



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 05:58 AM UTC

PDB ID : 4XGW / pdb_00004xgw
Title : Crystal structure of Escherichia coli Flavin trafficking protein, an FMN transferase, E169K mutant
Authors : Tomchick, D.R.; Brautigam, C.A.; Deka, R.K.; Norgard, M.V.
Deposited on : 2015-01-02
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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

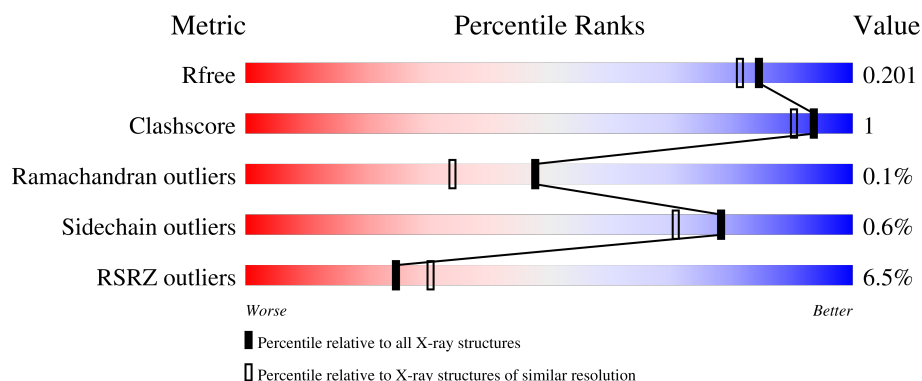
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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}	180053	1187 (1.74-1.74)
Clashscore	190562	1207 (1.74-1.74)
Ramachandran outliers	187476	1200 (1.74-1.74)
Sidechain outliers	187428	1200 (1.74-1.74)
RSRZ outliers	180081	1188 (1.74-1.74)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	340	6% 87% 11%
1	B	340	6% 87% 9%
1	C	340	7% 87% 10%
1	D	340	5% 86% 11%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 19641 atoms, of which 9481 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 FAD:protein FMN transferase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	304	Total	C	H	N	O	S	0	3	0
			4704	1484	2347	404	459	10			
1	B	308	Total	C	H	N	O	S	0	0	0
			4757	1501	2377	409	460	10			
1	C	307	Total	C	H	N	O	S	0	2	0
			4766	1501	2386	409	460	10			
1	D	303	Total	C	H	N	O	S	0	3	0
			4688	1473	2347	404	454	10			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP P0AB85
A	169	LYS	GLU	engineered mutation	UNP P0AB85
A	333	LEU	-	expression tag	UNP P0AB85
A	334	GLU	-	expression tag	UNP P0AB85
A	335	HIS	-	expression tag	UNP P0AB85
A	336	HIS	-	expression tag	UNP P0AB85
A	337	HIS	-	expression tag	UNP P0AB85
A	338	HIS	-	expression tag	UNP P0AB85
A	339	HIS	-	expression tag	UNP P0AB85
A	340	HIS	-	expression tag	UNP P0AB85
B	1	MET	-	initiating methionine	UNP P0AB85
B	169	LYS	GLU	engineered mutation	UNP P0AB85
B	333	LEU	-	expression tag	UNP P0AB85
B	334	GLU	-	expression tag	UNP P0AB85
B	335	HIS	-	expression tag	UNP P0AB85
B	336	HIS	-	expression tag	UNP P0AB85
B	337	HIS	-	expression tag	UNP P0AB85
B	338	HIS	-	expression tag	UNP P0AB85
B	339	HIS	-	expression tag	UNP P0AB85
B	340	HIS	-	expression tag	UNP P0AB85
C	1	MET	-	initiating methionine	UNP P0AB85

