



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 13, 2024 – 09:00 AM EDT

PDB ID : 1PS1
Title : PENTALENENE SYNTHASE
Authors : Lesburg, C.A.; Christianson, D.W.
Deposited on : 1997-03-23
Resolution : 2.60 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	:	4.02b-467
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

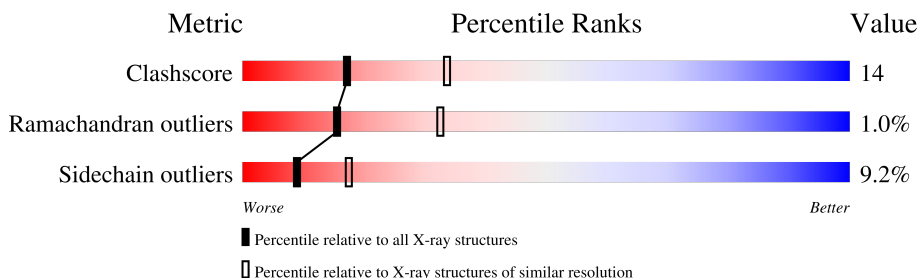
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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))
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	337	
1	B	337	

2 Entry composition [i](#)

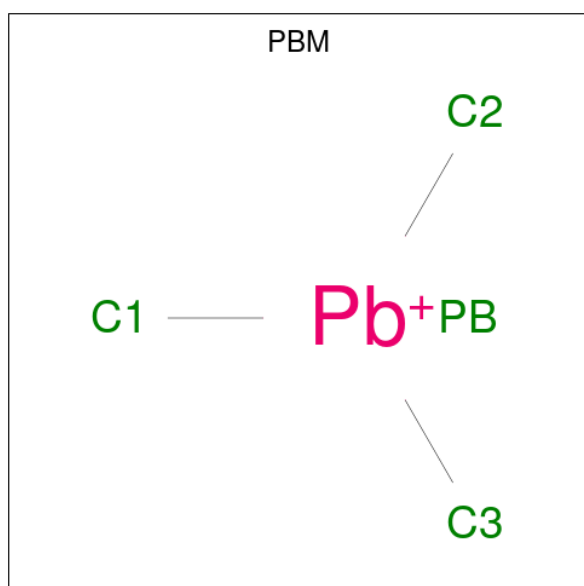
There are 3 unique types of molecules in this entry. The entry contains 4917 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 PENTALENENE SYNTHASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	304	Total	C	N	O	S	0	0	0
			2425	1509	449	456	11			
1	B	304	Total	C	N	O	S	0	0	0
			2425	1509	449	456	11			

- Molecule 2 is TRIMETHYL LEAD ION (three-letter code: PBM) (formula: C_3H_9Pb).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Pb	0	0
			1	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	32	Total	O	0	0
			32	32		

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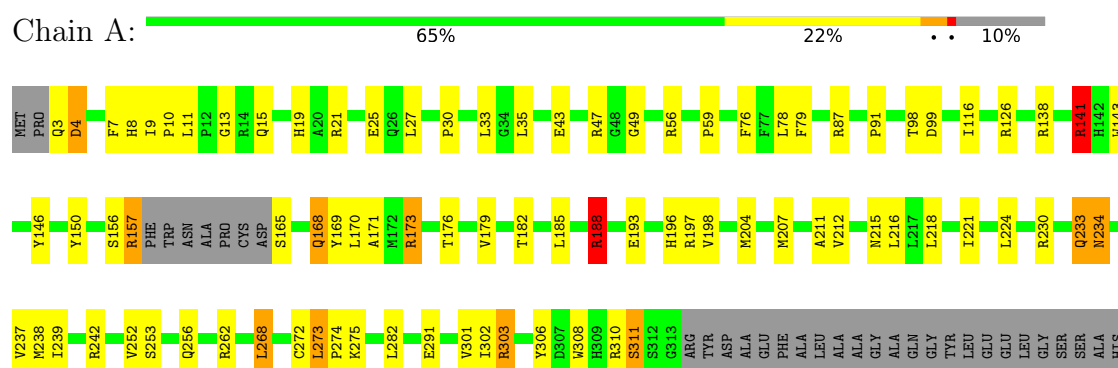
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	34	Total	O	0	0
			34	34		

