



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 03:50 PM UTC

PDB ID : 1B6R / pdb_00001b6r
Title : N5-CARBOXYAMINOIMIDAZOLE RIBONUCLEOTIDE SYNTHETASE
FROM E. COLI
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Deposited on : 1999-01-17
Resolution : 2.10 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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

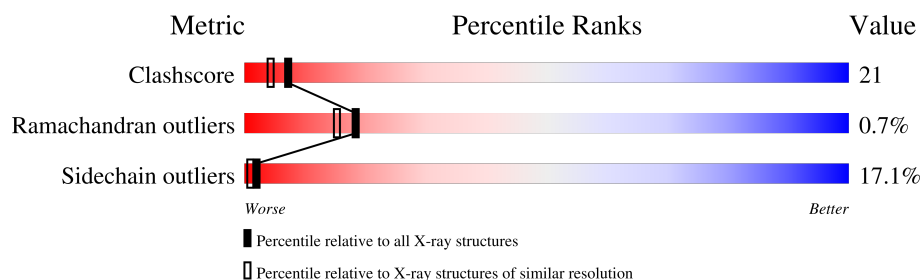
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)

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	355	 56% 30% 10% . .

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 2834 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.

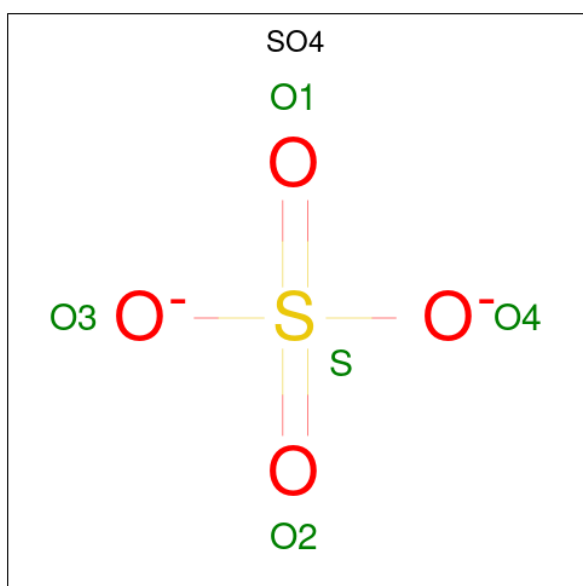
- Molecule 1 is a protein called PROTEIN (N5-CARBOXYAMINOIMIDAZOLE RIBONUCLEOTIDE SYNTHETASE).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	349	2737	1742	486	498	11	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	61	GLN	GLU	conflict	UNP P09029
A	205	ARG	GLN	conflict	UNP P09029

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
2	A	1	5	4	1	0	0

- Molecule 3 is water.

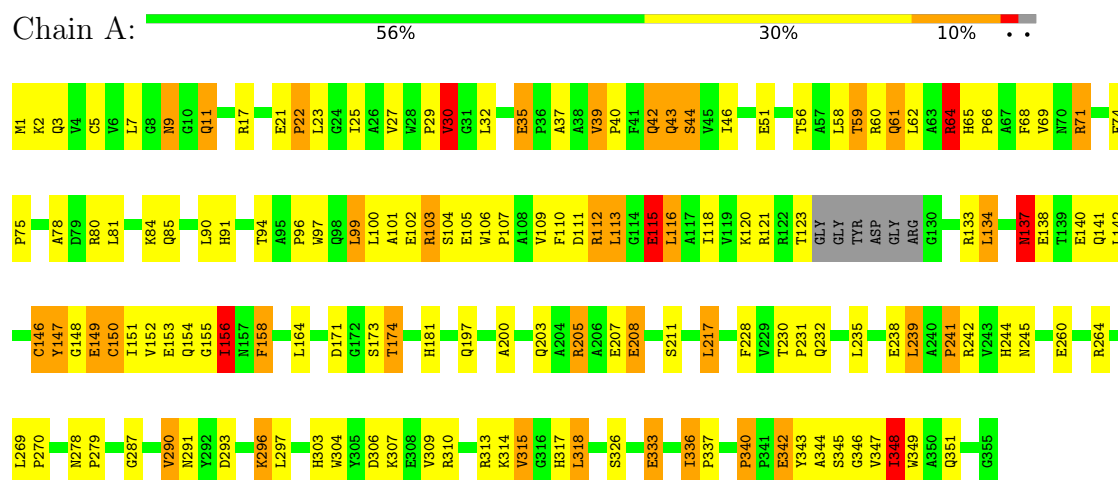
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	92	Total 92	O 92	0	0

