



Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2017 – 01:38 PM EDT

PDB ID : 5X03
Title : Crystal structure of the C-terminal domain of Bacillus subtilis GabR reveals a closed conformation by the binding of gamma-aminobutyric acid, inducing the transcriptional activation
Authors : Park, S.A.; Lee, K.S.
Deposited on : 2017-01-19
Resolution : 2.00 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 : rb-20029077
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) : rb-20029077

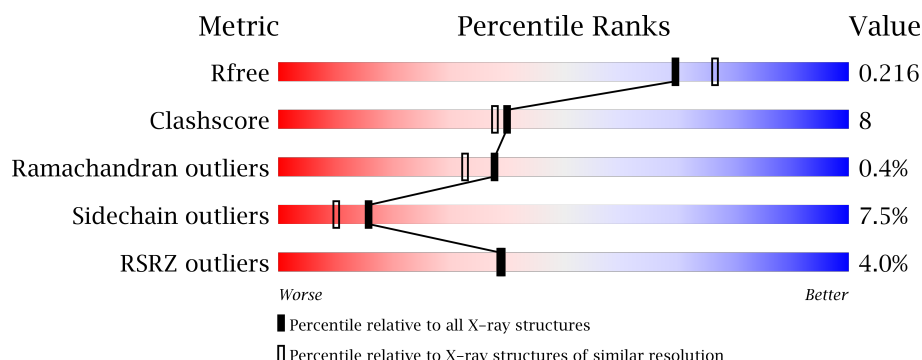
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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}	100719	6609 (2.00-2.00)
Clashscore	112137	7775 (2.00-2.00)
Ramachandran outliers	110173	7679 (2.00-2.00)
Sidechain outliers	110143	7678 (2.00-2.00)
RSRZ outliers	101464	6696 (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. 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	363	<div> <div>3%</div> <div>79%</div> <div>19%</div> <div>.</div> </div>
2	B	365	<div> <div>5%</div> <div>75%</div> <div>21%</div> <div>.</div> </div>

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 6176 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 HTH-type transcriptional regulatory protein GabR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	363	Total	C	N	O	S	0	0	0
			2935	1860	514	545	16			

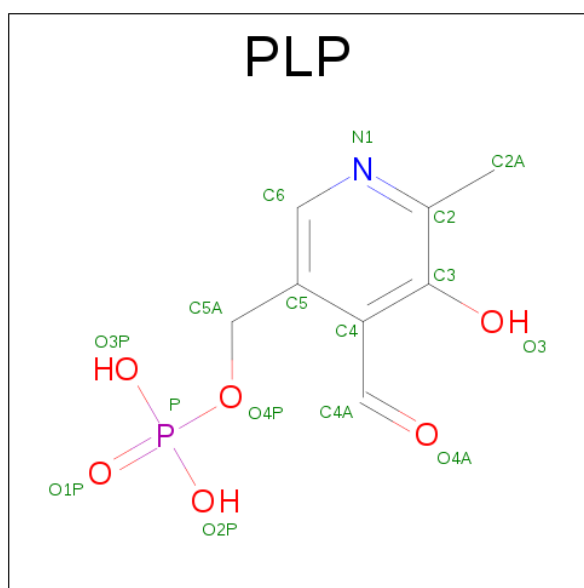
- Molecule 2 is a protein called HTH-type transcriptional regulatory protein GabR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	365	Total	C	N	O	S	0	0	0
			2956	1872	521	547	16			

There is a discrepancy between the modelled and reference sequences:

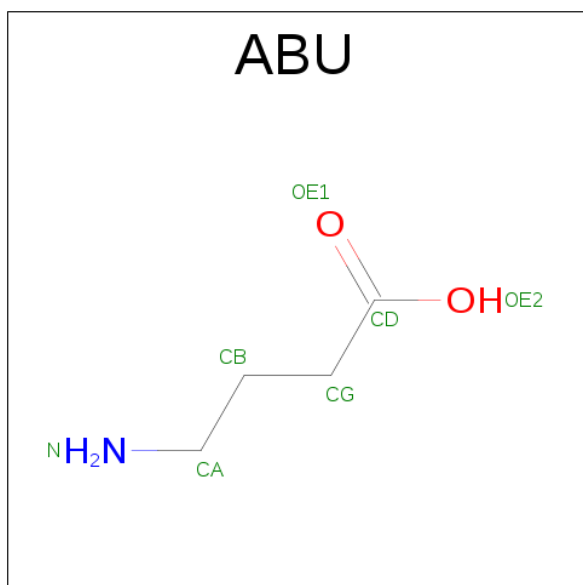
Chain	Residue	Modelled	Actual	Comment	Reference
B	472	ARG	LYS	engineered mutation	UNP P94426

