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 ⓘ

May 16, 2020 – 03:58 am BST

PDB ID	:	1PMM
Title	:	Crystal structure of Escherichia coli GadB (low pH)
Authors	:	Capitani, G.; De Biase, D.; Aurizi, C.; Gut, H.; Bossa, F.; Grutter, M.G.
Deposited on	:	2003-06-11
Resolution	:	2.00 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 following versions of software and data (see references ⓘ) were used in the production of this report:

|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 2.00 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.
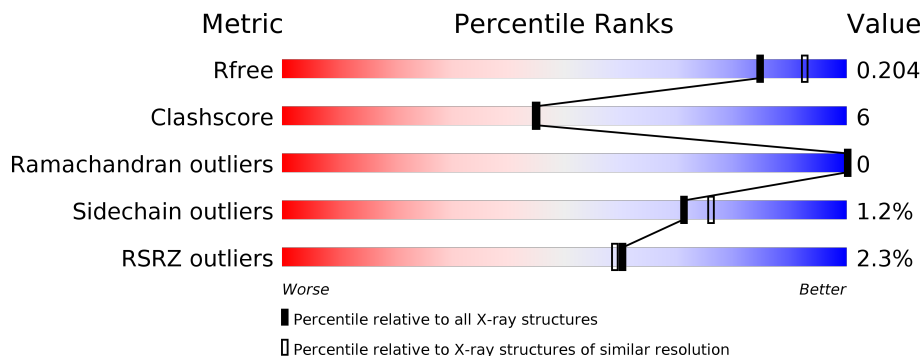
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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 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 <=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	466	
1	B	466	
1	C	466	
1	D	466	
1	E	466	
1	F	466	

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 23447 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 Glutamate decarboxylase beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	450	Total	C	N	O	S	0	3	0
			3584	2287	610	661	26			
1	B	450	Total	C	N	O	S	0	3	0
			3585	2287	611	662	25			
1	C	449	Total	C	N	O	S	0	4	0
			3579	2282	608	664	25			
1	D	450	Total	C	N	O	S	0	3	0
			3584	2287	610	661	26			
1	E	449	Total	C	N	O	S	0	3	0
			3575	2281	608	660	26			
1	F	450	Total	C	N	O	S	0	3	0
			3584	2287	610	661	26			

- Molecule 2 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula: $C_8H_{10}NO_6P$).
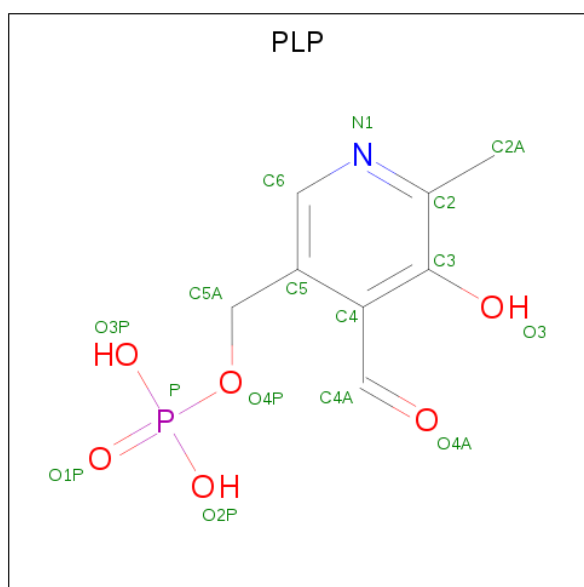
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	N	O	P		0	0
			15	8	1	5	1			
2	B	1	Total	C	N	O	P		0	0
			15	8	1	5	1			
2	C	1	Total	C	N	O	P		0	0
			15	8	1	5	1			
2	D	1	Total	C	N	O	P		0	0
			15	8	1	5	1			
2	E	1	Total	C	N	O	P		0	0
			15	8	1	5	1			
2	F	1	Total	C	N	O	P		0	0
			15	8	1	5	1			