3 Residue-property plots [i](#)

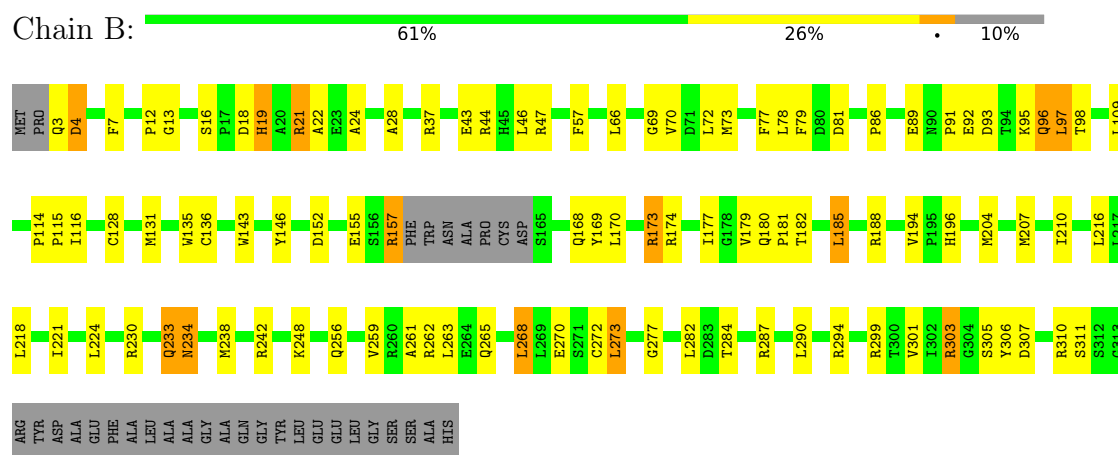
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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.

Note EDS was not executed.

• Molecule 1: PENTALENENE SYNTHASE



• Molecule 1: PENTALENENE SYNTHASE



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, α , β , γ	178.72Å 178.72Å 56.62Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 2.60	Depositor
% Data completeness (in resolution range)	82.6 (20.00-2.60)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.198 , 0.273	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4917	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PBM

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	0.85	2/2482 (0.1%)	0.92	2/3365 (0.1%)
1	B	0.73	0/2482	0.85	4/3365 (0.1%)
All	All	0.79	2/4964 (0.0%)	0.89	6/6730 (0.1%)

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
1	B	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	272	CYS	CB-SG	5.78	1.92	1.82
1	A	141	ARG	CG-CD	5.78	1.66	1.51

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	128	CYS	CA-CB-SG	-6.37	102.54	114.00
1	A	4	ASP	N-CA-C	6.32	128.06	111.00
1	B	4	ASP	N-CA-C	5.32	125.36	111.00
1	B	109	LEU	CA-CB-CG	5.31	127.52	115.30
1	A	188	ARG	CG-CD-NE	-5.27	100.73	111.80
1	B	19	HIS	N-CA-C	5.03	124.58	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	306	TYR	Sidechain

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	2425	0	2317	72	0
1	B	2425	0	2317	62	0
2	A	1	0	0	0	0
3	A	32	0	0	1	0
3	B	34	0	0	1	0
All	All	4917	0	4634	131	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 14.