- Molecule 3 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula: C₈H₁₀NO₆P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
3	B	1	Total	C	N	O	P	0	0
			15	8	1	5	1		

- Molecule 4 is GAMMA-AMINO-BUTANOIC ACID (three-letter code: ABU) (formula: $C_4H_9NO_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			7	4	1	2		

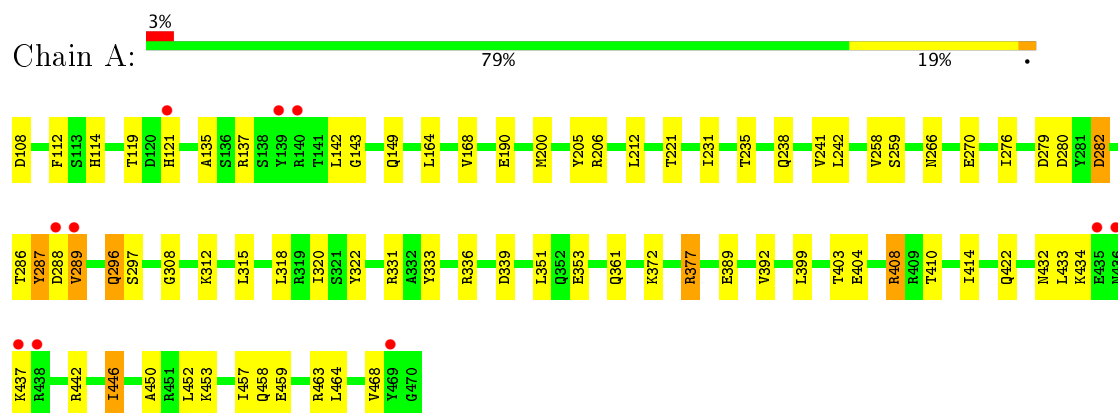
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	140	Total	O	0	0
			140	140		
5	B	108	Total	O	0	0
			108	108		

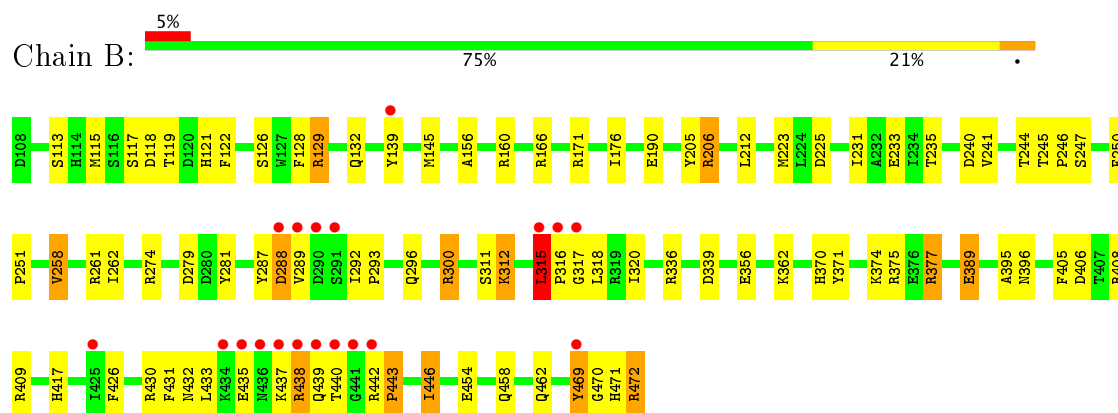
3 Residue-property plots

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: HTH-type transcriptional regulatory protein GabR



- Molecule 2: HTH-type transcriptional regulatory protein GabR



4 Data and refinement statistics

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, α , β , γ	118.50Å 118.50Å 75.86Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.47 – 2.00 37.47 – 2.00	Depositor EDS
% Data completeness (in resolution range)	96.6 (37.47-2.00) 96.5 (37.47-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.98 (at 2.00Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.173 , 0.216 0.173 , 0.216	Depositor DCC
R_{free} test set	1928 reflections (2.81%)	DCC
Wilson B-factor (Å ²)	25.3	Xtriage
Anisotropy	0.237	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 39.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.37$, $\langle L^2 \rangle = 0.19$	Xtriage
Estimated twinning fraction	0.253 for h,-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6176	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.63% 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: ABU, 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	0.44	0/2993	0.55	0/4032
2	B	0.43	0/3015	0.57	0/4061
All	All	0.43	0/6008	0.56	0/8093

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	315	LEU	Peptide

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	2935	0	2952	40	0
2	B	2956	0	2972	61	0
3	A	15	0	6	1	0
3	B	15	0	6	3	0
4	A	7	0	5	0	0
5	A	140	0	0	5	0
5	B	108	0	0	7	0
All	All	6176	0	5941	98	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 8.

