



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 11:11 pm GMT

PDB ID : 3AB1
Title : Crystal Structure of Ferredoxin NADP+ Oxidoreductase
Authors : Muraki, N.; Seo, D.; Kurisu, G.
Deposited on : 2009-11-30
Resolution : 2.39 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 ⓘ 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

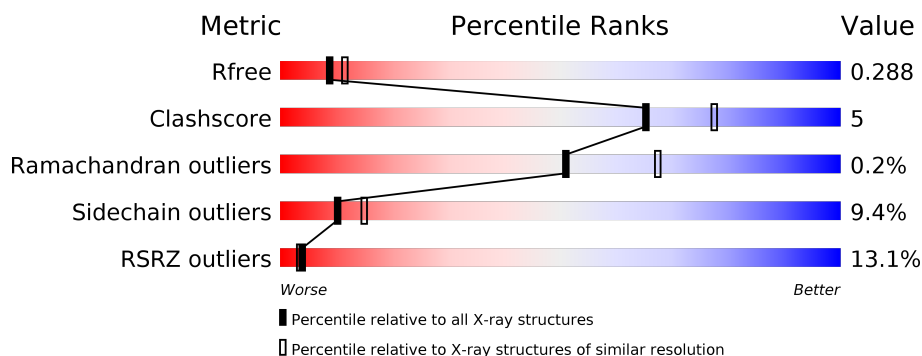
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION



The reported resolution of this entry is 2.39 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	3166 (2.40-2.40)
Clashscore	112137	3674 (2.40-2.40)
Ramachandran outliers	110173	3616 (2.40-2.40)
Sidechain outliers	110143	3617 (2.40-2.40)
RSRZ outliers	101464	3195 (2.40-2.40)

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	360	 <p>9% 73% 14% • 12%</p>
1	B	360	 <p>15% 79% 12% • 7%</p>

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 5216 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 Ferredoxin–NADP reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	318	Total	C	N	O	S	0	0	0
			2438	1543	422	466	7			
1	B	336	Total	C	N	O	S	0	0	0
			2575	1629	447	491	8			

- 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		

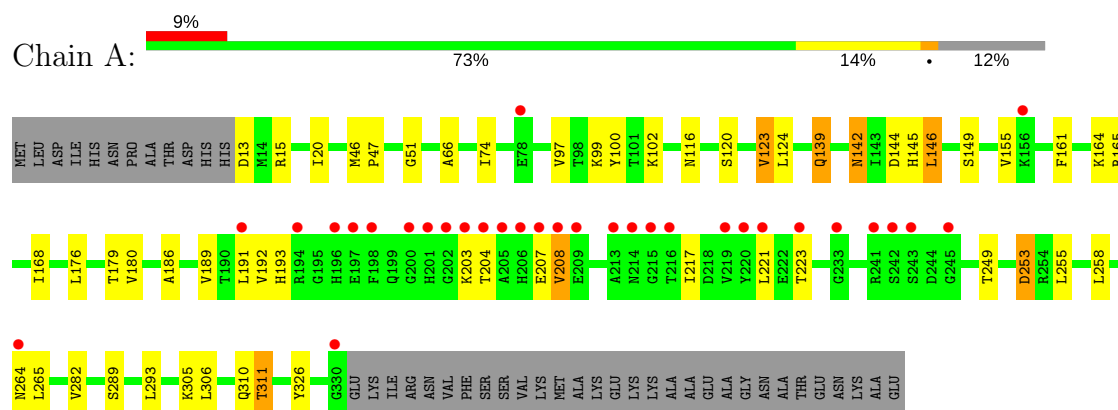
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	48	Total 48	O 48	0	0
3	B	49	Total 49	O 49	0	0

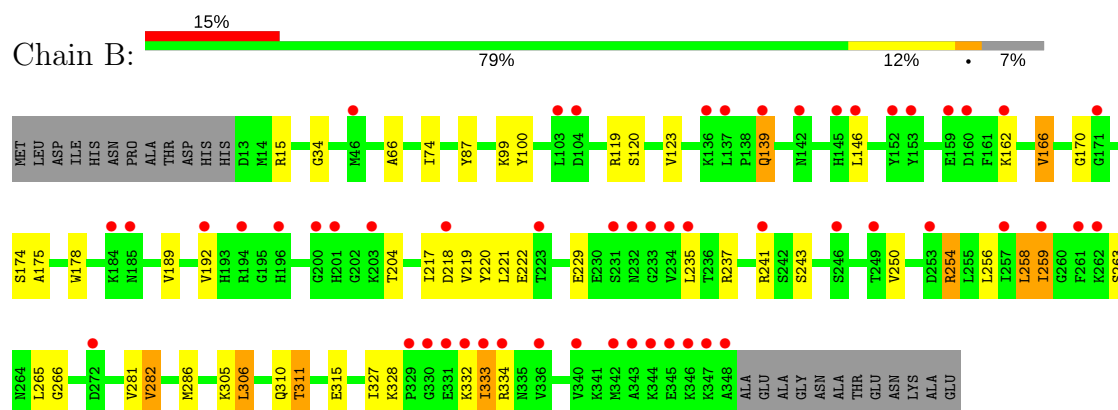
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: Ferredoxin–NADP reductase