All (131) 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:7:PHE:HE1	1:B:256:GLN:HA	1.37	0.90
1:B:157:ARG:NH1	1:B:157:ARG:HA	1.89	0.88
1:A:157:ARG:HA	1:A:157:ARG:NH1	1.93	0.84
1:A:7:PHE:HE1	1:A:256:GLN:HA	1.43	0.83
1:B:157:ARG:HH11	1:B:157:ARG:N	1.80	0.80
1:B:157:ARG:HH11	1:B:157:ARG:H	1.31	0.78
1:A:253:SER:HA	1:A:256:GLN:OE1	1.84	0.77
1:A:233:GLN:HB2	1:A:242:ARG:NH2	2.00	0.76
1:A:157:ARG:HA	1:A:157:ARG:HH11	1.52	0.73
1:B:152:ASP:O	1:B:155:GLU:HB3	1.89	0.71
1:B:262:ARG:HG2	1:B:262:ARG:HH11	1.57	0.69
1:A:15:GLN:OE1	1:A:19:HIS:CD2	2.46	0.68
1:A:156:SER:O	1:A:157:ARG:HB2	1.93	0.68
1:B:233:GLN:HB2	1:B:242:ARG:NH2	2.07	0.68
1:A:204:MET:HE3	1:A:207:MET:SD	2.35	0.66
1:A:234:ASN:H	1:A:234:ASN:HD22	1.42	0.66
1:A:157:ARG:HH11	1:A:157:ARG:CA	2.07	0.66
1:B:13:GLY:HA2	1:B:303:ARG:HD3	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:234:ASN:H	1:B:234:ASN:HD22	1.42	0.66
1:B:157:ARG:NH1	1:B:157:ARG:CA	2.60	0.64
1:B:204:MET:HE3	1:B:207:MET:HB2	1.81	0.63
1:A:7:PHE:HB2	1:A:306:TYR:CE1	2.34	0.63
1:B:66:LEU:O	1:B:70:VAL:HG23	2.01	0.61
1:A:8:HIS:O	1:A:9:ILE:HD13	2.01	0.60
1:A:138:ARG:HG3	1:A:141:ARG:NH1	2.17	0.60
1:B:157:ARG:HA	1:B:157:ARG:CZ	2.33	0.59
1:A:7:PHE:HB2	1:A:306:TYR:HE1	1.67	0.59
1:A:252:VAL:O	1:A:256:GLN:HG3	2.02	0.59
1:A:196:HIS:H	1:A:196:HIS:CD2	2.21	0.59
1:A:150:TYR:CD1	1:A:176:THR:HG22	2.38	0.59
1:B:7:PHE:CE1	1:B:256:GLN:HA	2.28	0.58
1:A:179:VAL:O	1:A:182:THR:HB	2.03	0.58
1:A:262:ARG:HH11	1:A:262:ARG:HG2	1.69	0.57
1:B:204:MET:CE	1:B:207:MET:HB2	2.34	0.57
1:B:270:GLU:O	1:B:273:LEU:HB2	2.04	0.57
1:A:126:ARG:O	1:A:188:ARG:NH1	2.38	0.56
1:A:197:ARG:NH2	1:A:282:LEU:HD23	2.20	0.56
1:B:169:TYR:CZ	1:B:173:ARG:HG3	2.41	0.56
1:B:157:ARG:HH11	1:B:157:ARG:CA	2.18	0.56
1:A:49:GLY:HA2	3:A:515:HOH:O	2.06	0.56
1:A:239:ILE:HG12	1:A:242:ARG:HH12	1.71	0.55
1:B:21:ARG:O	1:B:24:ALA:HB3	2.06	0.55
1:A:13:GLY:HA2	1:A:303:ARG:HD3	1.90	0.54
1:A:157:ARG:HH11	1:A:157:ARG:N	2.04	0.54
1:A:233:GLN:HB2	1:A:242:ARG:HH22	1.71	0.54
1:B:180:GLN:HB3	1:B:181:PRO:HD3	1.90	0.54
1:B:91:PRO:HG3	1:B:155:GLU:HA	1.90	0.54
1:B:18:ASP:OD1	1:B:21:ARG:HD3	2.08	0.53
1:A:169:TYR:CZ	1:A:173:ARG:HG3	2.43	0.53
1:A:43:GLU:O	1:A:47:ARG:HG2	2.08	0.53
1:A:15:GLN:HE21	1:A:56:ARG:CZ	2.22	0.53
1:A:291:GLU:OE1	1:A:291:GLU:HA	2.09	0.52
1:B:179:VAL:O	1:B:182:THR:HB	2.09	0.52
1:B:224:LEU:HD21	1:B:248:LYS:HE2	1.92	0.52
1:A:211:ALA:HA	1:A:302:ILE:CD1	2.39	0.51
1:B:294:ARG:O	1:B:299:ARG:HG3	2.10	0.50
1:B:73:MET:O	1:B:77:PHE:HD1	1.94	0.50
1:A:8:HIS:C	1:A:9:ILE:HD13	2.32	0.50
1:B:93:ASP:O	1:B:96:GLN:HB3	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:21:ARG:HH12	1:B:22:ALA:HB2	1.76	0.49
1:B:210:ILE:HG23	1:B:262:ARG:HB3	1.93	0.49
1:A:224:LEU:HD22	1:A:237:VAL:HG21	1.92	0.49
1:B:307:ASP:O	1:B:310:ARG:HB2	2.12	0.49
1:A:170:LEU:HD21	1:A:216:LEU:HD11	1.95	0.49
1:B:16:SER:O	1:B:19:HIS:HB3	2.13	0.49
1:A:87:ARG:O	1:A:87:ARG:HG2	2.13	0.49
1:A:179:VAL:HB	1:A:212:VAL:HG22	1.95	0.48