All (98) 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)
2:B:312:LYS:HZ3	3:B:501:PLP:C4A	1.54	1.09
2:B:312:LYS:HZ1	3:B:501:PLP:C4A	1.61	1.04
2:B:389:GLU:OE1	2:B:469:TYR:OH	1.98	0.82
1:A:114:HIS:HB3	1:A:446:ILE:HD11	1.63	0.81
2:B:292:ILE:O	5:B:602:HOH:O	1.98	0.80
2:B:315:LEU:HG	2:B:317:GLY:H	1.44	0.80
3:B:501:PLP:O2P	5:B:601:HOH:O	1.98	0.80
2:B:206:ARG:NH1	2:B:433:LEU:O	2.15	0.78
2:B:118:ASP:OD1	2:B:121:HIS:ND1	2.19	0.74
2:B:362:LYS:NZ	5:B:604:HOH:O	2.21	0.74
1:A:282:ASP:HB3	1:A:312:LYS:HG3	1.71	0.73
2:B:190:GLU:OE1	2:B:336:ARG:NH2	2.22	0.73
1:A:143:GLY:HA2	2:B:316:PRO:HA	1.71	0.72
1:A:190:GLU:OE1	1:A:336:ARG:NH2	2.23	0.71
1:A:377:ARG:HD3	1:A:457:ILE:HD12	1.76	0.67
2:B:417:HIS:CE1	2:B:470:GLY:HA2	2.29	0.67
2:B:311:SER:O	2:B:315:LEU:HB3	1.96	0.64
2:B:117:SER:HG	2:B:371:TYR:HH	1.45	0.62
1:A:408:ARG:NH2	5:A:610:HOH:O	2.32	0.61
2:B:251:PRO:HG3	2:B:431:PHE:CG	2.36	0.60
2:B:132:GLN:NE2	5:B:610:HOH:O	2.33	0.60
2:B:113:SER:HB2	2:B:426:PHE:CE2	2.37	0.60
2:B:288:ASP:HB2	2:B:396:ASN:ND2	2.17	0.59
2:B:126:SER:HA	2:B:129:ARG:HD2	1.84	0.58
1:A:137:ARG:NH1	1:A:353:GLU:OE2	2.37	0.58
1:A:231:ILE:O	1:A:235:THR:HG23	2.03	0.58
2:B:244:THR:HG23	2:B:246:PRO:HD3	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:437:LYS:O	2:B:438:ARG:NE	2.37	0.57
1:A:135:ALA:HA	1:A:142:LEU:HD11	1.87	0.56
2:B:389:GLU:HG2	2:B:406:ASP:HB3	1.90	0.54
1:A:266:ASN:O	1:A:270:GLU:HG3	2.08	0.53
2:B:409:ARG:HH21	2:B:470:GLY:HA3	1.74	0.53
1:A:392:VAL:HG22	1:A:403:THR:HG22	1.89	0.53
2:B:432:ASN:OD1	5:B:603:HOH:O	2.19	0.53
1:A:143:GLY:HA2	2:B:316:PRO:CA	2.37	0.52
2:B:300:ARG:H	2:B:300:ARG:HD3	1.75	0.51
2:B:336:ARG:HD3	2:B:339:ASP:OD2	2.11	0.51
2:B:442:ARG:HB3	2:B:443:PRO:HD2	1.92	0.50
1:A:238:GLN:HG2	5:A:687:HOH:O	2.10	0.50
2:B:409:ARG:NH2	2:B:470:GLY:HA3	2.27	0.50
2:B:405:PHE:HB2	2:B:443:PRO:HB2	1.93	0.50
1:A:404:GLU:HB3	1:A:442:ARG:HD3	1.92	0.49
2:B:288:ASP:HB2	2:B:396:ASN:HD22	1.78	0.49
1:A:308:GLY:HA3	1:A:322:TYR:CZ	2.48	0.49
1:A:221:THR:HG21	1:A:434:LYS:HG2	1.95	0.48
2:B:231:ILE:O	2:B:235:THR:HG23	2.13	0.48
2:B:258:VAL:O	2:B:262:ILE:HG12	2.14	0.48
2:B:377:ARG:NH2	2:B:458:GLN:HG2	2.29	0.47
2:B:281:TYR:O	2:B:312:LYS:HG3	2.14	0.47
1:A:168:VAL:HG22	1:A:296:GLN:HG2	1.97	0.47
2:B:431:PHE:CE2	2:B:446:ILE:HD12	2.51	0.46