• Molecule 1: Ferredoxin–NADP reductase



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	100.51Å 127.97Å 128.35Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.57 – 2.39 39.57 – 2.39	Depositor EDS
% Data completeness (in resolution range)	99.5 (39.57-2.39) 99.6 (39.57-2.39)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.11 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.240 , 0.289 0.238 , 0.288	Depositor DCC
R_{free} test set	1668 reflections (5.34%)	DCC
Wilson B-factor (Å ²)	39.8	Xtriage
Anisotropy	0.098	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 42.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	5216	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.58% 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: 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	0.40	0/2486	0.56	0/3374
1	B	0.41	0/2624	0.57	0/3557
All	All	0.41	0/5110	0.57	0/6931

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	2438	0	2426	27	0
1	B	2575	0	2567	21	0
2	A	53	0	31	1	0
2	B	53	0	31	0	0
3	A	48	0	0	0	0
3	B	49	0	0	0	0
All	All	5216	0	5055	48	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 5.

All (48) 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:66:ALA:H	1:B:310:GLN:HE22	1.21	0.87
1:B:139:GLN:H	1:B:139:GLN:HE21	1.27	0.78
1:A:139:GLN:HE21	1:A:139:GLN:H	1.30	0.77
1:A:123:VAL:HG22	1:A:293:LEU:HD12	1.68	0.73
1:A:306:LEU:O	1:A:311:THR:HG21	1.90	0.71
1:A:66:ALA:H	1:A:310:GLN:HE22	1.40	0.70
1:A:123:VAL:HG22	1:A:293:LEU:CD1	2.30	0.61
1:B:66:ALA:H	1:B:310:GLN:NE2	1.95	0.60
1:A:15:ARG:O	1:A:120:SER:HA	2.02	0.58
1:A:264:ASN:OD1	1:A:265:LEU:N	2.39	0.56
1:A:176:LEU:HG	1:A:208:VAL:HG11	1.88	0.56
1:B:222:GLU:HB3	1:B:243:SER:HB2	1.91	0.53
1:B:333:ILE:H	1:B:333:ILE:HD13	1.74	0.51
1:A:168:ILE:HD12	1:A:179:THR:HG22	1.92	0.50
1:B:306:LEU:O	1:B:311:THR:HG21	2.11	0.50
1:B:34:GLY:HA3	1:B:87:TYR:CD2	2.47	0.48
1:B:218:ASP:HB3	1:B:220:TYR:CE1	2.49	0.48
1:A:142:ASN:C	1:A:142:ASN:HD22	2.16	0.48
1:B:305:LYS:NZ	1:B:311:THR:HG22	2.29	0.47
1:B:175:ALA:HA	1:B:258:LEU:HD23	1.95	0.46
1:A:179:THR:HG21	1:A:191:LEU:HB2	1.98	0.46
1:A:155:VAL:HG13	1:A:161:PHE:CE2	2.51	0.45
1:A:142:ASN:C	1:A:142:ASN:ND2	2.71	0.44
1:A:102:LYS:HE3	1:A:326:TYR:OH	2.17	0.44
1:B:256:LEU:HG	1:B:258:LEU:HD22	1.98	0.44
1:A:99:LYS:HG2	1:A:100:TYR:H	1.83	0.44
1:B:229:GLU:HB2	1:B:237:ARG:HB2	2.00	0.44
1:B:282:VAL:HG13	1:B:286:MET:HA	2.00	0.44
1:A:204:THR:O	1:A:208:VAL:HG13	2.18	0.43
1:B:99:LYS:HD2	1:B:100:TYR:H	1.83	0.43
1:A:99:LYS:HG2	1:A:100:TYR:N	2.34	0.43
1:A:142:ASN:ND2	1:A:144:ASP:H	2.16	0.43
1:A:51:GLY:HA2	2:A:361:FAD:O3B	2.19	0.42
1:B:189:VAL:HB	1:B:217:ILE:HG22	2.01	0.42
1:A:145:HIS:CD2	1:A:146:LEU:HD13	2.55	0.42
1:A:165:ARG:O	1:A:253:ASP:N	2.44	0.42
1:B:15:ARG:O	1:B:120:SER:HA	2.19	0.42
1:B:311:THR:HG23	1:B:315:GLU:OE1	2.19	0.42
1:A:46:MET:HB3	1:A:47:PRO:CD	2.50	0.42
1:A:203:LYS:HG2	1:A:203:LYS:H	1.65	0.41
1:B:170:GLY:HA2	1:B:259:ILE:HG22	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:20:ILE:HG12	1:A:97:VAL:HG21	2.01	0.41
1:A:193:HIS:HB3	1:A:221:LEU:HD23	2.03	0.41
1:A:164:LYS:O	1:A:186:ALA:HB1	2.21	0.41
1:B:327:ILE:HG22	1:B:328:LYS:HG3	2.02	0.41
1:A:189:VAL:HB	1:A:217:ILE:HG22	2.03	0.41
1:B:218:ASP:HB3	1:B:220:TYR:HE1	1.86	0.40
1:B:166:VAL:HB	1:B:254:ARG:HB3	2.04	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	316/360 (88%)	306 (97%)	10 (3%)	0	100	100
1	B	334/360 (93%)	321 (96%)	12 (4%)	1 (0%)	44	60
All	All	650/720 (90%)	627 (96%)	22 (3%)	1 (0%)	51	67