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. 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: PROTEIN (N5-CARBOXYAMINOIMIDAZOLE RIBONUCLEOTIDE SYNTHETASE)



4 Data and refinement statistics

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

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	93.40 Å 95.20 Å 120.60 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.10	Depositor
% Data completeness (in resolution range)	95.6 (30.00-2.10)	Depositor
R_{merge}	0.05	Depositor
R_{sym}	0.05	Depositor
Refinement program	TNT 5D	Depositor
R, R_{free}	0.197 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2834	wwPDB-VP
Average B, all atoms (Å ²)	44.0	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: SO4

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	1.14	3/2804 (0.1%)	1.69	41/3822 (1.1%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	260	GLU	CD-OE2	6.62	1.38	1.25
1	A	115	GLU	CD-OE2	5.59	1.35	1.25
1	A	208	GLU	CD-OE1	5.12	1.35	1.25

All (41) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	205	ARG	CD-NE-CZ	-10.42	109.82	124.40
1	A	205	ARG	NE-CZ-NH2	9.97	128.18	119.20
1	A	245	ASN	CA-CB-CG	9.68	122.28	112.60
1	A	205	ARG	NE-CZ-NH1	-8.29	113.21	121.50
1	A	336	ILE	N-CA-CB	7.90	115.81	110.52
1	A	340	PRO	N-CA-CB	7.83	107.57	103.19
1	A	260	GLU	CG-CD-OE2	-7.62	100.87	118.40
1	A	264	ARG	NE-CZ-NH1	7.45	128.95	121.50
1	A	264	ARG	CD-NE-CZ	6.19	133.06	124.40
1	A	9	ASN	N-CA-CB	-6.12	101.14	111.17
1	A	264	ARG	NE-CZ-NH2	-6.08	113.73	119.20
1	A	340	PRO	CA-C-N	6.07	126.24	119.32
1	A	340	PRO	C-N-CA	6.07	126.24	119.32
1	A	156	ILE	N-CA-C	6.04	117.28	108.58
1	A	318	LEU	CB-CA-C	-5.96	98.81	109.71
1	A	239	LEU	CB-CA-C	-5.95	97.60	109.33
1	A	158	PHE	CA-CB-CG	-5.85	107.95	113.80
1	A	296	LYS	N-CA-CB	5.85	120.24	110.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	270	PRO	N-CA-CB	5.84	108.76	103.33
1	A	111	ASP	CA-CB-CG	5.64	118.24	112.60
1	A	137	ASN	N-CA-CB	-5.61	101.65	110.46
1	A	241	PRO	N-CA-CB	-5.61	98.08	102.28
1	A	29	PRO	N-CA-CB	5.60	108.29	103.36
1	A	336	ILE	CA-C-O	5.53	122.92	118.71
1	A	164	LEU	N-CA-CB	5.53	119.27	110.65
1	A	348	ILE	CB-CA-C	-5.51	104.62	112.22
1	A	297	LEU	CB-CA-C	5.50	115.62	110.17
1	A	315	VAL	N-CA-CB	-5.47	106.19	112.21
1	A	244	HIS	N-CA-CB	-5.45	101.45	111.37
1	A	174	THR	N-CA-CB	-5.43	101.69	110.81
1	A	150	CYS	CB-CA-C	5.33	120.51	109.38
1	A	91	HIS	CA-CB-CG	-5.29	108.51	113.80
1	A	69	VAL	N-CA-C	5.26	115.78	108.84
1	A	64	ARG	CB-CA-C	-5.25	99.74	109.29
1	A	181	HIS	CA-CB-CG	-5.11	108.69	113.80
1	A	260	GLU	CB-CA-C	-5.07	102.92	110.88
1	A	200	ALA	N-CA-C	5.06	116.80	111.28
1	A	5	CYS	N-CA-CB	5.05	118.83	110.69
1	A	22	PRO	N-CA-CB	5.04	108.15	103.41
1	A	30	VAL	N-CA-CB	-5.01	102.66	111.39
1	A	340	PRO	O-C-N	5.00	123.61	121.31