- Molecule 3 is ACETIC ACID (three-letter code: ACY) (formula: $C_2H_4O_2$).
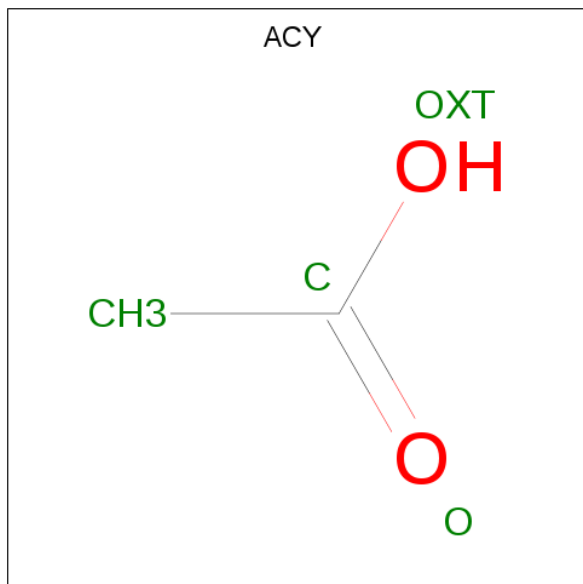
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	C	1	Total	C	O	0	0
			4	2	2		
3	D	1	Total	C	O	0	0
			4	2	2		
3	E	1	Total	C	O	0	0
			4	2	2		
3	E	1	Total	C	O	0	0
			4	2	2		

• Molecule 4 is water.

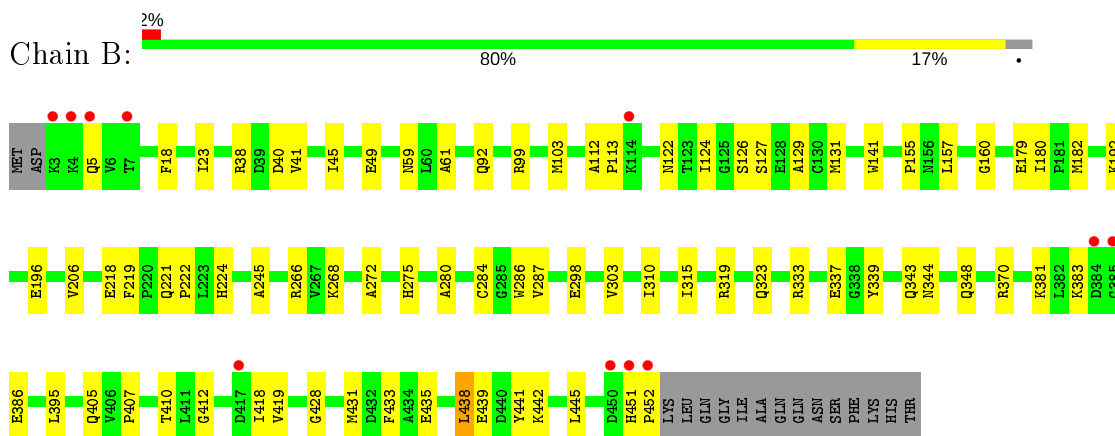| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	309	Total 309	O 309	0	0
4	B	320	Total 320	O 320	0	0
4	C	284	Total 284	O 284	0	0
4	D	333	Total 333	O 333	0	0
4	E	292	Total 292	O 292	0	0
4	F	304	Total 304	O 304	0	0