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	266	GLY

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	258/292 (88%)	236 (92%)	22 (8%)	12	19
1	B	272/292 (93%)	244 (90%)	28 (10%)	8	12
All	All	530/584 (91%)	480 (91%)	50 (9%)	10	15

All (50) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	ASP
1	A	74	ILE
1	A	116	ASN
1	A	123	VAL
1	A	124	LEU
1	A	139	GLN
1	A	142	ASN
1	A	146	LEU
1	A	149	SER
1	A	180	VAL
1	A	192	VAL
1	A	207	GLU
1	A	208	VAL
1	A	223	THR
1	A	249	THR
1	A	253	ASP
1	A	255	LEU
1	A	258	LEU
1	A	282	VAL
1	A	289	SER
1	A	305	LYS
1	A	311	THR
1	B	74	ILE
1	B	119	ARG
1	B	123	VAL
1	B	139	GLN
1	B	146	LEU
1	B	162	LYS
1	B	166	VAL
1	B	174	SER
1	B	178	TRP
1	B	192	VAL
1	B	204	THR
1	B	219	VAL
1	B	221	LEU

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Mol	Chain	Res	Type
1	B	235	LEU
1	B	241	ARG
1	B	250	VAL
1	B	254	ARG
1	B	258	LEU
1	B	259	ILE
1	B	263	SER
1	B	265	LEU
1	B	281	VAL
1	B	282	VAL
1	B	306	LEU
1	B	311	THR
1	B	332	LYS
1	B	333	ILE
1	B	334	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	94	ASN
1	A	116	ASN
1	A	139	GLN
1	A	142	ASN
1	A	199	GLN
1	A	239	HIS
1	A	310	GLN
1	B	32	GLN
1	B	37	ASN
1	B	94	ASN
1	B	116	ASN
1	B	139	GLN
1	B	201	HIS
1	B	264	ASN
1	B	310	GLN

5.3.3 RNA ⓘ

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](#)

2 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	FAD	A	361	-	51,58,58	1.29	7 (13%)	54,89,89	2.01	7 (12%)
2	FAD	B	361	-	51,58,58	1.41	7 (13%)	54,89,89	1.93	6 (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	FAD	A	361	-	-	0/28/50/50	0/6/6/6
2	FAD	B	361	-	-	0/28/50/50	0/6/6/6

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	361	FAD	C5X-N5	2.16	1.38	1.35
2	A	361	FAD	C5X-N5	2.29	1.38	1.35
2	A	361	FAD	C2A-N1A	2.53	1.38	1.33
2	A	361	FAD	C1'-N10	2.65	1.51	1.48
2	B	361	FAD	C2A-N1A	2.85	1.39	1.33
2	A	361	FAD	C4-N3	3.00	1.38	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	361	FAD	C1'-N10	3.05	1.51	1.48
2	B	361	FAD	C4-N3	3.14	1.38	1.33
2	A	361	FAD	C4X-N5	3.53	1.38	1.33
2	A	361	FAD	C10-N1	3.58	1.38	1.33
2	A	361	FAD	C2A-N3A	3.63	1.38	1.32
2	B	361	FAD	C4X-N5	3.79	1.38	1.33
2	B	361	FAD	C10-N1	3.95	1.38	1.33
2	B	361	FAD	C2A-N3A	4.38	1.39	1.32