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	2737	0	2723	113	0
2	A	5	0	0	1	0
3	A	92	0	0	2	0
All	All	2834	0	2723	113	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 21.

All (113) 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:A:278:ASN:HB3	1:A:279:PRO:HD2	1.60	0.83
1:A:230:THR:HB	1:A:231:PRO:HD2	1.66	0.77
1:A:138:GLU:O	1:A:141:GLN:HB2	1.87	0.75
1:A:74:PHE:HB2	1:A:75:PRO:HD3	1.67	0.74
1:A:112:ARG:HG2	1:A:113:LEU:HD13	1.69	0.73
1:A:11:GLN:HE21	1:A:11:GLN:H	1.38	0.71
1:A:121:ARG:HG2	1:A:150:CYS:SG	2.30	0.71
1:A:103:ARG:HA	1:A:106:TRP:CD1	2.26	0.69
1:A:203:GLN:O	1:A:207:GLU:HG3	1.94	0.68
1:A:137:ASN:OD1	1:A:137:ASN:N	2.22	0.67
1:A:61:GLN:O	1:A:64:ARG:HB2	1.95	0.66
1:A:84:LYS:HE2	1:A:153:GLU:OE1	1.95	0.66
1:A:346:GLY:HA3	3:A:456:HOH:O	1.96	0.66
1:A:84:LYS:NZ	1:A:94:THR:OG1	2.28	0.66
1:A:105:GLU:C	1:A:107:PRO:HD2	2.21	0.66
1:A:100:LEU:O	1:A:148:GLY:N	2.29	0.65
1:A:242:ARG:NH2	2:A:500:SO4:O3	2.25	0.65
1:A:46:ILE:HD12	1:A:65:HIS:CG	2.32	0.65
1:A:142:LEU:HD11	1:A:146:CYS:SG	2.37	0.65
1:A:65:HIS:O	1:A:71:ARG:NH1	2.30	0.65
1:A:171:ASP:OD1	1:A:173:SER:HB2	1.97	0.64
1:A:336:ILE:N	1:A:337:PRO:HD2	2.15	0.62
1:A:97:TRP:HB3	1:A:153:GLU:HG2	1.80	0.62
1:A:109:VAL:O	1:A:113:LEU:HB2	2.00	0.60
1:A:103:ARG:HA	1:A:106:TRP:HD1	1.67	0.60
1:A:3:GLN:HB3	1:A:44:SER:HB3	1.86	0.58
1:A:146:CYS:SG	1:A:150:CYS:HB2	2.43	0.58
1:A:146:CYS:SG	1:A:150:CYS:CB	2.93	0.57
1:A:340:PRO:HB2	1:A:342:GLU:OE2	2.06	0.55
1:A:205:ARG:HH11	1:A:205:ARG:CG	2.15	0.55
1:A:278:ASN:HB3	1:A:279:PRO:CD	2.35	0.55
1:A:205:ARG:HH11	1:A:205:ARG:HG2	1.71	0.55
1:A:104:SER:O	1:A:107:PRO:HD2	2.07	0.55
1:A:30:VAL:CG2	1:A:39:VAL:HG11	2.38	0.55
1:A:74:PHE:N	1:A:75:PRO:HD2	2.22	0.54
1:A:290:VAL:HG22	1:A:304:TRP:CZ2	2.44	0.53
1:A:21:GLU:HB3	1:A:22:PRO:HD3	1.90	0.52
1:A:116:LEU:HD23	1:A:133:ARG:HB3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:121:ARG:HA	1:A:150:CYS:SG	2.50	0.52
1:A:30:VAL:HG23	1:A:39:VAL:HG11	1.93	0.51
1:A:116:LEU:CD2	1:A:133:ARG:HB3	2.40	0.51
1:A:102:GLU:HG3	1:A:104:SER:H	1.74	0.51
1:A:99:LEU:HD12	1:A:150:CYS:O	2.11	0.51
1:A:344:ALA:O	1:A:348:ILE:HD12	2.11	0.50
1:A:106:TRP:N	1:A:107:PRO:HD2	2.27	0.50
1:A:333:GLU:HA	1:A:336:ILE:HD12	1.93	0.50
1:A:113:LEU:HD12	1:A:154:GLN:HB2	1.92	0.50
1:A:158:PHE:HB3	1:A:228:PHE:HB3	1.93	0.50
1:A:106:TRP:O	1:A:110:PHE:HD2	1.94	0.49
1:A:313:ARG:O	1:A:315:VAL:HG13	2.11	0.49
1:A:147:TYR:N	1:A:147:TYR:CD1	2.81	0.49
1:A:7:LEU:HD11	1:A:32:LEU:HD23	1.95	0.49
1:A:205:ARG:HG2	1:A:205:ARG:NH1	2.28	0.48
1:A:42:GLN:H	1:A:42:GLN:HG3	1.30	0.48