2:B:128:PHE:O	2:B:132:GLN:HG2	2.16	0.46
1:A:464:LEU:O	1:A:468:VAL:HG23	2.16	0.46
1:A:112:PHE:HE1	1:A:452:LEU:HD22	1.81	0.46
1:A:422:GLN:O	1:A:463:ARG:NH1	2.49	0.46
1:A:259:SER:HB3	5:A:686:HOH:O	2.15	0.45
2:B:426:PHE:HB2	2:B:446:ILE:CD1	2.46	0.45
2:B:375:ARG:NH2	2:B:395:ALA:O	2.49	0.45
2:B:471:HIS:O	2:B:472:ARG:HB3	2.17	0.45
1:A:279:ASP:OD2	3:A:501:PLP:N1	2.50	0.45
2:B:129:ARG:NH2	5:B:614:HOH:O	2.49	0.45
1:A:459:GLU:N	5:A:614:HOH:O	2.34	0.45
2:B:439:GLN:HG2	2:B:440:THR:HG23	2.00	0.44
1:A:288:ASP:CG	1:A:289:VAL:H	2.21	0.44
2:B:370:HIS:NE2	2:B:374:LYS:HE3	2.32	0.44
2:B:377:ARG:HD2	2:B:454:GLU:OE1	2.18	0.44
1:A:121:HIS:HB3	5:A:725:HOH:O	2.16	0.44
2:B:240:ASP:O	2:B:274:ARG:HA	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:171:ARG:HH11	2:B:171:ARG:HG2	1.82	0.43
2:B:160:ARG:NH2	2:B:356:GLU:OE2	2.49	0.43
2:B:245:THR:HG22	2:B:279:ASP:HB3	2.01	0.43
2:B:156:ALA:O	2:B:160:ARG:HG3	2.19	0.43
1:A:434:LYS:HD3	1:A:434:LYS:HA	1.70	0.43
2:B:223:MET:HG2	2:B:233:GLU:HG3	2.01	0.43
1:A:149:GLN:HG2	1:A:333:TYR:CE2	2.54	0.42
1:A:242:LEU:HD12	1:A:276:ILE:HG12	2.02	0.42
1:A:287:TYR:HB3	1:A:372:LYS:NZ	2.35	0.42
1:A:200:MET:HE2	1:A:433:LEU:HD21	2.00	0.42
1:A:320:ILE:HG21	1:A:351:LEU:HD22	2.01	0.42
1:A:336:ARG:HD3	1:A:339:ASP:OD2	2.20	0.42
1:A:410:THR:O	1:A:414:ILE:HG13	2.19	0.42
1:A:119:THR:HG21	2:B:139:TYR:O	2.19	0.42
1:A:399:LEU:HD13	1:A:450:ALA:HB2	2.02	0.42
2:B:166:ARG:NH2	2:B:247:SER:OG	2.53	0.41
2:B:288:ASP:HB3	2:B:289:VAL:H	1.52	0.41
2:B:261:ARG:NH1	2:B:293:PRO:O	2.52	0.41
2:B:122:PHE:CD2	2:B:316:PRO:HG3	2.54	0.41
1:A:296:GLN:HG3	1:A:297:SER:N	2.35	0.41
2:B:225:ASP:OD2	5:B:606:HOH:O	2.22	0.41
1:A:206:ARG:O	1:A:206:ARG:HG3	2.21	0.41
1:A:437:LYS:HB3	1:A:437:LYS:HE2	1.85	0.41
2:B:311:SER:HA	2:B:315:LEU:HB2	2.03	0.41
2:B:458:GLN:OE1	2:B:462:GLN:NE2	2.54	0.41
2:B:250:PHE:HA	2:B:251:PRO:HA	1.68	0.41
2:B:287:TYR:HB2	2:B:396:ASN:CG	2.40	0.41
1:A:143:GLY:O	2:B:317:GLY:N	2.54	0.40
1:A:206:ARG:NH1	1:A:433:LEU:O	2.55	0.40
2:B:417:HIS:ND1	2:B:470:GLY:HA2	2.35	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	361/363 (99%)	343 (95%)	17 (5%)	1 (0%)	44	40
2	B	363/365 (100%)	347 (96%)	14 (4%)	2 (1%)	28	21
All	All	724/728 (100%)	690 (95%)	31 (4%)	3 (0%)	38	33