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 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.
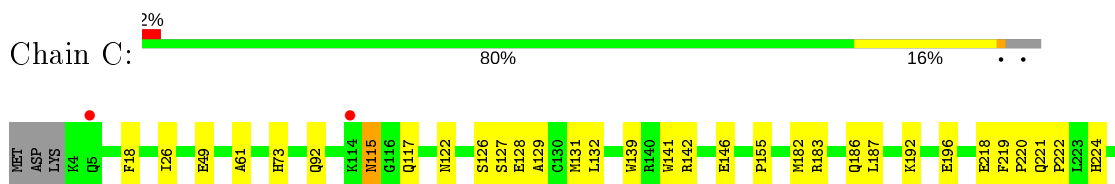
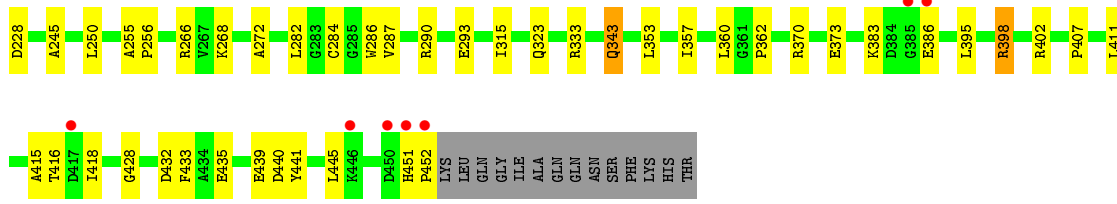- Molecule 1: Glutamate decarboxylase beta

Chain A:

- Molecule 1: Glutamate decarboxylase beta

Chain B:

- Molecule 1: Glutamate decarboxylase beta

Chain C:

D228 A245 L250 A255 P256 R266 V267 K268 A272 L282 G283 C284 G285 W286 V287 R290 E293 I315 Q323 R333 Q343 L353 I357 L360 G361 P362 R370 E373 K383 D384 G385 E386 L395 R398 R402 P407 L411

A415 T416 D417 I418 G428 D432 F433 A434 E435 E439 D440 Y441 L445 K446 D450 H451 P452 LYS GLN GLY ILE ALA GLN GLN ASN SER PHE LYS HIS THR

• Molecule 1: Glutamate decarboxylase beta

Chain D:

MET ASP K3 Q5 V6 L9 F18 I23 I26 V41 I45 E49 A61 E70 K74 D77 E89 Y90 P91 Q92 K114 I124 G125 S126 S127 M131 W141 P155 I180 M189 K192 R193 M194 I195 E196 P207 E218

F219 P220 Q221 P222 H224 M240 A245 R266 A272 E293 V303 D304 Y305 I306 G307 I310 I315 R319 P320 R333 Y339 Q343 Q348 I375 P376 K383 D384 G385 E386 R400 P407 L411 E414 A415 T416 D417 I418 M431

L436 L437 L438 K442 D450 H451 P452 LYS LEU GLN GLY ILE ALA GLN GLN ASN SER PHE LYS HIS THR

• Molecule 1: Glutamate decarboxylase beta

Chain E:

MET ASP LYS K4 Q5 K21 S24 E28 R31 F32 R38 D39 D40 E49 A61 N83 W84 I85 D86 Q92 K114 S126 S127 E128 A129 G130 M131 L132 W141 R142 E146 P155 G160 E179 I180 G185 E218 Q221 P222 L223 H224

A245 D261 F262 R263 L264 S269 A272 E275 A280 C284 V287 I288 W289 L299 D304 G307 G308 I315 A321 G322 Q323 V324 R333 Y339 Q343 E364 R370 I375 K381 L382 K383 E386 L395 P407 D417