1:A:118:ILE:HD12	1:A:155:GLY:HA2	1.96	0.48
1:A:118:ILE:CD1	1:A:155:GLY:HA2	2.44	0.47
1:A:134:LEU:HD13	1:A:134:LEU:N	2.29	0.47
1:A:11:GLN:H	1:A:11:GLN:NE2	2.09	0.47
1:A:96:PRO:HG2	1:A:154:GLN:OE1	2.15	0.47
1:A:346:GLY:O	1:A:349:TRP:HB3	2.15	0.47
1:A:347:VAL:O	1:A:351:GLN:HB2	2.15	0.47
1:A:102:GLU:O	1:A:105:GLU:HB2	2.15	0.46
1:A:68:PHE:CD1	1:A:68:PHE:C	2.94	0.46
1:A:242:ARG:HB3	3:A:483:HOH:O	2.15	0.46
1:A:46:ILE:HD12	1:A:65:HIS:CD2	2.50	0.46
1:A:205:ARG:HE	1:A:208:GLU:CD	2.23	0.46
1:A:97:TRP:CD1	1:A:97:TRP:N	2.83	0.46
1:A:149:GLU:C	1:A:150:CYS:SG	2.99	0.46
1:A:309:VAL:O	1:A:310:ARG:HG3	2.15	0.46
1:A:74:PHE:O	1:A:78:ALA:N	2.45	0.46
1:A:154:GLN:CG	1:A:155:GLY:N	2.78	0.46
1:A:17:ARG:HA	1:A:27:VAL:HB	1.97	0.46
1:A:74:PHE:HB2	1:A:75:PRO:CD	2.42	0.46
1:A:74:PHE:CB	1:A:75:PRO:HD3	2.43	0.46
1:A:56:THR:O	1:A:60:ARG:HB2	2.15	0.45
1:A:101:ALA:HB3	1:A:105:GLU:OE2	2.16	0.45
1:A:147:TYR:H	1:A:147:TYR:HD1	1.65	0.45
1:A:46:ILE:CD1	1:A:65:HIS:CD2	3.00	0.45
1:A:133:ARG:C	1:A:134:LEU:HD13	2.42	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:291:ASN:C	1:A:293:ASP:N	2.74	0.45
1:A:115:GLU:H	1:A:115:GLU:HG3	1.51	0.44
1:A:68:PHE:C	1:A:68:PHE:HD1	2.25	0.44
1:A:290:VAL:HG22	1:A:304:TRP:CH2	2.53	0.44
1:A:291:ASN:C	1:A:293:ASP:H	2.24	0.44
1:A:134:LEU:N	1:A:134:LEU:CD1	2.79	0.44
1:A:291:ASN:OD1	1:A:293:ASP:HB2	2.17	0.44
1:A:149:GLU:C	1:A:150:CYS:HG	2.25	0.44
1:A:113:LEU:HD12	1:A:113:LEU:HA	1.86	0.43
1:A:151:ILE:CG2	1:A:152:VAL:N	2.80	0.43
1:A:287:GLY:HA2	1:A:310:ARG:O	2.18	0.43
1:A:156:ILE:HA	1:A:156:ILE:HD13	1.59	0.43
1:A:230:THR:HB	1:A:231:PRO:CD	2.42	0.43
1:A:74:PHE:N	1:A:75:PRO:CD	2.80	0.43
1:A:106:TRP:N	1:A:107:PRO:CD	2.82	0.43
1:A:25:ILE:HD13	1:A:25:ILE:HG21	1.80	0.43
1:A:106:TRP:HB2	1:A:107:PRO:HD3	2.00	0.43
1:A:40:PRO:HB3	1:A:43:GLN:NE2	2.33	0.43
1:A:278:ASN:CB	1:A:279:PRO:CD	2.97	0.42
1:A:336:ILE:HB	1:A:337:PRO:HD3	2.00	0.42
1:A:217:LEU:HA	1:A:217:LEU:HD12	1.75	0.42
1:A:120:LYS:HE3	1:A:153:GLU:OE2	2.20	0.42
1:A:65:HIS:HA	1:A:66:PRO:HD2	1.89	0.42
1:A:81:LEU:O	1:A:85:GLN:HG3	2.19	0.42
1:A:241:PRO:O	1:A:242:ARG:HB3	2.19	0.42
1:A:58:LEU:HB3	1:A:59:THR:H	1.69	0.42
1:A:84:LYS:HA	1:A:84:LYS:HD2	1.84	0.41
1:A:307:LYS:NZ	1:A:314:LYS:O	2.53	0.41
1:A:35:GLU:C	1:A:37:ALA:H	2.28	0.41
1:A:81:LEU:HA	1:A:151:ILE:HD11	2.02	0.41
1:A:7:LEU:HD11	1:A:32:LEU:CD2	2.49	0.41
1:A:74:PHE:CB	1:A:75:PRO:CD	2.98	0.41
1:A:303:HIS:HB2	1:A:317:HIS:CE1	2.56	0.41
1:A:343:TYR:O	1:A:347:VAL:HG23	2.21	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	135/355 (38%)	132 (98%)	2 (2%)	1 (1%)	18	15

