



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 03:31 AM UTC

PDB ID : 4NA2 / pdb_00004na2
Title : Crystal Structure of the second ketosynthase from the bacillaene polyketide synthase bound to its natural intermediate
Authors : Gay, D.C.; Gay, G.R.; Keatinge-Clay, A.T.
Deposited on : 2013-10-21
Resolution : 2.30 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

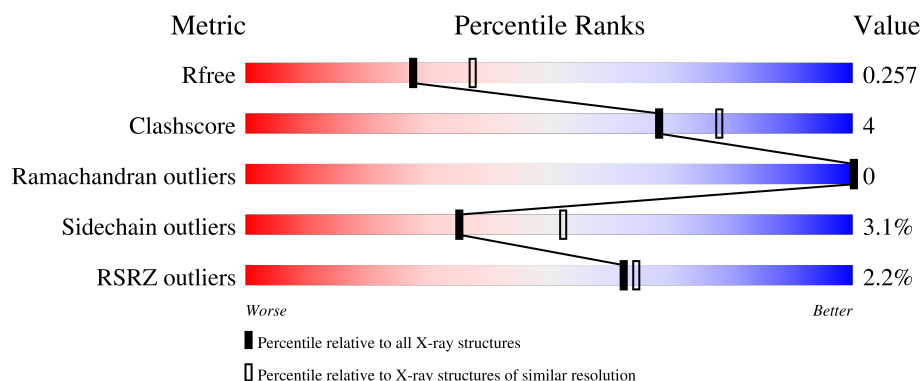
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	637	 2% 81% 12% 7%
1	B	637	 2% 83% 8% 9%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 9432 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 Polyketide synthase PksJ.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	594	Total	C	N	O	S	0	0	0
			4644	2925	811	887	21			
1	B	581	Total	C	N	O	S	0	0	0
			4545	2868	790	866	21			

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-18	GLY	-	expression tag	UNP P40806
A	-17	SER	-	expression tag	UNP P40806
A	-16	SER	-	expression tag	UNP P40806
A	-15	HIS	-	expression tag	UNP P40806
A	-14	HIS	-	expression tag	UNP P40806
A	-13	HIS	-	expression tag	UNP P40806
A	-12	HIS	-	expression tag	UNP P40806
A	-11	HIS	-	expression tag	UNP P40806
A	-10	HIS	-	expression tag	UNP P40806
A	-9	SER	-	expression tag	UNP P40806
A	-8	SER	-	expression tag	UNP P40806
A	-7	GLY	-	expression tag	UNP P40806
A	-6	LEU	-	expression tag	UNP P40806
A	-5	VAL	-	expression tag	UNP P40806
A	-4	PRO	-	expression tag	UNP P40806
A	-3	ARG	-	expression tag	UNP P40806
A	-2	GLY	-	expression tag	UNP P40806
A	-1	SER	-	expression tag	UNP P40806
A	0	SER	-	expression tag	UNP P40806
A	176	2JF	CYS	engineered mutation	UNP P40806
A	617	GLY	GLU	SEE REMARK 999	UNP P40806
B	-18	GLY	-	expression tag	UNP P40806
B	-17	SER	-	expression tag	UNP P40806
B	-16	SER	-	expression tag	UNP P40806
B	-15	HIS	-	expression tag	UNP P40806

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-14	HIS	-	expression tag	UNP P40806
B	-13	HIS	-	expression tag	UNP P40806
B	-12	HIS	-	expression tag	UNP P40806
B	-11	HIS	-	expression tag	UNP P40806
B	-10	HIS	-	expression tag	UNP P40806
B	-9	SER	-	expression tag	UNP P40806
B	-8	SER	-	expression tag	UNP P40806
B	-7	GLY	-	expression tag	UNP P40806
B	-6	LEU	-	expression tag	UNP P40806
B	-5	VAL	-	expression tag	UNP P40806
B	-4	PRO	-	expression tag	UNP P40806
B	-3	ARG	-	expression tag	UNP P40806
B	-2	GLY	-	expression tag	UNP P40806
B	-1	SER	-	expression tag	UNP P40806
B	0	SER	-	expression tag	UNP P40806
B	176	2JF	CYS	engineered mutation	UNP P40806
B	617	GLY	GLU	SEE REMARK 999	UNP P40806