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	361	FAD	N3A-C2A-N1A	-11.11	119.18	128.86
2	B	361	FAD	N3A-C2A-N1A	-10.63	119.60	128.86
2	A	361	FAD	C4X-C4-N3	-2.77	119.54	123.48
2	A	361	FAD	C4A-C5A-N7A	-2.49	107.01	109.41
2	B	361	FAD	C4X-C4-N3	-2.21	120.33	123.48
2	A	361	FAD	C1'-N10-C9A	2.39	120.54	118.35
2	A	361	FAD	C5X-C9A-N10	2.47	119.49	117.66
2	B	361	FAD	C4X-N5-C5X	2.94	119.86	116.76
2	B	361	FAD	C5X-C9A-N10	3.34	120.14	117.66
2	A	361	FAD	C4X-N5-C5X	3.49	120.45	116.76
2	B	361	FAD	C1'-N10-C9A	3.50	121.55	118.35
2	B	361	FAD	C4-N3-C2	5.35	119.83	115.16
2	A	361	FAD	C4-N3-C2	5.53	119.99	115.16

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	361	FAD	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, 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	318/360 (88%)	0.82	32 (10%) 8 7	23, 42, 70, 86	2 (0%)
1	B	336/360 (93%)	0.86	54 (16%) 2 2	22, 43, 69, 86	1 (0%)
All	All	654/720 (90%)	0.84	86 (13%) 4 3	22, 43, 70, 86	3 (0%)

All (86) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	200	GLY	10.1
1	A	205	ALA	9.3
1	B	330	GLY	5.9
1	A	206	HIS	5.8
1	B	234	VAL	5.4
1	A	78	GLU	5.1
1	A	330	GLY	5.0
1	B	348	ALA	4.8
1	B	185	ASN	4.5
1	A	216	THR	4.5
1	B	232	ASN	4.2
1	A	208	VAL	4.0
1	B	334	ARG	3.9
1	B	46	MET	3.9
1	B	347	LYS	3.8
1	B	235	LEU	3.7
1	A	196	HIS	3.7
1	A	215	GLY	3.6
1	A	201	HIS	3.5
1	B	332	LYS	3.4
1	B	200	GLY	3.4
1	B	201	HIS	3.4
1	B	343	ALA	3.4
1	B	329	PRO	3.4

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Mol	Chain	Res	Type	RSRZ
1	B	336	VAL	3.3
1	B	345	GLU	3.3
1	A	214	ASN	3.3
1	B	333	ILE	3.3
1	B	152	TYR	3.2
1	B	196	HIS	3.2
1	B	104	ASP	3.2
1	B	241	ARG	3.2
1	A	243	SER	3.1
1	A	198	PHE	3.1
1	A	220	TYR	3.1
1	B	340	VAL	3.1
1	B	159	GLU	3.0
1	B	231	SER	3.0
1	B	145	HIS	2.9
1	B	160	ASP	2.9
1	B	142	ASN	2.8
1	A	202	GLY	2.8
1	B	246	SER	2.8
1	A	204	THR	2.8
1	A	194	ARG	2.8
1	B	103	LEU	2.7
1	B	331	GLU	2.7
1	A	213	ALA	2.7
1	B	259	ILE	2.7
1	B	261	PHE	2.7
1	B	137	LEU	2.7
1	B	184	LYS	2.7
1	A	197	GLU	2.6
1	B	194	ARG	2.6
1	A	219	VAL	2.6
1	B	223	THR	2.6
1	A	245	GLY	2.6
1	B	139	GLN	2.5
1	B	171	GLY	2.5
1	B	249	THR	2.4
1	B	153	TYR	2.4
1	B	136	LYS	2.4
1	A	207	GLU	2.4
1	B	346	LYS	2.4
1	A	221	LEU	2.4
1	B	146	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	241	ARG	2.4
1	B	162	LYS	2.4
1	A	156	LYS	2.4
1	A	209	GLU	2.3
1	A	223	THR	2.3
1	B	344	LYS	2.3
1	A	191	LEU	2.2
1	B	253	ASP	2.2
1	A	203	LYS	2.2
1	A	242	SER	2.1
1	B	233	GLY	2.1
1	A	233	GLY	2.1
1	B	342	MET	2.1
1	B	257	ILE	2.1
1	B	272	ASP	2.1
1	A	264	ASN	2.1
1	B	262	LYS	2.1
1	B	192	VAL	2.0
1	B	218	ASP	2.0
1	B	203	LYS	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, 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	FAD	A	361	53/53	0.95	0.17	-0.04	27,30,39,39	0
2	FAD	B	361	53/53	0.98	0.12	-0.66	18,25,26,26	0

6.5 Other polymers ⓘ

There are no such residues in this entry.