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Chain	Residue	Modelled	Actual	Comment	Reference
C	169	LYS	GLU	engineered mutation	UNP P0AB85
C	333	LEU	-	expression tag	UNP P0AB85
C	334	GLU	-	expression tag	UNP P0AB85
C	335	HIS	-	expression tag	UNP P0AB85
C	336	HIS	-	expression tag	UNP P0AB85
C	337	HIS	-	expression tag	UNP P0AB85
C	338	HIS	-	expression tag	UNP P0AB85
C	339	HIS	-	expression tag	UNP P0AB85
C	340	HIS	-	expression tag	UNP P0AB85
D	1	MET	-	initiating methionine	UNP P0AB85
D	169	LYS	GLU	engineered mutation	UNP P0AB85
D	333	LEU	-	expression tag	UNP P0AB85
D	334	GLU	-	expression tag	UNP P0AB85
D	335	HIS	-	expression tag	UNP P0AB85
D	336	HIS	-	expression tag	UNP P0AB85
D	337	HIS	-	expression tag	UNP P0AB85
D	338	HIS	-	expression tag	UNP P0AB85
D	339	HIS	-	expression tag	UNP P0AB85
D	340	HIS	-	expression tag	UNP P0AB85

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

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

- Molecule 3 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Na 1 1	0	0
3	C	1	Total Na 1 1	0	0
3	D	1	Total Na 1 1	0	0

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



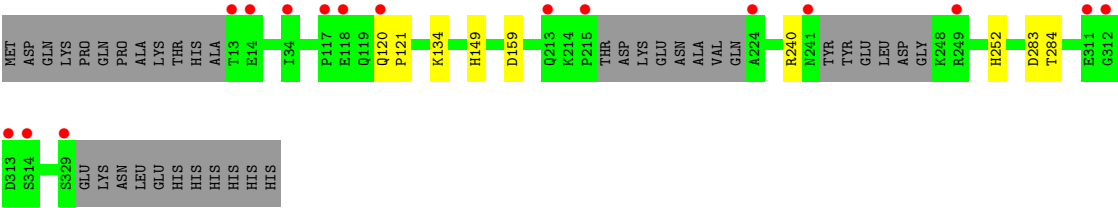
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	C	1	Total	C	H	O	0	0
			10	2	6	2		
4	C	1	Total	C	H	O	0	0
			10	2	6	2		
4	D	1	Total	C	H	O	0	0
			10	2	6	2		
4	D	1	Total	C	H	O	0	0
			10	2	6	2		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	181	Total	O	0	0
			181	181		
5	B	161	Total	O	0	0
			161	161		
5	C	147	Total	O	0	0
			147	147		
5	D	190	Total	O	0	0
			190	190		

- Molecule 1: FAD:protein FMN transferase





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	57.22Å 70.65Å 86.28Å 75.72° 71.91° 69.72°	Depositor
Resolution (Å)	33.92 – 1.75 33.92 – 1.75	Depositor EDS
% Data completeness (in resolution range)	96.5 (33.92-1.75) 96.6 (33.92-1.75)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.49 (at 1.75Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.172 , 0.199 0.176 , 0.201	Depositor DCC
R_{free} test set	5873 reflections (4.86%)	wwPDB-VP
Wilson B-factor (Å ²)	19.9	Xtriage
Anisotropy	0.562	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 41.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	19641	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.77% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NA, CA, EDO

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	0.32	0/2411	0.60	0/3264
1	B	0.32	0/2426	0.62	0/3289
1	C	0.32	0/2432	0.62	0/3294
1	D	0.33	0/2396	0.61	0/3247
All	All	0.32	0/9665	0.61	0/13094