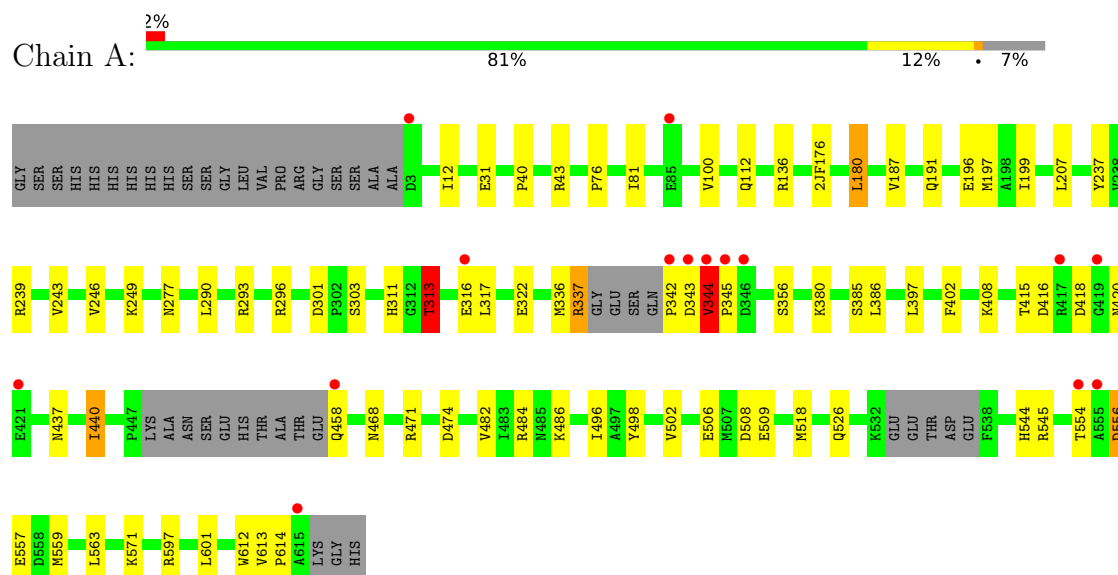
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	165	Total O 165 165	0	0
2	B	78	Total O 78 78	0	0

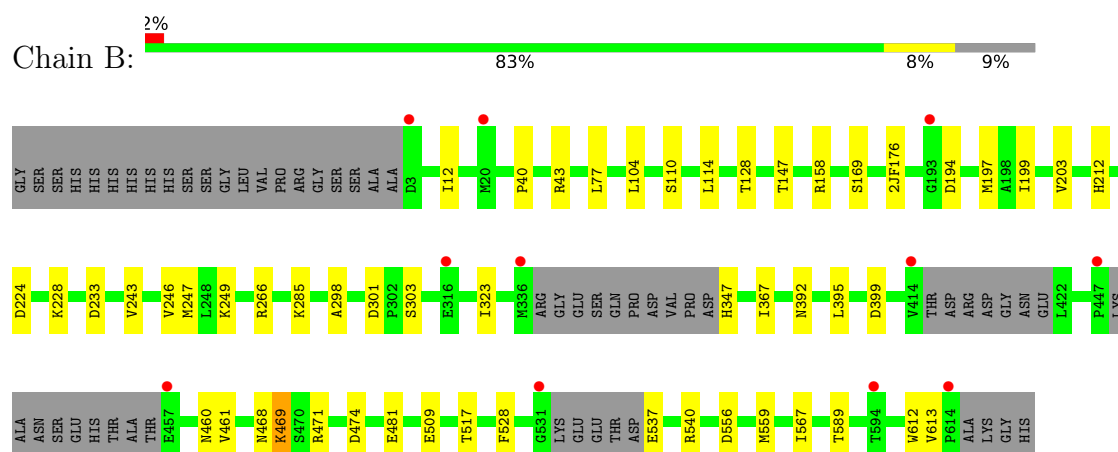
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: Polyketide synthase PksJ