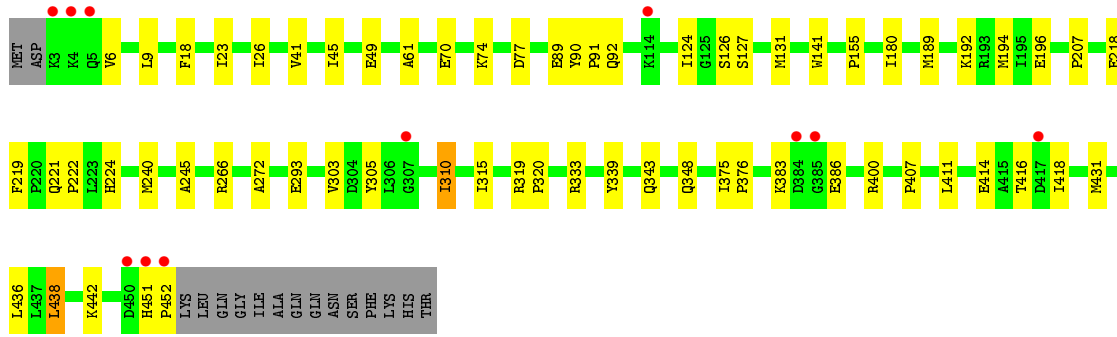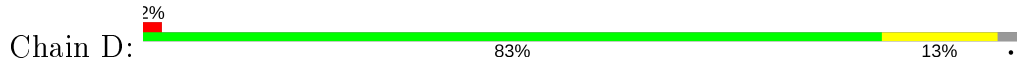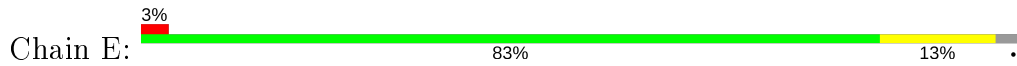M424 G428 E435 Y441 L445 S449 D450 H451 P452 LYS LEU GLN GLY ILE ALA GLN GLN ASN SER PHE LYS HIS THR

• Molecule 1: Glutamate decarboxylase beta

Chain F:

MET ASP K3 K4 Q5 V6 T7 D8 L9 E12 F18 L34 H35 R38 D39 D40 I45 E49 A61 Q92 K114 N122 S126 S127 M131 W139 R140 W141 R142 K143 K150 P151 P155 N156 L157 F169 I180 P181 M182 Q186 M189

K192 R193 M194 I195 E196 G204 V205 V206 E218 F219 P220 Q221 P222 A245 A272 H275 A280 W286 N302 V303 G308 Q309 I310 G311 I315 R319 P320 R333 Y339 Q343 Q348 L360 D372 E373 G374 I375 P376 D384 G385 L395

P407 T410 L411 G412 G413 E414 D417 I418 V419 M431 E435 L436 E439 D440 Y441 L445 D450 H451 P452 LYS LEU GLN GLY ILE ALA GLN GLN ASN SER PHE LYS HIS THR

![Worldwide Protein Data Bank logo]

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	90.78Å 91.41Å 93.69Å 76.80° 77.10° 78.24°	Depositor
Resolution (Å)	24.62 – 2.00 24.64 – 2.01	Depositor EDS
% Data completeness (in resolution range)	95.8 (24.62-2.00) 95.3 (24.64-2.01)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$<I/\sigma(I)>$ [1]	7.10 (at 2.01Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.182 , 0.213 0.174 , 0.204	Depositor DCC
R_{free} test set	5238 reflections (2.93%)	wwPDB-VP
Wilson B-factor (Å^2)	15.1	Xtriage
Anisotropy	0.045	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.39 , 51.8	EDS
L-test for twinning[2]	$<|L|> = 0.49, <L^2> = 0.32$	Xtriage
Estimated twinning fraction	0.146 for k,l,h 0.146 for l,h,k 0.019 for -k,-h,-l 0.012 for -l,-k,-h 0.012 for -h,-l,-k	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	23447	wwPDB-VP
Average B, all atoms (Å^2)	15.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.58% 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, 0.333 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: ACY, PLP

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	0/3691	0.58	1/5002 (0.0%)
1	B	0.32	0/3692	0.58	1/5004 (0.0%)
1	C	0.31	0/3691	0.57	1/5004 (0.0%)
1	D	0.32	0/3691	0.58	1/5002 (0.0%)
1	E	0.31	0/3682	0.58	1/4991 (0.0%)
1	F	0.32	0/3691	0.58	1/5002 (0.0%)
All	All	0.32	0/22138	0.58	6/30005 (0.0%)