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	2357	2347	2340	7	0
1	B	2380	2377	2376	7	0
1	C	2380	2386	2381	6	0
1	D	2341	2347	2340	6	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	C	8	12	12	0	0
4	D	8	12	12	0	0
5	A	181	0	0	1	0
5	B	161	0	0	3	0
5	C	147	0	0	2	0
5	D	190	0	0	0	0
All	All	10160	9481	9461	26	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 (26) 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:249:ARG:O	5:C:601:HOH:O	2.14	0.66
1:B:19:GLU:O	1:B:43:LYS:NZ	2.37	0.58
1:B:178:ARG:NH2	5:B:602:HOH:O	2.38	0.56
1:B:283:ASP:OD1	1:B:284:THR:N	2.40	0.55
1:C:283:ASP:OD1	1:C:284:THR:N	2.44	0.51
1:D:283:ASP:OD1	1:D:284:THR:N	2.45	0.49
1:A:267:VAL:HA	1:A:287:MET:HE1	1.94	0.49
1:C:178:ARG:NH2	5:C:605:HOH:O	2.44	0.49
1:A:38:ARG:NH2	1:A:183:GLU:O	2.46	0.48
1:C:239:TYR:HA	1:C:267:VAL:CG1	2.44	0.48
1:D:159:ASP:OD1	1:D:159:ASP:N	2.41	0.48
1:D:120:GLN:HB3	1:D:121:PRO:HD2	1.96	0.48
1:A:283:ASP:OD1	1:A:284:THR:N	2.48	0.47
1:C:120:GLN:HE21	1:C:120:GLN:N	2.12	0.47
1:A:247:GLY:N	5:A:606:HOH:O	2.48	0.45
1:B:119:GLN:NE2	1:B:241:ASN:O	2.50	0.44
1:D:240:ARG:HD2	1:D:252:HIS:CG	2.53	0.43
1:A:239:TYR:HA	1:A:242:TYR:HB2	2.00	0.43
1:B:42:LEU:HD11	1:B:185:ILE:HD11	2.00	0.43
1:A:267:VAL:CA	1:A:287:MET:HE1	2.49	0.42
1:B:178:ARG:CZ	5:B:602:HOH:O	2.69	0.41
1:B:169:LYS:HE3	5:B:708:HOH:O	2.20	0.41
1:D:240:ARG:HD2	1:D:252:HIS:CD2	2.55	0.41
1:C:266:LEU:HD21	1:C:269:VAL:CG2	2.51	0.41
1:A:38:ARG:NH2	1:A:183:GLU:HB3	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:120:GLN:HB3	1:D:121:PRO:CD	2.51	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	299/340 (88%)	292 (98%)	7 (2%)	0	100	100
1	B	304/340 (89%)	297 (98%)	6 (2%)	1 (0%)	36	23
1	C	303/340 (89%)	300 (99%)	3 (1%)	0	100	100
1	D	300/340 (88%)	293 (98%)	7 (2%)	0	100	100
All	All	1206/1360 (89%)	1182 (98%)	23 (2%)	1 (0%)	48	34

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	33	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	257/288 (89%)	257 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	259/288 (90%)	257 (99%)	2 (1%)	73	64
1	C	261/288 (91%)	259 (99%)	2 (1%)	73	64
1	D	258/288 (90%)	256 (99%)	2 (1%)	73	64
All	All	1035/1152 (90%)	1029 (99%)	6 (1%)	78	71

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	128	GLU
1	B	328	VAL
1	C	120	GLN
1	C	252	HIS
1	D	134	LYS
1	D	149	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	127	GLN
1	A	146	ASN
1	B	73	GLN
1	B	146	ASN
1	B	147	GLN
1	B	150	GLN
1	C	73	GLN
1	C	147	GLN
1	C	150	GLN
1	C	151	GLN
1	C	154	GLN
1	D	146	ASN
1	D	241	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 oligosaccharides in this entry.

5.6 Ligand geometry

Of 11 ligands modelled in this entry, 7 are monoatomic - leaving 4 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	$\# Z > 2$
4	EDO	C	503	-	3,3,3	0.43	0	2,2,2	0.42	0
4	EDO	D	503	-	3,3,3	0.44	0	2,2,2	0.36	0
4	EDO	C	504	-	3,3,3	0.42	0	2,2,2	0.35	0
4	EDO	D	504	-	3,3,3	0.42	0	2,2,2	0.36	0

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
4	EDO	C	503	-	-	0/1/1/1	-
4	EDO	D	503	-	-	1/1/1/1	-
4	EDO	C	504	-	-	0/1/1/1	-
4	EDO	D	504	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	503	EDO	O1-C1-C2-O2

There are no ring outliers.

No monomer is involved in short contacts.