• Molecule 1: Polyketide synthase PksJ



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	165.12Å 71.34Å 116.47Å 90.00° 95.10° 90.00°	Depositor
Resolution (Å)	43.50 – 2.30 43.50 – 2.30	Depositor EDS
% Data completeness (in resolution range)	93.1 (43.50-2.30) 93.1 (43.50-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.65 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.210 , 0.260 0.208 , 0.257	Depositor DCC
R_{free} test set	3039 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	30.3	Xtriage
Anisotropy	0.109	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 38.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9432	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 53.95 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 3.9153e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: 2JF

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	0.30	1/4723 (0.0%)	0.74	8/6389 (0.1%)
1	B	0.27	0/4621	0.70	0/6249
All	All	0.29	1/9344 (0.0%)	0.72	8/12638 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	554	THR	CA-CB	5.50	1.60	1.53

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	556	ASP	N-CA-C	8.68	123.09	110.42
1	A	458	GLN	CA-C-N	-7.59	112.66	120.85
1	A	458	GLN	C-N-CA	-7.59	112.66	120.85
1	A	556	ASP	CB-CA-C	-7.51	99.27	109.71
1	A	344	VAL	CA-C-N	5.45	125.35	119.85
1	A	344	VAL	C-N-CA	5.45	125.35	119.85
1	A	313	THR	N-CA-C	5.39	119.12	112.54
1	A	343	ASP	N-CA-C	5.21	119.20	113.21

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	4644	0	4556	42	0
1	B	4545	0	4461	26	0
2	A	165	0	0	5	1
2	B	78	0	0	3	0
All	All	9432	0	9017	66	1

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 4.