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	147	TYR

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	292/296 (99%)	242 (83%)	50 (17%)	2	1

All (50) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	2	LYS
1	A	9	ASN
1	A	11	GLN
1	A	23	LEU
1	A	30	VAL
1	A	35	GLU
1	A	39	VAL
1	A	42	GLN
1	A	43	GLN

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Mol	Chain	Res	Type
1	A	44	SER
1	A	51	GLU
1	A	59	THR
1	A	61	GLN
1	A	62	LEU
1	A	64	ARG
1	A	71	ARG
1	A	80	ARG
1	A	90	LEU
1	A	99	LEU
1	A	103	ARG
1	A	112	ARG
1	A	113	LEU
1	A	115	GLU
1	A	116	LEU
1	A	123	THR
1	A	134	LEU
1	A	137	ASN
1	A	140	GLU
1	A	146	CYS
1	A	149	GLU
1	A	156	ILE
1	A	174	THR
1	A	197	GLN
1	A	211	SER
1	A	217	LEU
1	A	232	GLN
1	A	235	LEU
1	A	238	GLU
1	A	239	LEU
1	A	269	LEU
1	A	290	VAL
1	A	296	LYS
1	A	306	ASP
1	A	318	LEU
1	A	326	SER
1	A	333	GLU
1	A	342	GLU
1	A	345	SER
1	A	348	ILE

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	3	GLN
1	A	9	ASN
1	A	11	GLN
1	A	42	GLN
1	A	43	GLN
1	A	85	GLN
1	A	141	GLN
1	A	185	GLN
1	A	278	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is 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	$\# Z > 2$
2	SO4	A	500	-	4,4,4	0.28	0	6,6,6	0.67	0

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	500	SO4	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

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.