1:A:165:SER:HB3	1:A:168:GLN:HE21	1.77	0.48
1:B:57:PHE:CD1	1:B:301:VAL:HA	2.47	0.48
1:B:284:THR:N	1:B:287:ARG:HH21	2.11	0.48
1:B:69:GLY:O	1:B:73:MET:HG2	2.14	0.48
1:B:95:LYS:HA	1:B:98:THR:HB	1.95	0.48
1:A:169:TYR:CE1	1:A:173:ARG:HG3	2.49	0.47
1:A:7:PHE:CE1	1:A:256:GLN:HA	2.35	0.47
1:B:277:GLY:HA2	1:B:282:LEU:HD12	1.96	0.47
1:B:177:ILE:HG23	1:B:179:VAL:H	1.78	0.47
1:A:239:ILE:HG12	1:A:242:ARG:NH1	2.30	0.47
1:A:10:PRO:O	1:A:11:LEU:HD23	2.14	0.47
1:A:268:LEU:HD22	1:B:272:CYS:HB3	1.96	0.47
1:A:98:THR:HG22	1:A:99:ASP:N	2.30	0.46
1:B:143:TRP:O	1:B:146:TYR:HB3	2.16	0.46
1:A:211:ALA:HA	1:A:302:ILE:HD11	1.96	0.46
1:A:138:ARG:HG3	1:A:141:ARG:HH11	1.79	0.46
1:A:98:THR:HG22	1:A:99:ASP:OD1	2.16	0.46
1:B:185:LEU:HD23	1:B:185:LEU:HA	1.79	0.46
1:B:194:VAL:HG23	1:B:290:LEU:HA	1.98	0.45
1:A:78:LEU:HD23	1:A:78:LEU:HA	1.72	0.45
1:A:33:LEU:CB	1:A:35:LEU:CD1	2.94	0.45
1:B:78:LEU:O	1:B:81:ASP:HB2	2.17	0.45
1:B:170:LEU:O	1:B:174:ARG:HG3	2.17	0.45
1:B:259:VAL:O	1:B:263:LEU:HD23	2.17	0.45
1:A:56:ARG:O	1:A:59:PRO:HD3	2.17	0.45
1:A:56:ARG:C	1:A:59:PRO:HD3	2.36	0.44
1:A:170:LEU:CD2	1:A:216:LEU:HD11	2.47	0.44
1:B:157:ARG:N	1:B:157:ARG:HD2	2.32	0.44
1:A:268:LEU:HD22	1:B:272:CYS:SG	2.57	0.44
1:A:157:ARG:HA	1:A:157:ARG:CZ	2.45	0.44
1:B:261:ALA:O	1:B:265:GLN:HG3	2.18	0.44
1:B:28:ALA:HB3	3:B:350:HOH:O	2.17	0.44
1:B:234:ASN:HD22	1:B:234:ASN:N	2.14	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:196:HIS:H	1:B:196:HIS:CD2	2.36	0.44
1:A:143:TRP:O	1:A:146:TYR:HB3	2.17	0.44
1:B:79:PHE:HB2	1:B:116:ILE:HD11	1.99	0.43
1:B:97:LEU:HD12	1:B:97:LEU:O	2.18	0.43
1:B:173:ARG:HB3	1:B:216:LEU:HD22	2.01	0.43
1:A:168:GLN:O	1:A:171:ALA:HB3	2.18	0.43
1:A:33:LEU:HB2	1:A:35:LEU:CD1	2.49	0.43
1:B:157:ARG:NH1	1:B:157:ARG:H	2.08	0.43
1:A:204:MET:CE	1:A:207:MET:HB2	2.48	0.42
1:B:262:ARG:HG2	1:B:262:ARG:NH1	2.30	0.42
1:A:173:ARG:HB3	1:A:216:LEU:HD22	2.01	0.42
1:B:46:LEU:HD23	1:B:46:LEU:HA	1.75	0.42
1:A:27:LEU:O	1:A:30:PRO:HD2	2.19	0.42
1:A:198:VAL:HG21	1:A:282:LEU:HD11	2.00	0.42
1:A:13:GLY:CA	1:A:303:ARG:HD3	2.49	0.42
1:A:310:ARG:O	1:A:311:SER:CB	2.68	0.42
1:A:79:PHE:HE1	1:A:150:TYR:CE2	2.37	0.42
1:A:33:LEU:HB3	1:A:35:LEU:CD1	2.49	0.42
1:A:196:HIS:CD2	1:A:196:HIS:N	2.86	0.42
1:B:86:PRO:HA	1:B:89:GLU:OE1	2.19	0.42
1:A:79:PHE:CE1	1:A:150:TYR:CE2	3.08	0.41
1:A:275:LYS:HB3	1:B:268:LEU:HD11	2.02	0.41
1:B:114:PRO:HA	1:B:115:PRO:HD3	1.94	0.41
1:B:72:LEU:HD22	1:B:185:LEU:HD12	2.02	0.41
1:A:211:ALA:HA	1:A:302:ILE:HD13	2.03	0.41
1:B:131:MET:HG3	1:B:135:TRP:CZ3	2.55	0.41
1:A:79:PHE:HB2	1:A:116:ILE:HD11	2.03	0.40
1:A:308:TRP:C	1:A:310:ARG:H	2.23	0.40
1:A:273:LEU:N	1:A:274:PRO:CD	2.84	0.40
1:A:170:LEU:HD23	1:A:170:LEU:HA	1.70	0.40
1:B:43:GLU:O	1:B:46:LEU:HB2	2.22	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	300/337 (89%)	279 (93%)	19 (6%)	2 (1%)	22	43
1	B	300/337 (89%)	281 (94%)	15 (5%)	4 (1%)	12	24
All	All	600/674 (89%)	560 (93%)	34 (6%)	6 (1%)	15	32