All (66) 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:12:ILE:HG22	1:B:246:VAL:HG12	1.72	0.72
1:A:31:GLU:O	2:A:848:HOH:O	2.10	0.69
1:A:197:MET:HG2	1:A:249:LYS:HG2	1.75	0.68
1:A:296:ARG:NH2	1:A:336:MET:SD	2.68	0.66
1:A:196:GLU:O	2:A:731:HOH:O	2.13	0.66
1:A:12:ILE:HG22	1:A:246:VAL:HG12	1.78	0.65
1:B:128:THR:OG1	2:B:731:HOH:O	2.14	0.65
1:A:506:GLU:OE2	2:A:769:HOH:O	2.15	0.60
1:A:559:MET:HE1	1:B:559:MET:HE1	1.88	0.56
1:B:301:ASP:OD2	1:B:303:SER:OG	2.24	0.55
1:A:556:ASP:O	1:A:559:MET:HB3	2.07	0.55
1:A:337:ARG:HH22	1:A:342:PRO:N	2.05	0.54
1:A:496:ILE:HD12	1:A:518:MET:HE1	1.88	0.54
1:B:471:ARG:NH1	1:B:474:ASP:OD2	2.41	0.54
1:B:347:HIS:N	2:B:747:HOH:O	2.42	0.53
1:A:416:ASP:HB2	1:A:420:ASN:H	1.75	0.52
1:A:544:HIS:CD2	1:A:545:ARG:HG3	2.45	0.52
1:B:460:ASN:OD1	1:B:461:VAL:N	2.39	0.52
1:A:496:ILE:HG12	1:A:601:LEU:HD21	1.92	0.51
1:B:469:LYS:HD3	1:B:540:ARG:HH12	1.76	0.50
1:B:567:ILE:HG21	1:B:589:THR:HB	1.94	0.50
1:B:323:ILE:HG13	1:B:395:LEU:HD22	1.94	0.49
1:A:316:GLU:HB3	1:A:317:LEU:HD12	1.94	0.49
1:B:197:MET:HG2	1:B:249:LYS:HG2	1.94	0.49
1:A:471:ARG:NH1	1:A:474:ASP:OD1	2.46	0.49
1:A:356:SER:HB2	1:A:386:LEU:HB2	1.94	0.49
1:A:313:THR:HG22	2:A:744:HOH:O	2.12	0.49
1:A:180:LEU:HG	1:A:440:ILE:HD13	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:468:ASN:HA	1:B:509:GLU:HG3	1.95	0.48
1:A:416:ASP:HB3	1:A:418:ASP:H	1.78	0.48
1:A:40:PRO:HG2	1:A:43:ARG:HG2	1.94	0.48
1:A:100:VAL:HG13	1:A:199:ILE:HD13	1.95	0.47
1:A:187:VAL:O	1:A:191:GLN:HG2	2.15	0.47
1:A:571:LYS:NZ	1:B:556:ASP:OD1	2.38	0.47
1:A:76:PRO:HB2	1:A:81:ILE:O	2.15	0.46
1:B:104:LEU:HD21	1:B:199:ILE:HD11	1.98	0.46
1:A:311:HIS:N	1:A:322:GLU:OE2	2.44	0.46
1:A:397:LEU:HD22	1:A:402:PHE:HB2	1.97	0.46
1:A:207:LEU:HD22	1:A:612:TRP:HH2	1.81	0.46
1:A:237:TYR:HE1	1:A:239:ARG:HG2	1.81	0.45
1:B:266:ARG:NH2	1:B:298:ALA:O	2.50	0.45
1:B:203:VAL:HG22	1:B:243:VAL:HG23	1.99	0.45
1:B:246:VAL:HG13	1:B:367:ILE:HD11	1.99	0.45
1:A:468:ASN:HA	1:A:509:GLU:HG3	1.98	0.44
1:B:469:LYS:HD3	1:B:540:ARG:NH1	2.33	0.43
1:B:612:TRP:CD1	1:B:613:VAL:HG22	2.53	0.43
1:A:559:MET:HE2	1:A:563:LEU:HG	1.99	0.43
1:B:147:THR:O	1:B:158:ARG:NH2	2.50	0.43
1:A:301:ASP:OD1	1:A:303:SER:OG	2.29	0.43
1:A:380:LYS:NZ	2:A:835:HOH:O	2.50	0.43
1:A:290:LEU:HD22	1:A:437:ASN:HB3	2.01	0.43
1:A:344:VAL:HA	1:A:345:PRO:HD3	1.75	0.43
1:B:392:ASN:HB3	1:B:395:LEU:HG	2.00	0.43
1:A:484:ARG:NH1	1:A:526:GLN:OE1	2.51	0.42
1:A:508:ASP:OD2	1:A:544:HIS:ND1	2.44	0.42
1:B:228:LYS:HE3	1:B:233:ASP:HB3	2.01	0.42
1:B:528:PHE:HE1	1:B:540:ARG:HD2	1.84	0.42
1:A:420:ASN:OD1	1:A:420:ASN:N	2.53	0.41
1:B:40:PRO:HG2	1:B:43:ARG:HG2	2.01	0.41
1:A:508:ASP:CG	1:A:544:HIS:HD1	2.25	0.41
1:A:556:ASP:HB3	1:A:559:MET:HB2	2.02	0.41
1:A:471:ARG:HA	1:A:471:ARG:HD3	1.81	0.41
1:A:613:VAL:HA	1:A:614:PRO:HD3	1.96	0.40
1:A:498:TYR:O	1:A:502:VAL:HG22	2.22	0.40
1:B:169:SER:HB2	2:B:735:HOH:O	2.21	0.40
1:B:528:PHE:CE1	1:B:540:ARG:HD2	2.55	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:784:HOH:O	2:A:784:HOH:O[2_655]	2.19	0.01