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	443	PRO
1	A	282	ASP
2	B	315	LEU

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	319/319 (100%)	297 (93%)	22 (7%)	18	12
2	B	321/321 (100%)	295 (92%)	26 (8%)	14	8
All	All	640/640 (100%)	592 (92%)	48 (8%)	16	10

All (48) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	108	ASP
1	A	164	LEU
1	A	205	TYR
1	A	212	LEU
1	A	241	VAL
1	A	258	VAL
1	A	280	ASP
1	A	286	THR
1	A	287	TYR
1	A	289	VAL

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Mol	Chain	Res	Type
1	A	296	GLN
1	A	315	LEU
1	A	318	LEU
1	A	331	ARG
1	A	361	GLN
1	A	377	ARG
1	A	389	GLU
1	A	408	ARG
1	A	432	ASN
1	A	446	ILE
1	A	453	LYS
1	A	458	GLN
2	B	115	MET
2	B	119	THR
2	B	129	ARG
2	B	145	MET
2	B	176	ILE
2	B	205	TYR
2	B	206	ARG
2	B	212	LEU
2	B	241	VAL
2	B	258	VAL
2	B	288	ASP
2	B	296	GLN
2	B	300	ARG
2	B	312	LYS
2	B	315	LEU
2	B	318	LEU
2	B	320	ILE
2	B	377	ARG
2	B	389	GLU
2	B	408	ARG
2	B	430	ARG
2	B	435	GLU
2	B	438	ARG
2	B	446	ILE
2	B	469	TYR
2	B	472	ARG

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

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](#)

3 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	PLP	A	501	4	15,15,16	3.70	3 (20%)	20,22,23	1.17	1 (5%)
4	ABU	A	502	3	3,6,6	0.21	0	2,6,6	0.58	0
3	PLP	B	501	2	15,15,16	3.65	3 (20%)	20,22,23	1.15	1 (5%)

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	PLP	A	501	4	-	0/6/6/8	0/1/1/1
4	ABU	A	502	3	-	0/2/4/4	0/0/0/0
3	PLP	B	501	2	-	0/6/6/8	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	501	PLP	C3-C4	3.78	1.48	1.40
3	B	501	PLP	C3-C4	3.80	1.48	1.40
3	B	501	PLP	C5-C4	6.95	1.48	1.40
3	A	501	PLP	C5-C4	7.02	1.48	1.40
3	B	501	PLP	C3-C2	11.39	1.48	1.40
3	A	501	PLP	C3-C2	11.62	1.48	1.40

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	501	PLP	C6-N1-C2	2.06	123.23	119.26
3	B	501	PLP	C6-N1-C2	2.08	123.27	119.26

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	501	PLP	1	0
3	B	501	PLP	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, 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	363/363 (100%)	0.18	10 (2%) 53 53	16, 27, 41, 82	0
2	B	365/365 (100%)	0.40	19 (5%) 28 28	15, 30, 49, 111	0
All	All	728/728 (100%)	0.29	29 (3%) 39 39	15, 28, 47, 111	0

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	441	GLY	11.8
2	B	436	ASN	8.0
2	B	316	PRO	6.9
1	A	437	LYS	6.7
2	B	289	VAL	6.2
2	B	442	ARG	6.0
2	B	439	GLN	5.8
2	B	437	LYS	5.5
2	B	440	THR	5.4
2	B	288	ASP	5.0
2	B	438	ARG	4.8
2	B	290	ASP	4.5
2	B	469	TYR	4.4
1	A	435	GLU	4.3
1	A	438	ARG	3.9
2	B	434	LYS	3.8
2	B	435	GLU	3.3
1	A	289	VAL	3.3
1	A	288	ASP	2.8
2	B	317	GLY	2.6
1	A	469	TYR	2.6
2	B	139	TYR	2.6
1	A	140	ARG	2.6
1	A	121	HIS	2.5

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Mol	Chain	Res	Type	RSRZ
2	B	425	ILE	2.4
1	A	139	TYR	2.3
2	B	315	LEU	2.2
2	B	291	SER	2.1
1	A	436	ASN	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
3	PLP	B	501	15/16	0.93	0.15	0.16	31,37,43,45	0
4	ABU	A	502	7/7	0.97	0.12	-0.67	22,26,31,37	0
3	PLP	A	501	15/16	0.98	0.12	-0.70	20,23,26,26	0

6.5 Other polymers [i](#)

There are no such residues in this entry.