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	311	SER
1	A	4	ASP
1	B	311	SER
1	B	4	ASP
1	B	12	PRO
1	B	47	ARG

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	250/273 (92%)	227 (91%)	23 (9%)	9	17
1	B	250/273 (92%)	227 (91%)	23 (9%)	9	17
All	All	500/546 (92%)	454 (91%)	46 (9%)	9	17

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	GLN
1	A	21	ARG
1	A	25	GLU
1	A	76	PHE
1	A	91	PRO
1	A	141	ARG
1	A	157	ARG

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Mol	Chain	Res	Type
1	A	168	GLN
1	A	173	ARG
1	A	185	LEU
1	A	188	ARG
1	A	193	GLU
1	A	215	ASN
1	A	218	LEU
1	A	221	ILE
1	A	230	ARG
1	A	233	GLN
1	A	234	ASN
1	A	238	MET
1	A	268	LEU
1	A	273	LEU
1	A	301	VAL
1	A	303	ARG
1	B	3	GLN
1	B	21	ARG
1	B	37	ARG
1	B	44	ARG
1	B	92	GLU
1	B	96	GLN
1	B	97	LEU
1	B	136	CYS
1	B	157	ARG
1	B	168	GLN
1	B	173	ARG
1	B	185	LEU
1	B	188	ARG
1	B	218	LEU
1	B	221	ILE
1	B	230	ARG
1	B	233	GLN
1	B	234	ASN
1	B	238	MET
1	B	268	LEU
1	B	273	LEU
1	B	303	ARG
1	B	305	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	3	GLN
1	A	15	GLN
1	A	19	HIS
1	A	26	GLN
1	A	96	GLN
1	A	100	GLN
1	A	168	GLN
1	A	196	HIS
1	A	233	GLN
1	A	234	ASN
1	A	281	GLN
1	B	3	GLN
1	B	26	GLN
1	B	96	GLN
1	B	100	GLN
1	B	196	HIS
1	B	219	ASN
1	B	233	GLN
1	B	234	ASN
1	B	265	GLN
1	B	281	GLN

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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 1 ligands modelled in this entry, 1 is modelled with single atom - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.