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	585/637 (92%)	564 (96%)	21 (4%)	0	100	100
1	B	570/637 (90%)	555 (97%)	15 (3%)	0	100	100
All	All	1155/1274 (91%)	1119 (97%)	36 (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	491/526 (93%)	474 (96%)	17 (4%)	32	48
1	B	480/526 (91%)	467 (97%)	13 (3%)	39	58
All	All	971/1052 (92%)	941 (97%)	30 (3%)	35	52

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	112	GLN
1	A	136	ARG
1	A	180	LEU

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Mol	Chain	Res	Type
1	A	243	VAL
1	A	277	ASN
1	A	293	ARG
1	A	313	THR
1	A	337	ARG
1	A	344	VAL
1	A	385	SER
1	A	408	LYS
1	A	415	THR
1	A	440	ILE
1	A	482	VAL
1	A	486	LYS
1	A	557	GLU
1	A	597	ARG
1	B	77	LEU
1	B	110	SER
1	B	114	LEU
1	B	194	ASP
1	B	212	HIS
1	B	224	ASP
1	B	247	MET
1	B	285	LYS
1	B	399	ASP
1	B	469	LYS
1	B	481	GLU
1	B	517	THR
1	B	537	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	92	GLN
1	A	204	ASN
1	A	437	ASN
1	A	501	GLN
1	B	92	GLN
1	B	112	GLN
1	B	164	ASN
1	B	204	ASN
1	B	478	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues 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$
1	2JF	A	176	1	18,19,19	1.18	2 (11%)	17,23,23	0.94	1 (5%)
1	2JF	B	176	1	18,19,19	1.18	2 (11%)	17,23,23	0.96	2 (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
1	2JF	A	176	1	-	2/20/22/22	-
1	2JF	B	176	1	-	1/20/22/22	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	176	2JF	OG-C8	4.17	1.45	1.33
1	B	176	2JF	OG-C8	4.16	1.45	1.33
1	B	176	2JF	C14-C13	-2.12	1.50	1.52
1	A	176	2JF	C14-C13	-2.09	1.50	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	176	2JF	OG-C8-C9	2.43	119.25	111.83
1	A	176	2JF	OG-C8-C9	2.43	119.23	111.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	176	2JF	OG-C8-O18	-2.06	118.48	123.63

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	176	2JF	C-CA-CB-OG
1	A	176	2JF	N12-C13-C14-O20
1	B	176	2JF	N12-C13-C14-O20

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	593/637 (93%)	-0.11	15 (2%) 58 60	12, 29, 64, 104	0
1	B	580/637 (91%)	0.27	11 (1%) 66 68	21, 41, 71, 99	0
All	All	1173/1274 (92%)	0.08	26 (2%) 62 64	12, 36, 68, 104	0

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	531	GLY	4.2
1	A	344	VAL	4.0
1	B	336	MET	3.9
1	A	555	ALA	3.6
1	A	342	PRO	3.6
1	A	3	ASP	3.1
1	B	594	THR	3.1
1	A	458	GLN	3.0
1	B	414	VAL	2.9
1	A	419	GLY	2.9
1	B	193	GLY	2.8
1	A	343	ASP	2.7
1	B	3	ASP	2.7
1	B	457	GLU	2.6
1	A	346	ASP	2.6
1	B	316	GLU	2.4
1	B	447	PRO	2.4
1	B	614	PRO	2.3
1	A	417	ARG	2.2
1	A	554	THR	2.2
1	B	20	MET	2.2
1	A	85	GLU	2.1
1	A	421	GLU	2.1
1	A	615	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	345	PRO	2.1
1	A	316	GLU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	2JF	B	176	20/20	0.94	0.11	19,41,67,73	0
1	2JF	A	176	20/20	0.95	0.08	13,25,38,42	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.