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, 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	304/340 (89%)	0.09	19 (6%) 26 32	15, 25, 64, 102	3 (0%)
1	B	308/340 (90%)	0.26	21 (6%) 23 29	17, 29, 69, 88	0
1	C	307/340 (90%)	0.24	24 (7%) 19 24	16, 29, 73, 99	2 (0%)
1	D	303/340 (89%)	-0.01	16 (5%) 32 39	15, 23, 65, 95	3 (0%)
All	All	1222/1360 (89%)	0.15	80 (6%) 25 30	15, 27, 69, 102	8 (0%)

All (80) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	12	ALA	5.4
1	B	215	PRO	5.2
1	C	60	TYR	5.0
1	C	247	GLY	5.0
1	A	328	VAL	4.4
1	B	111	ASN	4.4
1	B	328	VAL	4.3
1	C	13	THR	4.2
1	C	242	TYR	4.1
1	D	117	PRO	4.1
1	D	215	PRO	4.0
1	A	34	ILE	4.0
1	C	216	THR	4.0
1	D	241	ASN	3.9
1	D	329	SER	3.9
1	A	213	GLN	3.8
1	C	122	VAL	3.8
1	D	312	GLY	3.7
1	A	247	GLY	3.7
1	C	115	PHE	3.6
1	B	214	LYS	3.6

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Mol	Chain	Res	Type	RSRZ
1	A	60	TYR	3.6
1	A	212	ILE	3.6
1	B	245	LEU	3.6
1	D	13	THR	3.5
1	B	122	VAL	3.4
1	C	62	LYS	3.4
1	C	215	PRO	3.3
1	C	245	LEU	3.3
1	D	213	GLN	3.3
1	B	194	GLY	3.2
1	C	243	TYR	3.2
1	B	33	GLY	3.1
1	B	31	ILE	3.1
1	C	120	GLN	3.0
1	C	329	SER	3.0
1	D	311	GLU	3.0
1	A	223	GLN	2.9
1	C	212	ILE	2.9
1	C	26	PHE	2.8
1	A	117	PRO	2.8
1	C	114	GLY	2.8
1	D	34	ILE	2.8
1	A	116	GLY	2.8
1	C	223	GLN	2.7
1	B	247	GLY	2.7
1	C	246	ASP	2.7
1	D	118	GLU	2.7
1	A	123	GLN	2.6
1	C	203	GLY	2.6
1	B	128	GLU	2.6
1	C	244	GLU	2.6
1	B	131	ASP	2.6
1	B	123	GLN	2.6
1	D	14	GLU	2.6
1	D	120	GLN	2.5
1	D	314	SER	2.5
1	D	249	ARG	2.5
1	D	224	ALA	2.5
1	B	241	ASN	2.5
1	B	116	GLY	2.5
1	A	119	GLN	2.4
1	A	182	GLN	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	257	GLN	2.4
1	B	313	ASP	2.4
1	A	224	ALA	2.4
1	A	150	GLN	2.4
1	B	225	VAL	2.3
1	C	111	ASN	2.3
1	A	311	GLU	2.3
1	B	114	GLY	2.3
1	C	157	LEU	2.2
1	D	313	ASP	2.2
1	A	248	LYS	2.1
1	B	62	LYS	2.1
1	C	241	ASN	2.1
1	B	117	PRO	2.1
1	A	312	GLY	2.0
1	A	242	TYR	2.0
1	C	132	ALA	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 oligosaccharides 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. 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	B-factors($\text{\AA}^2$)	Q<0.9
4	EDO	C	504	4/4	0.70	0.20	63,76,80,84	0
4	EDO	D	504	4/4	0.74	0.17	40,49,53,54	0
4	EDO	D	503	4/4	0.79	0.25	41,53,63,63	0
3	NA	C	502	1/1	0.81	0.19	40,40,40,40	0
4	EDO	C	503	4/4	0.92	0.11	29,38,46,46	0
3	NA	D	502	1/1	0.92	0.16	31,31,31,31	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	NA	A	502	1/1	0.93	0.14	29,29,29,29	0
2	CA	C	501	1/1	0.97	0.10	26,26,26,26	0
2	CA	D	501	1/1	0.98	0.13	21,21,21,21	0
2	CA	A	501	1/1	0.98	0.10	24,24,24,24	0
2	CA	B	501	1/1	0.99	0.09	27,27,27,27	0

6.5 Other polymers [i](#)

There are no such residues in this entry.