
1	A	153	GLN	2.3
1	B	383	GLU	2.3
1	B	279	LEU	2.2
1	B	166	ASP	2.2
1	A	335	HIS	2.2
1	A	350	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	401	LYS	2.2
1	A	191	THR	2.2
1	B	357	LYS	2.1
1	B	182[A]	ARG	2.1
1	A	159	ALA	2.1
1	A	163	ALA	2.1
1	A	31	ARG	2.0
1	A	187	GLN	2.0
1	B	157	LYS	2.0
1	A	365	ASP	2.0
1	B	439	TRP	2.0

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
2	FAD	B	500	53/53	0.97	0.15	0.11	19,21,24,26	0
3	BE2	A	1476	10/10	0.90	0.12	0.02	41,45,49,55	0
2	FAD	A	500	53/53	0.97	0.10	-0.01	21,23,27,31	0
3	BE2	B	1476	10/10	0.92	0.13	-1.75	31,38,41,41	0

6.5 Other polymers (i)

There are no such residues in this entry.