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	218	GLU	N-CA-C	-5.64	95.78	111.00
1	A	218	GLU	N-CA-C	-5.50	96.15	111.00
1	F	218	GLU	N-CA-C	-5.47	96.23	111.00
1	D	218	GLU	N-CA-C	-5.42	96.36	111.00
1	E	218	GLU	N-CA-C	-5.41	96.39	111.00

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	3584	0	3494	56	0
1	B	3585	0	3493	56	0
1	C	3579	0	3478	56	0
1	D	3584	0	3494	51	0
1	E	3575	0	3481	43	0
1	F	3584	0	3494	52	0
2	A	15	0	6	1	0
2	B	15	0	6	1	0
2	C	15	0	6	1	0
2	D	15	0	6	1	0
2	E	15	0	6	1	0
2	F	15	0	6	1	0
3	A	4	0	3	0	0
3	B	4	0	3	0	0
3	C	4	0	3	0	0
3	D	4	0	3	0	0
3	E	8	0	6	1	0
4	A	309	0	0	2	0
4	B	320	0	0	0	0
4	C	284	0	0	1	0
4	D	333	0	0	1	0
4	E	292	0	0	0	0
4	F	304	0	0	1	0
All	All	23447	0	20988	277	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.

The worst 5 of 277 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:F:139:TRP:HE1	1:F:143:LYS:HE3	1.33	0.93
1:B:23:ILE:HG13	1:B:45:ILE:HD11	1.61	0.82
1:D:23:ILE:HG13	1:D:45:ILE:HD11	1.60	0.81
1:F:139:TRP:NE1	1:F:143:LYS:HE3	1.94	0.81
1:C:131[B]:MET:SD	1:D:315:ILE:HG23	2.22	0.80

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	451/466 (97%)	440 (98%)	11 (2%)	0	100	100
1	B	451/466 (97%)	440 (98%)	11 (2%)	0	100	100
1	C	451/466 (97%)	439 (97%)	12 (3%)	0	100	100
1	D	451/466 (97%)	438 (97%)	13 (3%)	0	100	100
1	E	450/466 (97%)	439 (98%)	11 (2%)	0	100	100
1	F	451/466 (97%)	440 (98%)	11 (2%)	0	100	100
All	All	2705/2796 (97%)	2636 (97%)	69 (3%)	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	379/390 (97%)	376 (99%)	3 (1%)	81	86
1	B	379/390 (97%)	375 (99%)	4 (1%)	73	78
1	C	379/390 (97%)	370 (98%)	9 (2%)	49	51
1	D	379/390 (97%)	374 (99%)	5 (1%)	69	74
1	E	378/390 (97%)	375 (99%)	3 (1%)	81	86
1	F	379/390 (97%)	376 (99%)	3 (1%)	81	86
All	All	2273/2340 (97%)	2246 (99%)	27 (1%)	71	76

5 of 27 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	333	ARG
1	C	433	PHE
1	F	333	ARG
1	C	343	GLN
1	B	333	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	115	ASN
1	D	81	ASN
1	F	302	ASN
1	C	297	GLN
1	B	5	GLN

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)

12 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	ACY	E	9519	-	1,3,3	2.83	1 (100%)	0,3,3	0.00	-
2	PLP	E	502	1	15,15,16	0.83	0	20,22,23	1.49	6 (30%)
3	ACY	C	8518	-	1,3,3	2.86	1 (100%)	0,3,3	0.00	-
3	ACY	D	7518	-	1,3,3	2.72	1 (100%)	0,3,3	0.00	-
3	ACY	B	6518	-	1,3,3	2.59	1 (100%)	0,3,3	0.00	-
2	PLP	A	500	1	15,15,16	0.85	0	20,22,23	1.46	5 (25%)
2	PLP	F	502	1	15,15,16	0.79	0	20,22,23	1.49	6 (30%)
3	ACY	A	5518	-	1,3,3	2.92	1 (100%)	0,3,3	0.00	-
3	ACY	E	9518	-	1,3,3	2.89	1 (100%)	0,3,3	0.00	-
2	PLP	C	501	1	15,15,16	0.85	0	20,22,23	1.48	6 (30%)
2	PLP	D	501	1	15,15,16	0.78	0	20,22,23	1.49	6 (30%)
2	PLP	B	500	1	15,15,16	0.77	0	20,22,23	1.49	6 (30%)

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	PLP	E	502	1	-	0/6/6/8	0/1/1/1
2	PLP	A	500	1	-	0/6/6/8	0/1/1/1
2	PLP	F	502	1	-	0/6/6/8	0/1/1/1
2	PLP	C	501	1	-	0/6/6/8	0/1/1/1
2	PLP	D	501	1	-	0/6/6/8	0/1/1/1
2	PLP	B	500	1	-	0/6/6/8	0/1/1/1

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	5518	ACY	CH3-C	2.92	1.52	1.48
3	E	9518	ACY	CH3-C	2.89	1.52	1.48
3	C	8518	ACY	CH3-C	2.86	1.52	1.48
3	E	9519	ACY	CH3-C	2.83	1.52	1.48
3	D	7518	ACY	CH3-C	2.72	1.52	1.48

The worst 5 of 35 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	501	PLP	C4A-C4-C5	3.13	124.16	120.94

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	E	502	PLP	C4A-C4-C5	3.00	124.02	120.94
2	F	502	PLP	C4A-C4-C5	2.99	124.02	120.94
2	B	500	PLP	C4A-C4-C5	2.97	123.99	120.94
2	D	501	PLP	C4A-C4-C5	2.95	123.97	120.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	502	PLP	1	0
2	A	500	PLP	1	0
2	F	502	PLP	1	0
3	E	9518	ACY	1	0
2	C	501	PLP	1	0
2	D	501	PLP	1	0
2	B	500	PLP	1	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(Å²)	Q<0.9
1	A	450/466 (96%)	-0.21	9 (2%)	65	63	7, 13, 25, 44	0
1	B	450/466 (96%)	-0.20	11 (2%)	59	57	7, 13, 26, 44	0
1	C	449/466 (96%)	-0.15	9 (2%)	65	63	9, 15, 26, 44	0
1	D	450/466 (96%)	-0.20	11 (2%)	59	57	5, 13, 27, 42	0
1	E	449/466 (96%)	-0.20	12 (2%)	54	53	7, 14, 26, 46	0
1	F	450/466 (96%)	-0.20	11 (2%)	59	57	6, 13, 26, 44	0
All	All	2698/2796 (96%)	-0.19	63 (2%)	60	59	5, 14, 26, 46	0

The worst 5 of 63 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	452	PRO	6.7
1	D	452	PRO	6.4
1	E	452	PRO	6.2
1	A	452	PRO	5.1
1	B	452	PRO	5.0

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. 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(Å^2)	Q<0.9
3	ACY	E	9519	4/4	0.96	0.12	17,17,17,17	0
2	PLP	C	501	15/16	0.96	0.09	12,13,14,15	0
3	ACY	D	7518	4/4	0.97	0.11	19,19,19,20	0
3	ACY	B	6518	4/4	0.97	0.13	14,15,15,15	0
2	PLP	A	500	15/16	0.97	0.10	11,12,13,13	0
2	PLP	F	502	15/16	0.97	0.09	10,11,11,12	0
3	ACY	E	9518	4/4	0.97	0.13	19,20,20,20	0
3	ACY	C	8518	4/4	0.97	0.10	17,18,18,18	0
2	PLP	D	501	15/16	0.97	0.09	10,10,10,11	0
2	PLP	B	500	15/16	0.97	0.08	11,11,12,12	0
2	PLP	E	502	15/16	0.98	0.08	11,12,13,13	0
3	ACY	A	5518	4/4	0.98	0.09	18,18,19,19	0

6.5 Other polymers (i)

There are no such residues in this entry.